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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : A01N 37/18, 43/04, C12Q 1/00, 1/02, 1/68, C12N 5/00, 5/06, 15/00, 15/06, 15/09, 15/10, 15/11, G01N 33/53		A2	(11) International Publication Number: WO 98/54963 (43) International Publication Date: 10 December 1998 (10.12.98)
(21) International Application Number: PCT/US98/11422 (22) International Filing Date: 4 June 1998 (04.06.98) (30) Priority Data: 60/048,915 6 June 1997 (06.06.97) US 60/048,882 6 June 1997 (06.06.97) US (Continued on the following page) (71) Applicant (for all designated States except US): HUMAN GENOME SCIENCES, INC. [US/US]; 9410 Key West Avenue, Rockville, MD 20850 (US). (72) Inventors; and (75) Inventors/Applicants (for US only): YOUNG, Paul [US/US]; 122 Beckwith Street, Gaithersburg, MD 20878 (US). GREENE, John, M. [US/US]; 872 Diamond Drive, Gaithersburg, MD 20878 (US). FERRIE, Ann, M. [US/US]; 13203 L Astoria Hill Court, Germantown, MD 20874 (US). RUBEN, Steven, M. [US/US]; 18528 Heritage Hills Drive, Olney, MD 20832 (US). ROSEN, Craig, A. [US/US]; 22400 Rolling Hill Road, Laytonsville, MD 20882 (US). HU, Jing-Shan [CN/US]; 1247 Lakeside Drive #3034, Sunnyvale, CA 94086 (US). OLSEN, Henrik, S. [DK/US]; 182 Kendrick Place #24, Gaithersburg, MD 20878 (US). EBNER, Reinhard [DE/US]; 9906 Shelburne Terrace #316,		<p>Gaithersburg, MD 20878 (US). BREWER, Laurie, A. [US/US]; 14920 Mt. Nebo Road, Poolesville, MD 20837 (US). MOORE, Paul, A. [GB/US]; Apartment 104, 1908 Holly Ridge Drive, McLean, VA 22102 (US). SHI, Yanggu [CN/US]; 437 West Side Drive, Gaithersburg, MD 20878 (US). FLORENCE, Charles [US/US]; (US). FLORENCE, Kimberly [US/US]; 12805 Atlantic Avenue, Rockville, MD 20851 (US). LAFLEUR, David, W. [US/US]; 1615 Q Street, N.W. #807, Washington, DC 20009 (US). NI, Jian [CN/US]; 5502 Manorfield Road, Rockville, MD 20853 (US). FAN, Ping [CN/US]; Apartment 302, 335 West Side Drive, Gaithersburg, MD 20878 (US). WEI, Ying-Fei [CN/US]; 13524 Straw Bale Lane, Darnestown, MD 20878 (US). FISCHER, Carrie, L. [US/US]; 5810 Hall Street, Burke, VA 22015 (US). SOPPET, Daniel, R. [US/US]; 15050 Stillfield Place, Centreville, VA 22020 (US). LI, Yi [CN/US]; 1247 Lakeside Drive #3034, Sunnyvale, CA 94086 (US). ZENG, Zhizhen [CN/US]; 13950 Saddleview Drive, Gaithersburg, MD 20878 (US). KYAW, Hla [MM/US]; 520 Sugarbush Circle, Frederick, MD 21703 (US). YU, Guo-Liang [CN/US]; 13524 Straw Bale Lane, Darnestown, MD 20878 (US). FENG, Ping [CN/US]; 4 Relda Court, Gaithersburg, MD 20878 (US). DILLON, Patrick, J. [US/US]; 1055 Snipe Court, Carlsbad, CA 92009 (US). ENDRESS, Gregory, A. [US/US]; 9729 Clagett Farm Drive, Potomac, MD 20854 (US). CARTER, Kenneth, C. [US/US]; 11601 Brandy Hall Lane, North Potomac, MD 20878 (US).</p> <p>(74) Agents: HOOVER, Kenley, K. et al.; Human Genome Sciences, Inc., 9410 Key West Avenue, Rockville, MD 10850 (US).</p> <p>(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).</p> <p>Published With declaration under Article 17(2)(a); without abstract; title not checked by the International Searching Authority.</p>	
(54) Title: 207 HUMAN SECRETED PROTEINS			

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207 Human Secreted Proteins

Field of the Invention

This invention relates to newly identified polynucleotides and the polypeptides encoded by these polynucleotides, uses of such polynucleotides and polypeptides, and their production.

Background of the Invention

Unlike bacterium, which exist as a single compartment surrounded by a membrane, human cells and other eucaryotes are subdivided by membranes into many functionally distinct compartments. Each membrane-bounded compartment, or organelle, contains different proteins essential for the function of the organelle. The cell uses "sorting signals," which are amino acid motifs located within the protein, to target proteins to particular cellular organelles.

One type of sorting signal, called a signal sequence, a signal peptide, or a leader sequence, directs a class of proteins to an organelle called the endoplasmic reticulum (ER). The ER separates the membrane-bounded proteins from all other types of proteins. Once localized to the ER, both groups of proteins can be further directed to another organelle called the Golgi apparatus. Here, the Golgi distributes the proteins to vesicles, including secretory vesicles, the cell membrane, lysosomes, and the other organelles.

Proteins targeted to the ER by a signal sequence can be released into the extracellular space as a secreted protein. For example, vesicles containing secreted proteins can fuse with the cell membrane and release their contents into the extracellular space - a process called exocytosis. Exocytosis can occur constitutively or after receipt of a triggering signal. In the latter case, the proteins are stored in secretory vesicles (or secretory granules) until exocytosis is triggered. Similarly, proteins residing on the cell membrane can also be secreted into the extracellular space by proteolytic cleavage of a "linker" holding the protein to the membrane.

Despite the great progress made in recent years, only a small number of genes encoding human secreted proteins have been identified. These secreted proteins include the commercially valuable human insulin, interferon, Factor VIII, human growth hormone, tissue plasminogen activator, and erythropoietin. Thus, in light of the pervasive role of secreted proteins in human physiology, a need exists for identifying and characterizing novel human secreted proteins and the genes that encode them. This knowledge will allow one to detect, to treat, and to prevent medical disorders by using secreted proteins or the genes that encode them.

Summary of the Invention

The present invention relates to novel polynucleotides and the encoded polypeptides. Moreover, the present invention relates to vectors, host cells, antibodies, and recombinant methods for producing the polypeptides and polynucleotides. Also provided are diagnostic methods for detecting disorders related to the polypeptides, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying binding partners of the polypeptides.

Detailed Description

Definitions

The following definitions are provided to facilitate understanding of certain terms used throughout this specification.

In the present invention, "isolated" refers to material removed from its original environment (e.g., the natural environment if it is naturally occurring), and thus is altered "by the hand of man" from its natural state. For example, an isolated polynucleotide could be part of a vector or a composition of matter, or could be contained within a cell, and still be "isolated" because that vector, composition of matter, or particular cell is not the original environment of the polynucleotide.

In the present invention, a "secreted" protein refers to those proteins capable of being directed to the ER, secretory vesicles, or the extracellular space as a result of a signal sequence, as well as those proteins released into the extracellular space without necessarily containing a signal sequence. If the secreted protein is released into the extracellular space, the secreted protein can undergo extracellular processing to produce a "mature" protein. Release into the extracellular space can occur by many mechanisms, including exocytosis and proteolytic cleavage.

As used herein, a "polynucleotide" refers to a molecule having a nucleic acid sequence contained in SEQ ID NO:X or the cDNA contained within the clone deposited with the ATCC. For example, the polynucleotide can contain the nucleotide sequence of the full length cDNA sequence, including the 5' and 3' untranslated sequences, the coding region, with or without the signal sequence, the secreted protein coding region, as well as fragments, epitopes, domains, and variants of the nucleic acid sequence. Moreover, as used herein, a "polypeptide" refers to a molecule having the translated amino acid sequence generated from the polynucleotide as broadly defined.

In the present invention, the full length sequence identified as SEQ ID NO:X was often generated by overlapping sequences contained in multiple clones (contig

analysis). A representative clone containing all or most of the sequence for SEQ ID NO:X was deposited with the American Type Culture Collection ("ATCC"). As shown in Table 1, each clone is identified by a cDNA Clone ID (Identifier) and the ATCC Deposit Number. The ATCC is located at 10801 University Boulevard,
5 Manassas, Virginia 20110-2209, USA. The ATCC deposit was made pursuant to the terms of the Budapest Treaty on the international recognition of the deposit of microorganisms for purposes of patent procedure.

A "polynucleotide" of the present invention also includes those polynucleotides capable of hybridizing, under stringent hybridization conditions, to sequences contained
10 in SEQ ID NO:X, the complement thereof, or the cDNA within the clone deposited with the ATCC. "Stringent hybridization conditions" refers to an overnight incubation at 42°C in a solution comprising 50% formamide, 5x SSC (750 mM NaCl, 75 mM sodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA, followed by washing the
15 filters in 0.1x SSC at about 65°C.

Also contemplated are nucleic acid molecules that hybridize to the polynucleotides of the present invention at lower stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily accomplished through the manipulation of formamide concentration (lower percentages
20 of formamide result in lowered stringency); salt conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37°C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M NaH₂PO₄; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 µg/ml salmon sperm blocking DNA; followed by washes at 50°C with 1XSSPE, 0.1% SDS. In addition, to achieve even
25 lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5X SSC).

Note that variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. Typical blocking reagents include
30 Denhardt's reagent, BLOTTO, heparin, denatured salmon sperm DNA, and commercially available proprietary formulations. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility.

Of course, a polynucleotide which hybridizes only to polyA+ sequences (such
35 as any 3' terminal polyA+ tract of a cDNA shown in the sequence listing), or to a

complementary stretch of T (or U) residues, would not be included in the definition of "polynucleotide," since such a polynucleotide would hybridize to any nucleic acid molecule containing a poly (A) stretch or the complement thereof (e.g., practically any double-stranded cDNA clone).

5 The polynucleotide of the present invention can be composed of any polyribonucleotide or polydeoxribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. For example, polynucleotides can be composed of single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and
10 double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, the polynucleotide can be composed of triple-stranded regions comprising RNA or DNA or both RNA and DNA. A polynucleotide may also contain one or more modified bases or DNA or RNA backbones modified for stability
15 or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications can be made to DNA and RNA; thus, "polynucleotide" embraces chemically, enzymatically, or metabolically modified forms.

 The polypeptide of the present invention can be composed of amino acids joined
20 to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres, and may contain amino acids other than the 20 gene-encoded amino acids. The polypeptides may be modified by either natural processes, such as posttranslational processing, or by chemical modification techniques which are well known in the art. Such modifications are well described in basic texts and in more detailed monographs,
25 as well as in a voluminous research literature. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be
30 branched, for example, as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched, and branched cyclic polypeptides may result from posttranslation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a
35 nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine,

formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, pegylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination. (See, for instance, PROTEINS - STRUCTURE AND MOLECULAR PROPERTIES, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York (1993); POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS, B. C. Johnson, Ed., Academic Press, New York, pgs. 1-12 (1983); Seifter et al., Meth Enzymol 182:626-646 (1990); Rattan et al., Ann NY Acad Sci 663:48-62 (1992).)

"SEQ ID NO:X" refers to a polynucleotide sequence while "SEQ ID NO:Y" refers to a polypeptide sequence, both sequences identified by an integer specified in Table 1.

"A polypeptide having biological activity" refers to polypeptides exhibiting activity similar, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. In the case where dose dependency does exist, it need not be identical to that of the polypeptide, but rather substantially similar to the dose-dependence in a given activity as compared to the polypeptide of the present invention (i.e., the candidate polypeptide will exhibit greater activity or not more than about 25-fold less and, preferably, not more than about tenfold less activity, and most preferably, not more than about three-fold less activity relative to the polypeptide of the present invention.)

Polynucleotides and Polypeptides of the Invention

FEATURES OF PROTEIN ENCODED BY GENE NO: 1

This gene is expressed primarily in melanocytes and, to a lesser extent, in testes, ovary, kidney and other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cancer, disorders of neural crest derived cells including pigmentation defects, melanoma, reproductive organ defects, and defects of the kidney. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the skin,

reproductive, and renal systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating disorders that arise from alterations in the number or fate of neural crest derived cells including cancers such as melanoma and defects of the developing reproductive system.

FEATURES OF PROTEIN ENCODED BY GENE NO: 2

This gene is expressed primarily in infant brain and fetal lung.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, developmental disorders of the brain or lung. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous and pulmonary systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating or diagnosing disorders associated with abnormal proliferation of cells in the Central nervous system and developing lung.

FEATURES OF PROTEIN ENCODED BY GENE NO: 3

This gene is expressed primarily in breast lymph node and to a lesser extent in ovarian cancer and chondrosarcoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune responses such as inflammation or immune surveillance for

tumors. This gene may be important for inflammatory responses associated with tumors. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 236 as residues: Lys-45 to Val-50, Lys-69 to Arg-76.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment or diagnosis of immune responses including those associated with tumor-induced inflammation.

FEATURES OF PROTEIN ENCODED BY GENE NO: 4

This gene is expressed primarily in T-cells and T-cell lymphomas.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immunological diseases involving T-cells such as inflammation, autoimmunity, and cancers including T-cell lymphomas. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of T-cells and other cells of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosing and treating T-cell based disorders such as inflammatory diseases, autoimmune disease and tumors including T-cell lymphomas.

FEATURES OF PROTEIN ENCODED BY GENE NO: 5

This gene is expressed primarily in activated monocytes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, inflammation, autoimmunity, infection, or disorders involving activation of monocytes. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 238 as residues: Asp-19 to Arg-31.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosing or treating diseases that result in activation of monocytes including infections, inflammatory responses or autoimmune diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 6

The translation product of this gene shares sequence homology with terminal deoxynucleotidyltransferase which is thought to be important in catalyzing the elongation of oligo- or polydeoxynucleotide chains.

This gene is expressed primarily in activated human neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancer, particularly those of the blood such as leukemia and deficiencies in neutrophils such as neutropenia. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the cardiovascular system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having

such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to terminal deoxynucleotidyltransferase indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and differential diagnosis of acute leukemia's. Alternatively, this gene may function in the proliferation of neutrophils and be useful as a treatment for neutropenia, for example, following neutropenia as a result of chemotherapy.

FEATURES OF PROTEIN ENCODED BY GENE NO: 7

The contig exhibits a reasonable homology to the human chorionic gonadotropic (HCG) analogue-GT beta-subunit as disclosed in U.S. Patent No. 5,508,261 and PCT Publication No. WO 92/22568. There is a high degree of conservation of the structurally important cysteine residues in these identities.

This gene is expressed primarily in IL-1 and LPS induced neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, diseases of the immune system, including inflammatory diseases and allergies. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/diagnosis of diseases of the immune system since expression is primarily in neutrophils, and may be useful as a growth factor for the differentiation or proliferation of neutrophils for the treatment of neutropenia following chemotherapy.

FEATURES OF PROTEIN ENCODED BY GENE NO: 8

This gene is expressed primarily in IL-1- and LPS-induced neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a

biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, diseases of the immune system, including inflammatory diseases and allergies. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 241 as residues: Ser-14 to Pro-22, Leu-43 to Val-53.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of diseases of the immune system since expression is primarily in neutrophils, and may be useful as a growth factor for the differentiation or proliferation of neutrophils for the treatment of neutropenia following chemotherapy.

FEATURES OF PROTEIN ENCODED BY GENE NO: 9

This gene is expressed primarily in IL-1 and LPS induced neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, diseases of the immune system, including inflammatory diseases and allergies. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 242 as residues: Tyr-22 to His-35.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/diagnosis of diseases of the immune system since expression is primarily in neutrophils, and may be useful as a growth

factor for the differentiation or proliferation of neutrophils for the treatment of neutropenia following chemotherapy.

FEATURES OF PROTEIN ENCODED BY GENE NO: 10

5 This gene is expressed primarily in activated T-cells and to a lesser extent in endothelial cells.

 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are
10 not limited to, immune dysfunctions including cancer of the T lymphocytes and autoimmune disorders and inflammation. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at
15 significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

20 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of immune disorders particularly of T-cell origin and may act as a growth factor for particular subsets of T-cells such as CD4 positive cells which would make this a useful therapeutic for the treatment of HIV and other immune compromising illnesses.

25

FEATURES OF PROTEIN ENCODED BY GENE NO: 11

 This gene is expressed primarily in fetal tissue.

 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
30 biological sample and for diagnosis of many developmental abnormalities. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the developing fetus, expression of this gene at significantly higher or lower levels may be routinely detected
35 in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e.,

the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful as a growth factor or differentiation factor for particular cell types in the developing fetus and may be useful in replacement or other types of therapy in cases where the gene is expressed aberrantly.

FEATURES OF PROTEIN ENCODED BY GENE NO: 12

This gene is expressed primarily in T-cells and to a lesser extent in tumor tissue including glioblastoma, meningioma, and Wilm's tumor.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, diseases of the immune system including autoimmune conditions such as rheumatoid arthritis, inflammatory disorders and cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 245 as residues: Thr-9 to Ser-14.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis/ modulation of immune function disorders, including rheumatoid arthritis and inflammatory responses.

FEATURES OF PROTEIN ENCODED BY GENE NO: 13

This gene is expressed primarily in placenta and to a lesser extent in fetal liver and bone marrow.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of hematological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of

disorders of the above tissues or cells, particularly of the hematological and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful as a growth factor for hematopoietic stem cells or progenitor cells in the treatment of chemotherapy patients or kidney disease.

FEATURES OF PROTEIN ENCODED BY GENE NO: 14

This gene is expressed primarily in stromal cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of hematopoietic disorders including cancer, neutropenia, anemia, and thrombocytopenia. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoietic and immune, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful as a growth factor for hematopoietic stem cells or progenitor cells, in particular following chemotherapy treatment.

FEATURES OF PROTEIN ENCODED BY GENE NO: 15

The translation product of this gene shares sequence homology with epsilon-COP from *Bos taurus* which is thought to be important as a component of coatamer, a complex of seven proteins, that is the major component of the non-clathrin membrane coat. Preferred polypeptides encoded by this gene comprise the following amino acid sequences:

MAPPAPGPASGGSGEVDELFDVKNAFYIGSYQQCINEAXXVKLSSPERDVERD

VFLYRAYLAQRKFGVVLDEIKPSSAPELQAVRMFADYLAHESRRDSIVAELDRE
 MSRSXDVTNTTFLMAASIYLHDQNPDAALRALHQGDSLECTAMTVQILLKLD
 RLDLARKELKRMQDLDEDATLTQLATAWVSLATGGEKLQDAYYIFQEMADKCS
 PTLNLLNGQAACHMAQGRWEAAEGLLQEALDKDSGYPETLVNLIVLSQHLGKP
 5 PEVTNRYLSQLKDAHRSHPIKEYQAKENDFDRLVLQYAPSAEAGPELSGP
 (SEQ ID NO:458); or RDVERDVFLYRAYLAQRKFGVVLDEIKPSSAPELQAVRMF
 ADYLAHESRRDSIVAELDREMSRSXDVTNTTFLMAASIYLHDQNPDAALRALH
 QGDSLECTAMTVQILLKLDRLDLARKELKRMQDLDEDATLTQLATAWVSLATG
 GEKLQDAYYIFQEMADKCSPTLNNNGQAACHMAQGRWEAAEGLLQEALDKD
 10 SGYPETLVNLIVLSQHLGKPPEVTNRYLSQLKDAHRSHPIKEYQAKENDFDRL
 VLQYAPSA (SEQ ID NO:459).

This gene is expressed primarily in activated monocytes and T-cells, and to a lesser extent in multiple other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as
 15 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immunomodulation, specifically relating to transport problems in these cells. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell
 20 type(s). For a number of disorders of the above tissues or cells, particularly of the immune, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene
 25 expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to epsilon-COP indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating
 /diagnosing problems with the cellular transport of proteins that may result in
 30 immunologic dysfunction.

FEATURES OF PROTEIN ENCODED BY GENE NO: 16

The translation product of this gene shares sequence homology with an RNA
 helicase which is thought to be important in polynucleotide metabolism. The translation
 35 product of this contig exhibits good homology to the LbeIF4A antigen of *Leishmania braziliensis*. The LbeIF4A antigen, or immunogenic portions of it, can be used to induce protective immunity against leishmaniasis, specifically *L. donovani*, *L. chagasi*,

L. infantum, *L. major*, *L. braziliensis*, *L. panamensis*, *L. tropica* and *L. guyanensis*. It can also be used diagnostically to detect *Leishmania* infection or to stimulate a cellular and/or humoral immune response or to stimulate the production of interleukin-12.

This gene is expressed primarily in colon cancer and to a lesser extent in pituitary.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of cancers particularly of the colon. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the gastrointestinal system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 249 as residues: Glu-93 to Ala-98, Gln-150 to Leu-156, Leu-220 to Leu-231, Leu-268 to Arg-273, Val-324 to Pro-341, Arg-372 to Asn-380, Ser-405 to Gly-410, Phe-426 to Ala-433, Glu-458 to Asp-470, Arg-506 to Ser-547.

The tissue distribution and homology to RNA helicase indicates that polynucleotides and polypeptides corresponding to this gene are useful for development of diagnostic tests for colon cancer.

FEATURES OF PROTEIN ENCODED BY GENE NO: 17

The translation product of this contig has sequence homology to a cytoplasmic protein that binds specifically to JNK designated the JNK interacting protein-1 or JIP-1 in mice. JIP-1 caused cytoplasmic retention of JNK and inhibition of JNK-regulated gene expression.

This gene is expressed primarily in brain including pituitary cerebellum frontal cortex, fetal brain and to a lesser extent in the kidney cortex.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of the central nervous system disorders including ischemia, epilepsy, Parkinson's disease, and schizophrenia. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological

probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Furthermore, the translation product of this contig may suppress the effects of the JNK signaling pathway on cellular proliferation, including transformation by the Bcr-Abl oncogene. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 250 as residues: Pro-6 to Ser-26, Ala-30 to Asp-41, Gly-55 to Ser-61, Gly-74 to Thr-80, Tyr-117 to Ala-123, Tyr-167 to Asp-172, Ala-212 to Cys-223, Pro-239 to Tyr-244.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for enhanced survival and/or differentiation of neurons as a treatment for neurodegenerative disease.

FEATURES OF PROTEIN ENCODED BY GENE NO: 18

The translation product of this gene shares sequence homology with a liver stage antigen from a protozoan parasite.

This gene is expressed primarily in fetal tissue and to a lesser extent in activated T-cells and other immune cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, developmental abnormalities and diseases of immune function. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to a protozoan antigen indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/immune modulation of parasitic infections.

5 FEATURES OF PROTEIN ENCODED BY GENE NO: 19

Preferred polypeptide encoded by this gene comprise the following polypeptide sequences:

MKAIGIEPSLATYHHIIRLFDQPGDPLKRSSFIIYDIMNELMGKRFSPKD
 PDDDKFFQSAMSICSSLRDLELAYQVHGLLKTGDNWKFIPDQHRNFYYSKFF
 10 DLICLMEQIDVTLKWYEDLIPSAYFPHSQTMHLLQALDVANRLEVIPKIWER
 (SEQ ID NO:460); and/or KDSKEYGHTFRSDLREEILMLMARDKHPPPELQVAF
 ADCAADIKSAYESQPIRQTAQDWPATSLNCIAILFLRAGRTQEAWKMLGLFRKH
 NKIPRSELLNELMDSAKVSNPSQAIEVVELASAFSLPICEGLTQRVMSDFAINQ
 EQKEALSNTALTSDSDTSDSSSDSDSDTSEGK (SEQ ID NO:461). Polynucleotides
 15 encoding such polypeptides are also provided.

This gene is expressed primarily in stromal and CD34 depleted bone marrow cells and to a lesser extent in tissues of embryonic origin.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
 20 biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, diseases of hematologic origin including cancers and immune dysfunction. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of
 25 the hematopoietic and immune, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily
 30 fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 252 as residues: Ser-28 to Gln-34.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful as a growth factor for hematopoietic stem cells or progenitor cells which may be useful in the treatment of chemotherapy patients
 35 suffering from neutropenia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 20

Preferred polypeptide fragments can be found in an alternative open reading frame. These preferred polypeptides comprise the amino acid sequence:

MSSDNESDIEDEDLKLELRRLRDKHLKEIQDLQSRQKHEIESLYTKLGKVPPAVI
 5 IPPAAPLSGRRRRPTKSKGSKSSRSSSLGNKSPQLSGNLSGQSAASVLHPQQTL
 HPPGNIPESGQNQLLQPLKPS SSDNLYSAFTSDGAISVPSLSAPGQGTSTNTV
 GATVNSQAAQAQPPAMTSSRKGTFTDDLHKLVDNWARDAMNLSGRRGSKGH
 MNYEGPGMARKFSAPGQLCISMTSNLGGAPISAASATSLGHFTKSMCPPQQY
 GFPATPFGAQWSGTGGPAPQPLGQFQPVGTASLQNFNISNLQKSISNPPGSNL
 10 RTT (SEQ ID NO:462); IQDLQSRQKHEIESLYTKLGKVPPAVIIPPAAPLSGRRRR
 PTKSKGSKSSRSSSLGNKSPQLSGNLSGQSAASVLHPQQTLHPPGNIPESGQN
 QLLQPLKPS SSDNLYSAFTSDGAISVPSLSAPGQGTSTT (SEQ ID NO:463);
 TSDGAISVPSLSAPGQGTSTNTV GATVNSQAAQAQPPAMTSSRKGTFTDDLH
 (SEQ ID NO:464); KGHMNYEGPGMARKFSAPGQLCISMTSNLGGAPISAAS
 15 ATSLGHFTK (SEQ ID NO:465); QPLKPS SSDNLYSAFTSDGAISVPSLSAPG
 (SEQ ID NO:466). Also preferred are polynucleotide fragments encoding these
 polypeptide fragments.

This gene is expressed in fetal liver and tissues associated with the CNS.

Therefore, polynucleotides and polypeptides of the invention are useful as
 20 reagents for differential identification of the tissue(s) or cell type(s) present in a
 biological sample and for diagnosis of diseases and conditions, which include, but are
 not limited to, liver and CNS diseases. Similarly, polypeptides and antibodies directed
 to these polypeptides are useful in providing immunological probes for differential
 identification of the tissue(s) or cell type(s). For a number of disorders of the above
 25 tissues or cells, particularly of the liver and CNS, expression of this gene at
 significantly higher or lower levels may be routinely detected in certain tissues (e.g.,
 cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial
 fluid or spinal fluid) or another tissue or cell sample taken from an individual having
 such a disorder, relative to the standard gene expression level, i.e., the expression level
 30 in healthy tissue or bodily fluid from an individual not having the disorder. Preferred
 epitopes include those comprising a sequence shown in SEQ ID NO: 253 as residues:
 Gln-26 to Lys-34.

The tissue distribution indicates that polynucleotides and polypeptides
 corresponding to this gene are useful for diagnosis and treatment for liver diseases such
 35 as hepatocellular carcinomas and diseases of the CNS.

FEATURES OF PROTEIN ENCODED BY GENE NO: 21

In an alternative reading frame, this gene shows sequence homology to two recently cloned genes, karyopherin beta 3 and Ran_GTP binding protein 5. (See Accession Nos. gil2102696 and gnllPIDle328731.) The Ran_GTP binding protein is related to importin-beta, the key mediator of nuclear localization signal (NLS)-dependent nuclear transport. Based on homology, it is likely that this gene may activity similar to the RAN_GTP binding protein. Preferred polypeptide fragments comprise the amino acid sequence: VRVAAESMXLLLECAAXVRGPEYLTQMWHFMCDALIKA IGTEPDSDVLSEIMHSFAK (SEQ ID NO:467). Also preferred are polynucleotide fragments encoding these polypeptide fragments.

This gene is expressed in thymus tissue.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment for immune disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 22

This gene is expressed primarily in prostate and osteoclastoma tissues. Preferred polypeptide fragments also comprise the amino acid sequence: MEINNQNCFIVIDLVRTVMENGVEGLLIFGAFLPESWLIGVRCSSPEPPKALLLIL AHSQKRRLDGWSFIRHLRVHYCVSLTIHFS (SEQ ID NO:468). Also preferred are polynucleotide sequences encoding this polypeptide fragment.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, bone and prostate diseases, and cancers, particularly of the bone and prostate. Similarly, polypeptides and antibodies directed to these polypeptides are

useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the bone and prostate systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded
5 tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 255 as residues: Met-1 to Ser-11.

10 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment for bone and prostate disorders, especially cancers of those systems.

FEATURES OF PROTEIN ENCODED BY GENE NO: 23

15 This gene shares sequence homology with the FK506-binding protein (FKBP-13) family, a known cytosolic receptor for the immunosuppressants. Recently, another group has cloned a very similar gene, recognizing the homology to FK506-binding protein family, calling their gene FKBP23. (See Accession No. 2827255.)

This gene is expressed primarily in lymphoid tissues.

20 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample, especially for those susceptible to immune suppressant therapies and for diagnosis of diseases and conditions, which include, but are not limited to, immune suppressant disorders. Similarly, polypeptides and antibodies directed to these
25 polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or
30 another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 256 as residues: Ala-19 to Val-31, Arg-38 to Gly-49, Ala-61 to Lys-66, Tyr-68 to Pro-78, Gly-116 to Ala-121, Asp-154 to
35 Ser-162, Glu-173 to Gln-186, Phe-194 to Gly-203, Pro-207 to Val-212.

The tissue distribution and homology to FKBP-12 and -13 indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment for immune suppressant disorders.

5 **FEATURES OF PROTEIN ENCODED BY GENE NO: 24**

This gene is expressed primarily in the brain and in the retina. This gene maps to chromosome 8, and therefore can be used in linkage analysis as a marker for chromosome 8.

Therefore, polynucleotides and polypeptides of the invention are useful as
10 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neurological and ocular associated disease states. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of
15 disorders of the above tissues or cells, particularly of the disorders of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard
20 gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 257 as residues: Cys-34 to Asp-40.

The tissue distribution in retina indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and/or detection of eye disorders
25 including blindness, color blindness, impaired vision, short and long sightedness, retinitis pigmentosa, retinitis proliferans, and retinoblastoma. Expression in the brain indicates a role in the is useful for the detection/treatment of neurodegenerative disease states and behavioral disorders such as Alzheimer's Disease, Parkinson's Disease, Huntington's Disease, schizophrenia, mania, dementia, paranoia, obsessive compulsive
30 disorder and panic disorder.

FEATURES OF PROTEIN ENCODED BY GENE NO: 25

This gene shows sequence homology to a newly identified class of proteins expressed in the nervous system, called stathmin family. (See Accession No. 2585991;
35 see also Eur. J. Biochem. 248 (3), 794-806 (1997).) The stathmin family appears to be an ubiquitous phosphoprotein involved as a relay integrating various intracellular signaling pathways. These pathways affect cell proliferation and differentiation.

Preferred polypeptide fragments comprise the amino acid sequence:

QDKHAEVRKNKELKEEASR (SEQ ID NO:469); QQDLSPWAAPVGCPLXXASX
TCHXLPLSGCLRRQXSXSLPVVAXLCFWFSCPLASLFVPGQPCVTCPPFSLPFQD
KHAEVRKNKELKEEASR (SEQ ID NO:470). Also preferred are the

5 polynucleotide fragments encoding these polypeptide fragments.

This gene is expressed primarily in brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neurological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioral disorders such as Alzheimer's Disease, Parkinson's Disease, Huntingtons Disease, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder and panic disorder.

25 **FEATURES OF PROTEIN ENCODED BY GENE NO: 26**

The polynucleotide sequence of this gene contains a domain similar to a Flt3 ligand peptide. Preferred polypeptide fragments comprise the amino acid sequence: PTRCCTTQPCRSSARRPCWVPMVPSPEGREXQPTCPS (SEQ ID NO:471). Thus, this gene may have activity as binding to Flt3 receptors, a process known to promote angiogenesis and/or lymphangiogenesis.

This gene is expressed in human tonsil, and to a lesser extent in teratocarcinoma, placenta, colon carcinoma, and fetal kidney.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, diseases of the tonsil, as well as cancers, such as colon, reproductive, and kidney cancers. Similarly, polypeptides and antibodies directed to these polypeptides are useful

in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the tonsils, colon, reproductive organs, and kidneys, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.,
 5 cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 259 as residues:
 10 Pro-22 to Glu-33.

The tissue distribution in tonsil and several cancers and fetal tissues indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of diseases of the tonsil or colon, such as tonsillitis, inflammatory diseases involving nose and paranasal sinuses, especially during the
 15 infection of influenza, adenoviruses, parainfluenza, rhinoviruses. The gene may also be useful in the diagnosis and treatment of neoplasms of nasopharynx or colon origins.

FEATURES OF PROTEIN ENCODED BY GENE NO: 27

In an alternative reading frame exists a large open reading frame that encodes a
 20 preferred polypeptide. Preferred polypeptide fragments comprise the amino acid sequence:
 MKRSLNENSARSTAGCLPVPLFNQKKRNRQPLTSNPLKDDSGISTPSDNYDFP
 PLPTDWAWEA VNPXAPVMKTVDTGQIPHVSRLRSQDSVFNSIQSNTGRSQ
 GGWSYRDGNKNTSLK TWXKND FKPQCKRTNLVANDGKNSCPMSSGAQQQK
 25 QLRTPEPPNLSRNKETELLRQTHSSKISGCTMRGLDKNSALQTLKPNFQQNQY
 KXQMLDDIPEDNTLKETSLYQLQFKEKASSLRISAVIESMKYWREHAQKTVLL
 FEVLAVLDSAVTPGPYYSKTFLMRDGKNTLPCVFYEIDRELPRIRGRVHRCVG
 NYDQKKNIFQCVSVRPASVSEQKTFQAFVKIADVEMQYYINVMNET (SEQ ID
 NO:472); SQDSVFNSIQSNTGRSQGGWSYRDGNKNTSLK TWXKND FKPQCKR
 30 (SEQ ID NO:473); NKETELLRQTHSSKISGCTMRGLDKNSALQTLKPNF (SEQ ID
 NO:474); SSLRIISAVIESMKYWREHAQKTVLLFEVLAVLDSAVTPGPYYSKTFLM
 (SEQ ID NO:475); and PRLIRGRVHRCVGNYDQKKNIFQCVSVRPASVSEQK
 TQAFV (SEQ ID NO:476).

This gene is expressed primarily in human testes.

35 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are

not limited to, male reproductive disorders, including cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the male reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful as a hormone with reproductive or other systemic functions; contraceptive development; male infertility of testicular causes, such as Klinefelter's syndrome, varicocele, orchitis; male sexual dysfunctions; testicular neoplasms; and inflammatory disorders such as epididymitis.

FEATURES OF PROTEIN ENCODED BY GENE NO: 28

This gene is expressed primarily in apoptotic T-cell.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, diseases relating to T cells, as well as cancer in general. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the disorders of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for immune disorders. Moreover, since the gene was isolated from an apoptotic cell and based on the understanding of the relationship of apoptosis and cancer, it is likely that this gene may play a role in the genesis of cancer.

FEATURES OF PROTEIN ENCODED BY GENE NO: 29

This gene is expressed primarily in human tonsils.

Therefore, polynucleotides and polypeptides of the invention are useful as
 5 reagents for differential identification of the tissue(s) or cell type(s) present in a
 biological sample and for diagnosis of diseases and conditions, which include, but are
 not limited to, gastrointestinal disorders. Similarly, polypeptides and antibodies directed
 to these polypeptides are useful in providing immunological probes for differential
 identification of the tissue(s) or cell type(s). For a number of disorders of the above
 10 tissues or cells, particularly of the gastrointestinal system, expression of this gene at
 significantly higher or lower levels may be routinely detected in certain tissues (e.g.,
 cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial
 fluid or spinal fluid) or another tissue or cell sample taken from an individual having
 such a disorder, relative to the standard gene expression level, i.e., the expression level
 15 in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
 corresponding to this gene are useful for the diagnosis and treatment of gastrointestinal
 diseases.

20 FEATURES OF PROTEIN ENCODED BY GENE NO: 30

The translation product of this gene shares sequence homology with C44C1.2
 gene product of *Caenorhabditis elegans* with unknown function. Preferred polypeptide
 fragments comprise the amino acid sequence:

GVFRPCVCGRPASLTCSPLDPEVGPYCDTPTMRTL FNLLWLALACSPVHTTLSK
 25 SDAKKAASKTLEKSQFSDKPVQDRGLVVTDLKAESVVLEHRSYCSAKARDRH
 FAGDVLGYVTPWNSHGYDVTKVFGSKFTQISPVWLQLKRRGREMF EVTGLHD
 VDQGWMRAVRKHAKGLHIVPRLLFEDWTYDDFRNVLDSEDEIEELSKTVVQVA
 KNQHFDG FVVEVWNQLLSQKR VGLIHMLTHLAEALH QARLLALLVIPPAITPGT
 DQLGMFTHKEFEQLAPVLDGFS LMTYDYSTA HQPGPNAPLSWVRACVQVLDP
 30 KXKWR TKSSWGSTSMXW TXRXPXDARXPVVGXR XIQXLKDXPRMVLD SK
 PQ (SEQ ID NO:477); TCSPLDPEVGPYCDTPTMRTL FNLLWLALACSPVHTTLS
 (SEQ ID NO:478); LVVTDLKAESVVLEHRSYCSAKARDRH FAGDVLGYVTPW
 NSHGYDVTKVFGSKF (SEQ ID NO:479); REMFEVTGLHDVDQGWMRAVRK
 HAKGLHIVPRLLFEDWTYDDFRNVLDSEDE (SEQ ID NO:480); HFDG FVVEVW
 35 NQLLSQKR VGLIHMLTHLAEALH QARLLALLVIPPAITPGTDQLGM (SEQ ID
 NO:481); DGFSLMTYDYSTA HQPGPNAPLSWVRACVQVLDPKXKWR TKSSW
 GST (SEQ ID NO:482). Also preferred are polynucleotide fragments encoding these

polypeptide fragments. This gene maps to human chromosome 11, and therefore is useful in linkage analysis as a marker for chromosome 11.

This gene is expressed primarily in human T cells and to a lesser extent in human colon carcinoma.

5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune disorders and cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for
10 differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and gastrointestinal systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from
15 an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 263 as residues: Leu-21 to Ala-30, Ser-38 to Asp-47, Pro-87 to Asp-94, Leu-197 to Thr-204, Pro-256 to Ser-262, Thr-277 to Arg-282, Thr-293 to Trp-303.

20 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of immune disorders and gastrointestinal diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 31

25 The translation product of this gene shares sequence homology with Ribosomal protein L11 of *Caenorhabditis elegans*. (See Accession No. 156201.) Preferred polypeptide fragments comprise the amino acid sequence:
ERGVSIHQFCKEFNERTKDIKEGIPLPTKILVKPDRTFEIKIGQPTVSYFLKAAAG
IEKGARQTGKEVAGLVTLKHVYEIARIKAQDEAFALQDVPLSSVVRISIIGSARSL
30 GIRVVKDLSSEELAAFQKERAIFLAAQKEADLAAQEEAAKK (SEQ ID NO:483).
Also preferred are polynucleotide fragments encoding these polypeptide fragments.

This gene is expressed in human embryo tissue and to a lesser extent in human epithelioid sarcoma and other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as
35 reagents for identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, development disorders and epithelial cell cancer. Similarly, polypeptides and antibodies

directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the embryonic and epithelial cell systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 264 as residues: Lys-34 to Gly-40.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of developmental disorders and epithelial cancer.

15 **FEATURES OF PROTEIN ENCODED BY GENE NO: 32**

This gene is expressed primarily in resting T cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, inflammatory and general immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of disorders of immune system.

FEATURES OF PROTEIN ENCODED BY GENE NO: 33

This gene is believed to reside on chromosome 1. Accordingly, polynucleotides derived from this gene are useful in linkage analysis as chromosome 1 markers.

This gene is expressed primarily in prostate and to a lesser extent in soares adult brain, human umbilical vein endothelial cells, and amniotic cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, prostate-related disorders. Similarly, polypeptides and antibodies
 5 directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the urinary system and nervous system expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum,
 10 plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein products of this gene are useful
 15 for the diagnosis and treatment of disorders of the urinary and nervous systems.

FEATURES OF PROTEIN ENCODED BY GENE NO: 34

This gene shares sequence homology with R05G6.4 gene product. (See Accession No. gil1326338.) This gene also shares sequence homology with the cyclophilin-like protein
 20 CyP-60. (See Accession No. 1199598, see also Biochem. J. 314 (1), 313-319 (1996).) Preferred polypeptide fragments comprise the amino acid sequence:
 AVYTYHEKKKDTAASGYGTQNIRLSRDAVKDFDCCCLSLQPCHDPVVTDPDGYL
 YEREAILEYILHQKKEIARQMKAIEKQGRGTRREEQKELQRAASQDHVRGFLEKE
 SAIVSRP LNPFTAKALSGTSPDDVQPGPSVGPPSKDKDKVLPSFWIPSLTPEAK
 25 ATKLEKPSRTVTCPMSGKPLRMSDLTPVHFTPLDSSVDRVGLITRSERYVCAVT
 RDSLSNATPCAVLRPSGAVVTLECVKLRKDMVDPVTGDKLTDRDIIVLQRG
 (SEQ ID NO:484); YLYEREAILEYILHQKKEIARQMKAIEKQGRGTRREEQKELQ
 RAASQDHVRGFLE (SEQ ID NO:485); and FTAKALSGTSPDDVQPGPSVGPP
 SKDKDKVLPSFWIPSLTPEAKATKLEKPSRTVTCPMSGKPL (SEQ ID NO:486).
 30 Also preferred are polynucleotide fragments that encode these polypeptide fragments.

This gene is expressed primarily in human testis and to a lesser extent in other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
 35 biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, male reproductive disorders and in particular testicular cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing

immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system. Expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of disorders of the male reproductive system and in particular of testicular cancer.

FEATURES OF PROTEIN ENCODED BY GENE NO: 35

The translation product of this gene shares sequence homology with Lpe5p of *Saccharomyces cerevisiae* which is thought to be important in the metabolism of phospholipids.

This gene is expressed primarily in liver and brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, metabolic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the metabolic and nervous systems expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 268 as residues: Pro-14 to Leu-20, Lys-28 to Asn-38, Arg-109 to Arg-114, Lys-119 to Asn-124, Glu-152 to Leu-157, Pro-172 to Val-180.

The tissue distribution and homology to Lpe5p of *Saccharomyces cerevisiae* indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of metabolic and nervous disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 36

This gene shares sequence homology with the nuclear ribonucleoprotein U (HNRNP U), encoded by *C. elegans* (See Accession gil1703576.) Preferred polypeptide fragments comprise the amino acid sequence:

- 5 MDTSENRPENDVPEPPMPIADQVSNDDRPEGSVEDEEKKESSLPKSFKRKISVV
 SATKGVPAGNSDTEGGQPGRKRRWGASTATTQKKPSISITTESLKSIPDIKPL
 AGQEAVVDLHADDSRISEDETERNGDDGTHDKGLKICRTVTQVVPAGQENGQ
 REEEEEKEPEAEPPVPPQVSVEVALPPPAEHEVKKVTLGDTLTRRSISQKSGV
 SITIDDPVRTAQVSPPRGKISNIVHISNLVRPFTLGQLKELLGRTGTLVEEAFWI
 10 DKKSHCFVTYSTVEEAVATRTALHGVKWPQSNPKFLCADYAEQDELDYHRGL
 LVDRPSETKTEEQGIPLHPPPPPVQPPQHPRAEQREQERAVREQWAERERE
 MERRERTRSEREWDKVRREGPRSRSRXRRRKERAKSKEKKSEKKEKAQE
 EPPAKLLDDLFRKTKAAPCIYWLPLTDSQIVQKEAERAERAKEREKRRKEQEEE
 EQKEREKEAERERNRQLEREKRREHSRERDRERERERERDRGDRDRERDRE
 15 RGRERDRRDTKRHSRSTPVRDRGGR (SEQ ID NO:488). Also preferred are
 the polynucleotide fragments encoding this polypeptide fragments.

This gene is expressed primarily in epididymus.

- Therefore, polynucleotides and polypeptides of the invention are useful as
 reagents for differential identification of the tissue(s) or cell type(s) present in a
 20 biological sample and for diagnosis of diseases and conditions, which include, but are
 not limited to, diseases of the male reproductive system. Similarly, polypeptides and
 antibodies directed to these polypeptides are useful in providing immunological probes
 for differential identification of the tissue(s) or cell type(s). For a number of disorders
 of the above tissues or cells, particularly of the male reproductive system, expression of
 25 this gene at significantly higher or lower levels may be routinely detected in certain
 tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma,
 urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an
 individual having such a disorder, relative to the standard gene expression level, i.e.,
 the expression level in healthy tissue or bodily fluid from an individual not having the
 30 disorder.

The tissue distribution indicates that polynucleotides and polypeptides
 corresponding to this gene are useful for the diagnosis and treatment of male
 reproductive disorders.

35 FEATURES OF PROTEIN ENCODED BY GENE NO: 37

This gene is expressed primarily in amygdala.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, inflammatory diseases and reproductive disorders. Similarly,

5 polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the amygdala, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum,

10 plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides

15 corresponding to this gene are useful for diagnosis and treatment of inflammatory diseases and reproductive disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 38

This gene shares sequence homology with human opsonin protein P35

20 fragment. (See Accession No. R94181.) The opsonin protein activates the phagocytosis of pathogenic microbes by phagocytic cells. Preferred polypeptide fragments comprise the amino acid sequence: GCDSCPPHLPREAFAQDTQAEGECSSRAERADMCPDAP PSQEVPEGPGAAP (SEQ ID NO:489). Also preferred are polynucleotide fragments encoding these polypeptide fragments.

25 This gene is expressed in immune-related tissues such as thymus, macrophage, T cells and to a lesser extent in many other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are

30 not limited to, immune disorders and infectious disease. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system and infectious disease, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum,

35 plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e.,

the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 271 as residues: Lys-9 to Arg-14, Met-38 to Asp-51.

- 5 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of immune disorders, as well as the treatment and/or diagnosis of infectious disease.

FEATURES OF PROTEIN ENCODED BY GENE NO: 39

- 10 The translation product of this gene shares sequence homology with alpha-2 type I collagen which is thought to be important in tissue repair. (See, e.g., 211607.) Preferred polypeptide fragments comprise the amino acid sequence: PQLPSCGRPWP GTASVFQSHTQGPREDPDPCRAQGSAGTHCPISLSPPRQ (SEQ ID NO:490). Also preferred are the polynucleotide sequences encoding these polypeptide sequences.

- 15 This gene is expressed primarily in the brain and to a lesser extent in the kidney and thymus

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, brain, kidney, and immune disorders. Similarly, polypeptides and
20 antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain, kidney, and immune disorders, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum,
25 plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

- 30 The tissue distribution and homology to alpha-2 type I collagen indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of tissue repair, and brain, kidney, immune disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 40

- 35 The translation product of this gene shares sequence homology with mini-collagen which is thought to be important in tissue repair tumor metastasis. (See Accession No. gnllPIDd1006976.) Preferred polypeptide fragments comprise the amino acid sequence: PGFRGPSGLGCSFFPRSLGRVLPPGCQRPGAHAD

SSPPPTP (SEQ ID NO:491). Also preferred are polynucleotides encoding this polypeptide fragment.

This gene is expressed in ovarian cancer and to a lesser extent in dendritic cells and smooth muscle.

5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, tumor metastasis and tissue repair. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes
10 for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the tumor metastasis and tissue repair, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from
15 an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 273 as residues: Asn-2 to His-11.

The tissue distribution and homology to mini-collagen gene indicates that
20 polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of tumor metastasis and tissue repair.

FEATURES OF PROTEIN ENCODED BY GENE NO: 41

This gene shares sequence homology with the HIV TAT protein. (See
25 Accession No. 328416.) Preferred polypeptide fragments comprise the amino acid sequence: EDLKKPD PASLRAASC GEGKKRKACKNCTCGLAE ELEKEK SREQMSSQPKSACGNCYLGD AFR CASC PYLGMPAFKPG EK VLLS (SEQ ID NO:492); EDLKKPD PASLRAASC GEGKKRKACKNCTCGLAE ELEKEK SREQMSSQPKSACGNCYLGD AFR CASC PYLGMPAFKPG EK VLLS SDSNLHD
30 (SEQ ID NO:493); CGNCYLGD AFR CASC PYLGMPAFKPG EK VLLS SDS (SEQ ID NO:494); SCGEGKKRKACKNCTCGLAE ELEKE (SEQ ID NO:495); SQPKSAC GNCYLGD AFR CASC (SEQ ID NO:496); and REAGQNSERQYVS LSRD (SEQ ID NO:497). Also preferred are polynucleotide fragments encoding these polypeptide fragments.

35 This gene is expressed primarily in the infant brain and to a lesser extent in the breast and testes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, brain, testes and breast disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain, testes and breast disorders, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 274 as residues: Pro-7 to Val-15.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of brain, testes and breast, and other related disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 42

This gene is expressed primarily in the infant brain, human cerebellum, and to a lesser extent in medulloblastoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, brain related disorders and medulloblastoma and other brain cancers. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain related disorders and brain cancers, including medulloblastoma, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 275 as residues: Thr-41 to Glu-47.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of human brain related disorders, brain cancers, and medulloblastoma.

5 FEATURES OF PROTEIN ENCODED BY GENE NO: 43

The translation product of this gene shares sequence homology with a phosphotyrosine-independent ligand for the lck SH2 domain which is thought to be important in signal transduction related to phosphotyrosine-independent ligand for the lck SH2 domain. (See Accession No. gill184951.) Preferred polypeptide fragments
 10 comprise the amino acid sequence: ESSGQARTLADPGPGWPRQQGMCFGSLT
 GLSTTPHGFLT VSAEADPRLIESLSQMLSMGFSDEGGWLTRLLQTKNYDIGAAL
 DTIQYSKH (SEQ ID NO:498). Also preferred are polynucleotide fragments encoding this polypeptide fragment. It is likely that this gene is a new member of a family of
 phosphotyrosine-independent ligands for the lck SH2 domains.

15 This gene is expressed primarily in the placenta and to a lesser extent in endothelial cells and neutrophil.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are
 20 not limited to, reproductive, cardiovascular, immune, and infectious diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the cardiovascular, reproductive, and immune system, and infectious diseases, expression
 25 of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the
 30 disorder.

The tissue distribution and homology to a phosphotyrosine-independent ligand for the lck SH2 domain indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of cardiovascular, reproductive, and immune system diseases, as well as infectious diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 44

This gene is expressed primarily in the fetal brain, cerebellum and to a lesser extent in the placenta.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neuronal cell related disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the neuronal cell related disorders, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 277 as residues: Thr-20 to Gly-28.

The tissue distribution and homology to proline-rich protein genes indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of neuronal cell related disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 45

The translation product of this gene shares sequence homology with precerebellin of human, which is thought to be important in synaptic physiology. (See Accession No. gil180251.) It has been observed that cerebellin-like immunoreactivity is associated with Purkinje cell postsynaptic structures. Thus, it is likely that this gene also have synaptic activity. Preferred polypeptide fragments comprise the amino acid sequence: QEGSEPVLLGECLVVCEPGRAAAGGPGGAALGEAPPGRVAFXAV RSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPVRGVYSFRFH VVKVYNRQTVQVSLMLNTWPVISAFANDPDVTREAATSSVLLPLDPGDRVSLR LRRGXSTGW (SEQ ID NO:499). Also preferred are polynucleotide fragments encoding these polypeptide fragments.

This gene is expressed primarily in cerebellum and infant brain. By Northern analysis, a single transcript of 2.4 kb was observed in brain tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are

not limited to, neuronal cell signal transduction and synaptic physiology. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the neuronal cell signal transduction and synaptic physiology expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to gene or gene family indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of neuronal cell related disorders.

15 **FEATURES OF PROTEIN ENCODED BY GENE NO: 46**

This gene is expressed in fetal liver and spleen, and to a lesser extent in bone marrow, umbilical vein, and T cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, disorders of the immune system, particularly hematopoiesis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoiesis and immune disorders, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 279 as residues: Asp-30 to Glu-57.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of hematopoietic and immune disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 47

The translation product of this gene shares sequence homology with a 12 kD nucleic acid binding protein of Feline calicivirus which is thought to be important in viral replication. (See Accession No. 59264)

- 5 This gene is expressed primarily in human cardiomyopathy and to a lesser extent in T helper cells, fetal brain and synovial sarcoma.

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cardiomyopathy as well as viral infection. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the cardiovascular system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 280 as residues: Trp-20 to Cys-26.

- The tissue distribution in cardiomyopathy and homology to viral 12 kD nucleic acid binding protein indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and intervention of cardiomyopathy, including those caused by ischemic, hypertensive, congenital, valvular, or pericardial abnormalities.
- 25 The gene expression pattern may be the consequence or the cause for these conditions.

FEATURES OF PROTEIN ENCODED BY GENE NO: 48

- The translation product of this gene shares sequence homology with tumor necrosis factor related gene product which is thought to be important in tumor necrosis, bacterial and viral infection, immune diseases and immunoreactions.

This gene is expressed primarily in colon and to a lesser extent in ovarian and breast cancers.

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, tumors of colon, ovary or breast origins. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes

for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the colon, ovary and breast, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to Tumor necrosis factors indicates that polynucleotides and polypeptides corresponding to this gene are useful for intervention of cancers of colon, ovary and breast origins, because TNF family members are known to be involved in the tumor development.

FEATURES OF PROTEIN ENCODED BY GENE NO: 49

The translation product of this gene shares sequence homology with mucins, such as epithelial mucin, which is thought to be important in extracellular matrix functions such as protection, lubrication and cell adhesion (See for example Accession No. R68002). Preferred polypeptide fragments comprise the following amino acid sequence: PRSRPALRPGRQRPPSHSATSGVLRPRKKPDP (SEQ ID NO:500).

Also preferred are polynucleotide fragments encoding these polypeptide fragments. Moreover, this gene maps to chromosome 22q11.2-qter, and therefore, can be used as a marker in linkage analysis for chromosome 22.

This gene is expressed primarily in corpus colosum.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, tumors, especially of corpus colosum, as well as metastatic lesions. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the corpus colosum and other solid tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to mucins indicates that polynucleotides and polypeptides corresponding to this gene are useful for serum tumor markers or immunotherapy targets because tumor cells have greatly elevated level of mucin expression and shed the molecules into the epithelial tissues.

5

FEATURES OF PROTEIN ENCODED BY GENE NO: 50

This gene is expressed primarily in CD34 depleted buffy coat cord blood and primary dendritic cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, hematopoietic disorders and immunological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoietic and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in CD34 depleted buffy coat cord blood and primary dendritic cells indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of hematopoietic and immune disorders. Secreted or cell surface proteins in the above tissue distribution often are involved in cell activation (e.g. cytokines) or molecules involved in cell surface activation.

FEATURES OF PROTEIN ENCODED BY GENE NO: 51

The translation product of this gene shares sequence homology with Interferon induced 1-8 gene encoded polypeptide which is thought to be important in binding to retroviral rev responsive element. Preferred polypeptide fragment comprise the following amino acid sequences: MTLITPSXKLTFXKGKNSWSSRACSSSTLVDP (SEQ ID NO:501). Also preferred are polynucleotide fragments encoding these polypeptide fragments.

This gene is expressed primarily in CD34 positive cells and neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a

biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, retroviral infection, such as AIDS, and other immune disorders.

Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell

5 type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard
10 gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 284 as residues: Gln-51 to Trp-62.

The tissue distribution and homology to interferon induced gene 1-8 indicates that polynucleotides and polypeptides corresponding to this gene are useful for
15 intervention of retroviral infection including HIV. The factor may be involved in viral stability or viral entry into the cells. Alternatively, the virus/factor complex may elicit the cellular immune reaction.

FEATURES OF PROTEIN ENCODED BY GENE NO: 52

20 This gene shares sequence homology to immunoglobulin lambda chain (See Accession No. 2865484). Therefore it is likely that this gene has activity similar to an immunoglobulin lambda chain. Preferred polypeptide fragments comprise the following amino acid sequence: GHPSPALSIAPSDGSQLPCDEVYPYGEAHVTRYCKKPLTNS HLETEAQSSSL (SEQ ID NO:502). Also preferred are polynucleotide fragments
25 encoding these polypeptide fragments.

This gene is expressed primarily in Hodgkin's lymphoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are
30 not limited to, Hodgkin's lymphoma and other immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected
35 in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e.,

the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 285 as residues: Pro-27 to Thr-32.

5 The tissue distribution in Hodgkin's lymphoma and the sequence homology indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis of Hodgkin's lymphoma, since the elevated expression and secretion by the tumor mass may be indicative of tumors of this type. Additionally the gene product may be used as a target in the immunotherapy of the cancer. Because the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune
10 functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, and leukemia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 53

This gene has extensive homology to cDNA for Homo sapiens mRNA for the
15 ISLR gene(See Accession No. AB003184). This protein is considered to be a new member of the Ig superfamily and contains a leucine-rich repeat (LRR) with conserved flanking sequences and a C2-type immunoglobulin (Ig)-like domain. These domains are important for protein-protein interaction or cell adhesion, and therefore it is possible that the novel protein ISLR may also interact with other proteins or cells. The ISLR gene
20 was mapped on human chromosome 15q23-q24 by fluorescence in situ hybridization (See Medline Article No. 97468140). Homology to the ISLR gene has been confirmed by another independent group as well (See Accession No. Hs.102171)

This gene is expressed in a number of tissues including human retina, heart, skeletal muscle, prostate, ovary, small intestine, thyroid, adrenal cortex, testis,
25 stomach, spinal cord, fetal lung and fetal kidney tissues, colon, tonsil and stomach cancer, and to a lesser extent in endometrial stromal cells treated with estradiol, breast tissue, synovium, lymphoma, and number of other tumors.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
30 biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, tumors of colon, ovary and breast origins. However, due to the wide range of expression in various tissues, protein may play a vital role in the development of cancer in other tissues as well, not just those mentioned above. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing
35 immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the colon, ovary and breast, expression of this gene at significantly higher or lower levels may be routinely

detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Additionally, this gene maps to chromosome 15q23-q24, and therefore, can be used as a marker in linkage analysis for chromosome 15.

The tissue distribution in tumors of colon, ovary, and breast origins indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and intervention of these tumors, in addition to other tumors where expression has been indicated. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues.

FEATURES OF PROTEIN ENCODED BY GENE NO: 54

Gene has homology to multidrug resistance gene 1 (See Accession No. P06795). Preferred polynucleotide fragments comprise the following sequence:
 GCTTCGTGTCCAACCCTCTTGCCCTTCGCCTGTGTGCCTGGAGCCAGTCCCA
 CCACGCTCGCGTTTCCTCCTGTAGTGCTCACAGGTCCCAGCACCGATGGCA
 TTCCCTTTGCCCTGAGTCTGCAGCGGGTCCCTTTTGTGCTTCCTTCCCCTCA
 GGTAGCCTCTCTCCCCCTGGGCCACTCCCGGGGGTGAGGGGGTTACCCCTT
 CCCAGTGTTTTTTATTCCTGTGGGGCTCACCCCAAAGTATTAAAAGTAGCTTT
 GTAA (SEQ ID NO:503). Also preferred are polypeptide fragments encoded by these polynucleotide fragments.

This gene is expressed primarily in lung, esophagus, leukemia (Jurkat cells) and breast cancers and to a lesser extent in macrophages treated with GM-CSF fetal tissues and wide range of tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancer of wide range of origins. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the solid tumors, lung and leukemia, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e.,

the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Furthermore, due to the high expression level in lung tissue and the proposed function of the multidrug resistance protein 1 gene as the efflux pump responsible for low-drug accumulation in multidrug-resistant cells, protein as well mutants thereof, may also be beneficial as a target for gene therapy, particularly for the chronic patient. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 287 as residues: Met-1 to Lys-16.

The tissue distribution in wide range of cancers and fetal tissues indicates that polynucleotides and polypeptides corresponding to this gene are useful for detection of cells in active proliferation, such as cancers. The gene products may be used for cancer markers or immunotherapy target.

FEATURES OF PROTEIN ENCODED BY GENE NO: 55

This gene maps to the X chromosome.

This gene is expressed primarily in the brain and to a lesser extent in the developing embryo.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neurodegenerative disease states and developmental disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders, including sex-linked disorders, of the above tissues or cells, particularly of the neurological, developmental systems, and cardiovascular system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Moreover, this gene maps to the X chromosome, and therefore, may be used as a marker in linkage analysis for this chromosome.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioral disorders such as Alzheimer's Disease, Parkinson's Disease, Huntington's Disease, Klinefelter's, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder and panic disorder. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental

disorders associated with the developing embryo, sexually-linked disorders, or disorders of the cardiovascular system.

FEATURES OF PROTEIN ENCODED BY GENE NO: 56

5 The translation product of this gene shares sequence homology with paxillin which is thought to be important in mediating signal transduction from growth factor receptors to the cytoskeleton. Preferred polynucleotide fragments comprise the following sequence: TGGCTCACTGTCTTACAATCACTGCTGTGGAATCATGA
TACCACTTTTAGCTCTTTGCATCTTCCITCAGTGTATTTTGTGTTTTCAAGAGG
10 AAGTAGATTTTAACTGGACAACTTTGAGTACTGACATCATTGATAAATAAACT
GGCTTGTGGTTTCAA (SEQ ID NO:506). Also preferred are polypeptide fragments encoded by these polynucleotide fragments. More preferably, polypeptide fragments comprise the amino acid sequence: LDELM AHLTEMQAKVAVRAD
AGKKHLPDKQD HKASLD SMLGGLEQELQDLGIATVPKGHCASCQKPIAGKVI
15 HALGQSWHPEHFVCTHCKEEIGSSPFFERSGLXYCPNDYHQLFSPRCAYCAAP
ILDKVLTAMNQ TWHP EHF FCSHCGEVFGAEGFHEKDKKPYCRKDFLAMFSPK
CGGCNRPVLENYLSAMDTVWHPECFVCGDCFTSFSTGSFFELDGRPFCELYH
HRRGTLCHGCGQPITGRCISAMGYKFHPEHFVCAFCLTQLSKGIFREQNDKTY
CQPCFNKLF (SEQ ID NO:507); KASLD SMLGGLEQELQDLGIATVPKGHC
20 ASCQKPIAGKVIHAL (SEQ ID NO:508); CPNDYHQLFSPRCAYCAAPILDKVL
TAMNQ TWHP EHF FCSHCGEVFGAEG (SEQ ID NO:509); DKKPYCRKDFLAM
FSPKCGGCNRPVLENYLSAMDTVWHPECFVCGDCFTSFSTGSFFELDGRPFCE
L (SEQ ID NO:510); CGQPITGRCISAMGYKFHPEHFVCAFCLTQLSKGIFRE
QNDKTYCQ (SEQ ID NO:511). Polynucleotide fragments encoding these preferred
25 polypeptide fragments are also contemplated.

This gene is expressed primarily in brain, and to a lesser extent in the developing embryo.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
30 biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neurological disease states and developmental abnormalities. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and
35 nervous systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or

cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Moreover, since this gene shares homology with a gene that maps to chromosome 11, (See Accession No.T87404), gene as well as its translated product may be used for linkage analysis on chromosome 11.

The tissue distribution and homology to paxillin indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and or detection of disease states associated with abnormal signal transduction in brain and/or the developing embryo. This would include treatment or detection of neurodegenerative disease states and behavioral disorders such as Alzheimer's Disease, Parkinson's Disease, Huntingtons Disease, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder and panic disorder and also in the treatment and or detection of embryonic development defects.

15 **FEATURES OF PROTEIN ENCODED BY GENE NO: 57**

This gene is expressed primarily in fetal spleen, brain, and to a lesser extent in six week old embryo.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune disorders, neurological disorders, and developmental abnormalities. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and developmental systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 290 as residues: Arg-28 to Gly-34.

The expression of this gene in fetal spleen indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/detection of immune disorders such as arthritis, asthma, immune deficiency diseases such as AIDS, and leukemia. In addition the expression of this gene in the early embryo, indicates a key role in embryo development and hence the gene or gene product could be used in the treatment and or detection of embryonic development defects. This would include

treatment or detection of neurodegenerative disease states and behavioral disorders such as Alzheimer's Disease, Parkinson's Disease, Huntintons Disease, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder and panic disorder and also in the treatment and or detection of embryonic development defects.

5

FEATURES OF PROTEIN ENCODED BY GENE NO: 58

The translation product of this gene shares sequence homology with the gene disrupted in the neurodegenerative disease dentatorubal-pallidoluysian atrophy. Moreover a long open reading frame exists in an alternative frame. Preferred polypeptide fragments

10 comprise the following:

MGSSQSVEIPGGGTEGYHVLRVQENSPGHRAGLEPFFDFIVSINGSRLNKDND
 TLKDLLKXNVEKPKV KMLIYSSKTLELRETSVTPSNLWGGQGLLGVSIRFCSFD
 GANENVWHVLEVESNSPAALAGLRPHSDYIIGADTMNESEDLSLIETHEAKP
 LKLYVYNTD TDNCREVIITPNSAWGGEGSLGCGIGYGYLHRIPTRPFEEGKKIS
 15 LPGQMAGTPITPLKDGFTVQLSSVNPPSLSPPGTTGIEQSLTGLSISSTPPAVSS
 VLSTGVPTVPLLPPQVNQSLTSVPPMNPATTLPGLMPLPAGLPNLPNLPNLP
 PHIMPGVGLPELVNPGLPPLPSMPPRNLPGLIAPLPSEFLPSFPLVPESSSAASS
 GELLSSLPPTSNA PSDPATTTAKADAASSLTVDVTPPTAKAPTTVEDRVGDSTPV
 SEKPVSAAVDANASEP (SEQ ID NO:512); SVEIPGGGTEGYHVLRVQENSPGH
 20 RAGLEPFFDFIVSINGSRLNKDNDTLKDLLKXNVEKPKV KMLIYSSKTLELRETS
 VTPSNLWGGQGLLGVSIRFCSFDGANENVWH (SEQ ID NO:513); ESNPAA
 LAGLRPHSDYIIGADTMNESEDLSLIETHEAKPLKLYVYNTD TDNCREVIITP
 NSAWGGEGSLGCGIGYGYLHRIPTRPFEEGKKISLPGQMAGTPITPLKDGFTV
 QLSSVNPPSLSPPGTTGIEQSLTG LSIS (SEQ ID NO:514); RIPTRPFEEGKKI
 25 SLPGQMAGTPITPLKDGFTVQLSSVNPPSLSPPGTTGIEQSLTGLSISSTPPAVS
 SVLSTGVPTVPLLPPQVNQSLTSVPPMNPATTLPGLMPLPAGLPNLPNLPNLP
 APHIMPGVGLPELVNPGLPPLPSMPPRN (SEQ ID NO:516); PGLPPLPSMPPRN
 LPGIAPLPSEFLPSFPLVPESSSAASSGELLSSLPPTSNA PSDPATTTAKADAA
 SSLTVDVTPPTAKAPTTVEDRVGDSTPVSEKPVSAAVDAN (SEQ ID NO:517).

30 This gene is expressed primarily in prostate cancer, and to a lesser extent in the pineal glands and in fetal lung.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are
 35 not limited to, neurological conditions and pulmonary disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For

a number of disorders of the above tissues or cells, particularly of the nervous, pulmonary, and endocrine systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or
5 another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 291 as residues: Asn-9 to Leu-14.

The abundance of this gene in the pineal gland and its homology to a gene
10 disrupted in the neurodegenerative disease state Dentatorubral-pallidolusian atrophy indicates that this gene may be useful in the treatment and/or detection of other neurodegenerative disease states and behavioral disorders such as Alzheimer's Disease, Parkinson's Disease, Huntingtons Disease, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder and panic disorder. The abundance of this gene in fetal
15 lung would suggest that misregulation of the expression of this protein product in the adult could lead to lymphoma or sarcoma formation, particularly in the lung; that it may also be involved in predisposition to certain pulmonary defects such as pulmonary edema and embolism, bronchitis and cystic fibrosis; and thus the gen or the gene protein encoded by the gene could be used in the detection and/or treatment of these
20 pulmonary disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 59

This gene is expressed primarily in the developing embryo.

Therefore, polynucleotides and polypeptides of the invention are useful as
25 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, developmental abnormalities. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of
30 the above tissues or cells, particularly of the developmental system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the
35 expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The expression of this gene primarily in the embryo, indicates the gene plays a key role in embryo development and that the gene or the protein encoded by the gene could be used in the treatment and or detection of developmental defects in the embryo or in infants.

5

FEATURES OF PROTEIN ENCODED BY GENE NO: 60

This gene displays homology to nestin, an intermediate filament protein, the expression of which correlates with the proliferation of Central Nervous System progenitor cells and that is useful in the identification of brain tumors. This gene maps
10 to chromosome 1, and therefore, may be used as a marker in linkage analysis for chromosome 1 (See Accession No. AA527348).

This gene is expressed primarily in kidney and to a lesser extent in brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
15 biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, renal disorders and neurodegenerative conditions. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the excretory and
20 nervous systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an
25 individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 293 as residues: Thr-128 to Asn-135.

The tissue distribution and homology to nestin indicates that polynucleotides and polypeptides corresponding to this gene are useful for detection and/or treatment of neurodegenerative disease states and behavioral disorders such as Alzheimer's Disease,
30 Parkinson's Disease, Huntingtons Disease, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder and panic disorder. In addition, its abundance in kidney indicates that it is useful in the treatment and detection of acute renal failure and other disease states associated with the kidney.

35 FEATURES OF PROTEIN ENCODED BY GENE NO: 61

Gene shares homology with the latrophilin-related protein 1 precursor as well as the calcium-independent alpha-latrotoxin receptor. Preferred polypeptide fragments

comprise the following amino acid sequence:

IYKVFRTAGLKPEVSCFENIRSCARXXXXXXXXXXXXWIFGVLHVHVASV
TAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNVPCC (SEQ ID NO:518);
WIFGVLHVHVASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNVPC

- 5 C (SEQ ID NO:519). Also preferred are polynucleotide fragments encoding these polypeptide fragments. (See Accession No. 2213659) The translation product of this gene shares sequence homology with CD 97, a seven transmembrane bound receptor.

This gene is expressed primarily in infant brain and in endothelial cells.

- Therefore, polynucleotides and polypeptides of the invention are useful as
10 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neurological disorders and hematopoietic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For
15 a number of disorders of the above tissues or cells, particularly of the neurological and hematopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the
20 standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 294 as residues: Lys-13 to Leu-21.

- The tissue distribution of this gene suggest that it may be useful in the detection and/or treatment of neurodegenerative disease states and behavioral disorders such as
25 Alzheimer's Disease, Parkinson's Disease, Huntingtons Disease, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder and panic disorder, while its expression in hematopoietic cell types indicates that the gene could be important for the treatment or detection of immune or hematopoietic disorders including arthritis, asthma and immunodeficiency diseases.

30

FEATURES OF PROTEIN ENCODED BY GENE NO: 62

This gene is expressed primarily in fetal liver and fetal spleen.

- Therefore, polynucleotides and polypeptides of the invention are useful as
35 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, hematological and immunological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes

for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and hematopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 295 as residues: Ser-91 to Lys-98.

The tissue distribution of this gene fetal liver and spleen indicates that the gene could be important for the treatment or detection of immune or hematopoietic disorders including arthritis, leukemia, asthma and immunodeficiency diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 63

Gene shares homology with human serum amyloid protein. Preferred polypeptide fragments comprise the following amino acid sequence:
ALTRIPPGDWVINVTAVSFAGKTTARFFHSSPPSLGDQARTDPGHQRRD (SEQ ID NO:520) (See Accession No. W13671). Also preferred are polynucleotide fragments encoding these polypeptide fragments This gene maps to chromosome 9, and therefore, may be used as a marker in linkage analysis for chromosome 9 (See Accession No. AA004342).

This gene is expressed primarily in fetal liver and spleen.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, hematopoietic and immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoietic and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution of this gene in fetal liver-spleen indicates that the gene could be important for the treatment or detection of immune or hematopoietic disorders including arthritis, leukemia, asthma, and immunodeficiency diseases.

5 **FEATURES OF PROTEIN ENCODED BY GENE NO: 64**

This gene maps to chromosome 3, and therefore, may be used as a marker in linkage analysis for chromosome 3 (See Accession No. AA219669).

This gene is expressed specifically in the brain.

Therefore, polynucleotides and polypeptides of the invention are useful as
10 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neurodegenerative disease states. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of
15 the above tissues or cells, particularly of the neurological systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the
20 expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioral disorders such as Alzheimer's Disease, Parkinson's
25 Disease, Huntingtons Disease, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder and panic disorder.

FEATURES OF PROTEIN ENCODED BY GENE NO: 65

Gene shares homology with a yeast protein. Preferred polypeptide fragments
30 comprise the following amino acid sequence: LQEVNITLPENSVWYERYKFDIP VFHL (SEQ ID NO:521). Also preferred are polynucleotide fragments encoding these polypeptide fragments. (See Accession No. 1332638)

This gene is expressed primarily in fetal tissue (fetus and fetal liver).

Therefore, polynucleotides and polypeptides of the invention are useful as
35 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, liver disorders and cancers (e.g. hepatoblastoma). Similarly,

polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hepatic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 298 as residues: Asn-59 to Glu-64.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection and treatment of liver disorders and cancers (e.g. hepatoblastoma, jaundice, hepatitis, liver metabolic diseases and conditions that are attributable to the differentiation of hepatocyte progenitor cells). In addition the expression in fetus would suggest a useful role for the protein product in developmental abnormalities, fetal deficiencies, pre-natal disorders and various wound-healing models and/or tissue trauma.

FEATURES OF PROTEIN ENCODED BY GENE NO: 66

Gene has homology with a B-cell surface antigen which may indicate gene plays a role in the immune response, including, but not limited to disorders and infections of the immune system. Preferred polynucleotide fragments comprise the following sequence: TAGCATGTAGCCAGTCGAATAACNTATAAGGACAAAGTGGAGTCCACGCGTGCGGCCGTCTAGACTAGTGGATCCCCGGCTGCAGGATTCCGGCACGAG (SEQ ID NO:523). Also preferred are polypeptide fragments encoded by these polynucleotide fragments (See Accession No.T94535). Additionally, this gene shares homology with an interferon-gamma receptor. Preferred polypeptide fragments also comprise the following amino acid sequence: MQSGSQFRACLLCLCFSCPCSPGGPRWNSRQGRRFPKTCRAISQNLVFKYKTFCPVRYMQPHRSSLCLHFTSYVFILSTWGLRITYSTDLLKKKKNSRGGPVPIRPKS (SEQ ID NO:522); MQSGSQFRACLLCLCFSCPCSPGGPRWNSRQGRRFPKTCRAISQNLVFK (SEQ ID NO:524); PVRYMQPHRSSLCLHFTSYVFILSTWGLRITYSTDLLKKKKNSRGGPVPIRPKS (SEQ ID NO:525); and GEEQRDCSLGWRGVGMRATHCQAA RMFVLFSLPKYAGL (SEQ ID NO:526). Also preferred are polynucleotide fragments encoding these polypeptide fragments

This gene is expressed primarily in T-cells and gall bladder.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immunological disorders and conditions (immunodeficiencies, cancer, leukemia, hematopoiesis). Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and digestive systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 299 as residues: Thr-41 to Gly-52.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of immune disorders including: leukemias, lymphomas, auto-immune disorders, immunosuppressive (transplantation) and immunodeficiencies (e.g. AIDS), inflammation and hematopoietic disorders. The expression of this gene in gall bladder would suggest a possible role for this gene product in digestive disorders, particularly of the pancreas.

FEATURES OF PROTEIN ENCODED BY GENE NO: 67

This gene maps to chromosome 11, and therefore, may be used as a marker in linkage analysis for chromosome 11 (See Accession No. AA011622).

This gene is expressed primarily in a variety of fetal and developmental tissues (e.g. fetal spleen, infant brain).

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, developmental, immune or neurological abnormalities. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the developing immune and central nervous systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or

another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 300 as residues: Ser-38 to Ser-43.

- 5 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for developmental abnormalities or fetal deficiencies. The detection in infant brain would suggest a role in neurological disorders (both developmental and neurodegenerative conditions of the brain and nervous system, behavioral disorders, depression, schizophrenia, Alzheimer's disease, Parkinson's
- 10 disease, Huntington's disease, mania, dementia). In addition, the detection in spleen would similarly suggest a role in detection and treatment of immunologically mediated disorders (e.g. immunodeficiency, inflammation, cancer, wound healing, tissue repair, hematopoiesis).

15 **FEATURES OF PROTEIN ENCODED BY GENE NO: 68**

 This gene is expressed primarily in spleen, T-cells, and fetal heart.

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are
- 20 not limited to, immunological deficiencies, including AIDS and cardiovascular disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and cardiovascular systems, expression of this gene at significantly higher
- 25 or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

- 30 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of immune disorders including: leukemias, lymphomas, autoimmune disorders, immunodeficiencies (e.g. AIDS), immuno-suppressive conditions (transplantation) and hematopoietic disorders. The expression in fetal heart indicates that polynucleotides and
- 35 polypeptides corresponding to this gene are useful for the treatment and diagnosis of cardiovascular disorders (e.g. heart disease, restenosis, atherosclerosis, stroke, angina, thrombosis).

FEATURES OF PROTEIN ENCODED BY GENE NO: 69

Gene shares homology with a human collagen protein. Preferred polypeptide fragments comprise the following amino acid sequence:

- 5 MPRKTSKCRQLLCSGASRNADTAARQSTCSSHRPPGKIPSLGPRRXPGCXSV
 SSRGEQSTGSPAAPRCGRRDAHRGLPGGAAMTPGDTWASFNPRAGHSKSQGE
 GQESSGASRQDRHPVSHWVERQREAWGAPRSSSAGGVKVAATTEREPEFKIK
 TGKA (SEQ ID NO:527); CSGASRNADTAARQSTCSSHRPPGKIPSLGPRRXPG
 CXSVPSRGEQSTGSPAAPRCGRRDAHRGLPGGAAMTPGDTWASFNPRAGHS
 10 (SEQ ID NO:528); QGEGQESSGASRQDRHPVSHWVERQREAWGAPRSSSAGG
 VKVAATTEREPEFKIKTGKA (SEQ ID NO:529) (See Accession No. 124886). Also
 preferred are polynucleotide fragments encoding these polypeptide fragments

This gene is expressed primarily in fetal heart.

- Therefore, polynucleotides and polypeptides of the invention are useful as
 15 reagents for differential identification of the tissue(s) or cell type(s) present in a
 biological sample and for diagnosis of diseases and conditions, which include, but are
 not limited to, cardiovascular disorders. Similarly, polypeptides and antibodies directed
 to these polypeptides are useful in providing immunological probes for differential
 identification of the tissue(s) or cell type(s). For a number of disorders of the above
 20 tissues or cells, particularly of the cardiovascular system, expression of this gene at
 significantly higher or lower levels may be routinely detected in certain tissues (e.g.,
 cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial
 fluid or spinal fluid) or another tissue or cell sample taken from an individual having
 such a disorder, relative to the standard gene expression level, i.e., the expression level
 25 in healthy tissue or bodily fluid from an individual not having the disorder. Preferred
 epitopes include those comprising a sequence shown in SEQ ID NO: 302 as residues:
 Pro-32 to Ser-39.

- The tissue distribution indicates that polynucleotides and polypeptides
 corresponding to this gene are useful for the treatment and diagnosis of cardiovascular
 30 disorders (e.g. heart disease, restenosis, atherosclerosis, stroke, angina, thrombosis).

FEATURES OF PROTEIN ENCODED BY GENE NO: 70

- The translation product of this gene shares sequence homology with a chicken
 single-strand DNA-binding protein. Preferred polypeptide fragments comprise the
 35 following amino acid sequence:

MSPRYPGGPRPPLRIPNQALGGVPGSQPLLPSGMDPTRQQGHPNMGGPMQRM
 TPPRGMVPLGPQNYGGAMRPPNLALGGPGMPGMNMGPGGGRWPNPNTNAN

SIPYSSASPGNYVGPPGGGGPPGTPIMPSPADSTNSGDNMYTLMNAVPPGPNR
 PNFPMPGSDGPMGGLGGMESHMHMNGSLGSGDMDSSISKNSPNNMSLSNQ
 GTPRDDGEMGGNFLNPFQSESYSPSMTMSV (SEQ ID NO:530); MSPRYPGG
 PRPPLRIPNQALGGVPGSQPLLPSGMDPTRQQGHPNMGGPMQRMTPPRGMV
 5 LGPQNYGGAMRPPLNALGGPGMPGMNMGPGGGRPWPNTNANSIPYSSASP
 GNY (SEQ ID. NO:531); LNALGGPGMPGMNMGPGGGRPWPNTNANSIPYSS
 ASPGNYVGPPGGGGPPGTPIMPSPADSTNSGDNMYTLMNAVPPGPN (SEQ ID
 NO:532); GPMGGLGGMESHMHMNGSLGSGDMDSSISKNSPNNMSLSNQPGTPR
 DDGEMGGNFLNPFQSESYSPSMTMSV (SEQ ID NO:533); TCEHSSEAKAFHDY
 10 (SEQ ID NO:534). Also preferred are polynucleotide fragments encoding these
 polypeptide fragments. (See Accession No. 1562534)

This gene is expressed primarily in placenta and to a lesser extent in the fetal heart and a variety of other tissues and cell types.

Therefore, polynucleotides and polypeptides of the invention are useful as
 15 reagents for differential identification of the tissue(s) or cell type(s) present in a
 biological sample and for diagnosis of diseases and conditions, which include, but are
 not limited to, developmental abnormalities, fetal deficiencies, and particularly of the
 cardiovascular system. Similarly, polypeptides and antibodies directed to these
 polypeptides are useful in providing immunological probes for differential identification
 20 of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells,
 particularly of the reproductive system, expression of this gene at significantly higher or
 lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded
 tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or
 another tissue or cell sample taken from an individual having such a disorder, relative to
 25 the standard gene expression level, i.e., the expression level in healthy tissue or bodily
 fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
 corresponding to this gene are useful for the detection and treatment of developmental
 abnormalities or fetal deficiencies, ovarian and other endometrial cancers, reproductive
 30 dysfunction, cardiovascular disorders, and pre-natal disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 71

This gene is expressed primarily in fetal liver and to a lesser extent in the breast and testes.

35 Therefore, polynucleotides and polypeptides of the invention are useful as
 reagents for differential identification of the tissue(s) or cell type(s) present in a
 biological sample and for diagnosis of diseases and conditions, which include, but are

not limited to, liver disorders (including hepatoblastomas) and reproductive disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hepatic and reproductive systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for detection and treatment of liver disorders and cancers (e.g. hepatoblastoma, jaundice, hepatitis, liver metabolic diseases and conditions that are attributable to the differentiation of hepatocyte progenitor cells). The expression in testes and breast indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection and treatment of endocrine and reproductive disorders (e.g. sperm maturation, milk production, testicular and breast cancers).

20 FEATURES OF PROTEIN ENCODED BY GENE NO: 72

This gene maps to chromosome 1, and therefore, may be used as a marker in linkage analysis for chromosome 1 (See Accession No. W93595).

This gene is expressed primarily in smooth muscle and to a lesser extent in brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cardiovascular and neurological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the cardiovascular and central nervous systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection and treatment of restenosis, atherosclerosis, stroke, angina, thrombosis, wound healing and other conditions of heart disease. In addition, the expression in brain would suggest that polynucleotides and polypeptides corresponding to this gene are useful for the detection and treatment of developmental, degenerative and behavioral conditions of the brain and nervous system (e.g. schizophrenia, depression, Alzheimer's disease, Parkinson's disease, Huntington's disease, mania, dementia, paranoia, addictive behavior and sleep disorders).

FEATURES OF PROTEIN ENCODED BY GENE NO: 73

Gene shares homology with human stromalin-2. Preferred polypeptide fragments comprise the following amino acid sequence:

QAFVLLSDLLLIFSPQMIVGGRDFLRPLVFFPEATLQSELASFLMDHVFQPGDL
 GSGA (SEQ ID NO:535); ACSYLLCNPEFTFFSRADFARSQVLDLLTDRFQQE
 LEELLQVG (SEQ ID NO:536), QKQLSSLRDRMVAFCCLCQSCLSVDVTEIQEQV
 ST (SEQ ID NO:537); QVILPALTLVYFSILWTLTHISKSDAS (SEQ ID NO:538);
 STHDLTRWELYEPCCQLLQKAVDTGXVPHQV (SEQ ID NO:539). Also preferred
 are polynucleotide fragments encoding these polypeptide fragments (See Accession
 No.R65208) This gene maps to chromosome 7, and therefore, may be used as a
 marker in linkage analysis for chromosome 7 (See Accession No. D52585).

This gene is expressed primarily in the brain (infant brain, adult brain, pituitary, cerebellum, hippocampus, schizophrenic hypothalamus, amygdala).

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, developmental and neurodegenerative diseases of the brain and nervous system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those

comprising a sequence shown in SEQ ID NO: 306 as residues: Thr-25 to Lys-36, Lys-55 to Ser-63.

- 5 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for detection and treatment of developmental, degenerative and behavioral conditions of the brain and nervous system (e.g. schizophrenia, depression, Alzheimer's disease, Parkinson's disease, Huntington's disease, mania, dementia, paranoia, addictive behavior and sleep disorders).

FEATURES OF PROTEIN ENCODED BY GENE NO: 74

- 10 This gene is expressed primarily in the hypothalamus of a human suffering from schizophrenia.

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, disorders of the CNS particularly schizophrenia. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the CNS, such as schizophrenia expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 307 as residues: Gly-38 to Ala-44.

The tissue distribution indicates that the protein products of this gene are useful for the study, diagnosis and treatment of schizophrenia and other disorders involving the CNS.

FEATURES OF PROTEIN ENCODED BY GENE NO: 75

Preferred polypeptides of the invention comprise the following amino acid sequence encoded by this gene:

LAVSTSFICCADISTALPLGSSRPAPAPRHREHEHGHQARPPRLIXTSLMPLSTP
AAAQLLWTQLTPMGGRPGGRHSPPTLHTGPRALPPGPPHPSLHVAALSLLR

- 35 (SEQ ID NO:540). Polynucleotides encoding such polypeptides are also provided.

This gene is expressed primarily in endometrial tumor and to a lesser extent in amniotic cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, reproductive and immune disorders particularly cancers of those systems. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 308 as residues: Ser-3 to Arg-9.

The tissue distribution indicates that the protein products of this gene are useful for study and treatment of immune and reproductive disorders particularly cancers of those systems.

FEATURES OF PROTEIN ENCODED BY GENE NO: 76

This gene is expressed primarily in kidney cortex and to a lesser extent in early stage human brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, renal disorders such as renal cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the kidney expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 309 as residues: Gly-38 to Gly-45, Gly-47 to Gly-52, Pro-92 to Lys-110.

The tissue distribution indicates that the protein products of this gene are useful for study, treatment and diagnosis of renal diseases such as cancer of the kidney.

FEATURES OF PROTEIN ENCODED BY GENE NO: 77

This gene is expressed primarily in kidney medulla.

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions, which include, but are
not limited to, metabolic and renal disorders. Similarly, polypeptides and antibodies
directed to these polypeptides are useful in providing immunological probes for
10 differential identification of the tissue(s) or cell type(s). For a number of disorders of
the above tissues or cells, particularly of the metabolic and renal systems, expression of
this gene at significantly higher or lower levels may be routinely detected in certain
tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma,
urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an
15 individual having such a disorder, relative to the standard gene expression level, i.e.,
the expression level in healthy tissue or bodily fluid from an individual not having the
disorder.

The tissue distribution indicates that the protein products of this gene are useful
for study, treatment and diagnosis of metabolic and renal diseases and disorders.

20 FEATURES OF PROTEIN ENCODED BY GENE NO: 78

This gene is expressed in chronic synovitis and microvascular endothelium.

Therefore, polynucleotides and polypeptides of the invention are useful as
reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions, which include, but are
25 not limited to, arthritis and atherosclerosis. Similarly, polypeptides and antibodies
directed to these polypeptides are useful in providing immunological probes for
differential identification of the tissue(s) or cell type(s). For a number of disorders of
the above tissues or cells, particularly of the vascular and skeletal systems, expression
of this gene at significantly higher or lower levels may be routinely detected in certain
30 tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma,
urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an
individual having such a disorder, relative to the standard gene expression level, i.e.,
the expression level in healthy tissue or bodily fluid from an individual not having the
disorder.

35 The tissue distribution indicates that the protein products of this gene are useful
for study, diagnosis and treatment of arthritic and other inflammatory diseases as well
as cardiovascular diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 79

This gene is expressed in resting T-cells and activated monocytes.

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions, which include, but are
not limited to, immune disorders. Similarly, polypeptides and antibodies directed to
these polypeptides are useful in providing immunological probes for differential
10 identification of the tissue(s) or cell type(s). For a number of disorders of the above
tissues or cells, particularly of the immune system, expression of this gene at
significantly higher or lower levels may be routinely detected in certain tissues (e.g.,
cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial
fluid or spinal fluid) or another tissue or cell sample taken from an individual having
15 such a disorder, relative to the standard gene expression level, i.e., the expression level
in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein products of this gene are useful
for the study and treatment of immune diseases such as inflammatory conditions.

FEATURES OF PROTEIN ENCODED BY GENE NO: 80

20 This gene is expressed in a variety of immune system tissues, e.g., neutrophils,
T-cells, and TNF induced epithelial and endothelial cells.

Therefore, polynucleotides and polypeptides of the invention are useful as
reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions, which include, but are
25 not limited to, infectious and immune disorders. Similarly, polypeptides and antibodies
directed to these polypeptides are useful in providing immunological probes for
differential identification of the tissue(s) or cell type(s). For a number of disorders of
the above tissues or cells, particularly of the immune and vascular systems, expression
of this gene at significantly higher or lower levels may be routinely detected in certain
30 tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma,
urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an
individual having such a disorder, relative to the standard gene expression level, i.e.,
the expression level in healthy tissue or bodily fluid from an individual not having the
disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID
35 NO: 313 as residues: Met-1 to Trp-6.

The tissue distribution indicates that the protein products of this gene are useful
for study and treatment of infectious diseases, immune and vascular disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 81

This gene is expressed in activated neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions, which include, but are
not limited to, inflammation and other immune conditions. Similarly, polypeptides and
antibodies directed to these polypeptides are useful in providing immunological probes
for differential identification of the tissue(s) or cell type(s). For a number of disorders
10 of the above tissues or cells, particularly of the immune system, expression of this gene
at significantly higher or lower levels may be routinely detected in certain tissues (e.g.,
cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial
fluid or spinal fluid) or another tissue or cell sample taken from an individual having
such a disorder, relative to the standard gene expression level, i.e., the expression level
15 in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein products of this gene are useful
for study and treatment of immune disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 82

20 This gene is expressed in neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as
reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions, which include, but are
not limited to, inflammatory and other immune conditions. Similarly, polypeptides and
25 antibodies directed to these polypeptides are useful in providing immunological probes
for differential identification of the tissue(s) or cell type(s). For a number of disorders
of the above tissues or cells, particularly of the immune system, expression of this gene
at significantly higher or lower levels may be routinely detected in certain tissues (e.g.,
cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial
30 fluid or spinal fluid) or another tissue or cell sample taken from an individual having
such a disorder, relative to the standard gene expression level, i.e., the expression level
in healthy tissue or bodily fluid from an individual not having the disorder. Preferred
epitopes include those comprising a sequence shown in SEQ ID NO: 315 as residues:
Ala-83 to Thr-91.

35 The tissue distribution indicates that the protein products of this gene are useful
for study and treatment of immune disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 83

This gene is expressed in human neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions, which include, but are
not limited to, inflammation and immune disorders. Similarly, polypeptides and
antibodies directed to these polypeptides are useful in providing immunological probes
for differential identification of the tissue(s) or cell type(s). For a number of disorders
10 of the above tissues or cells, particularly of the immune and inflammatory system,
expression of this gene at significantly higher or lower levels may be routinely detected
in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum,
plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from
an individual having such a disorder, relative to the standard gene expression level, i.e.,
15 the expression level in healthy tissue or bodily fluid from an individual not having the
disorder.

The tissue distribution indicates that the protein products of this gene are useful
for diagnosis and treatment of disorders of the inflammatory and immune systems.

20 FEATURES OF PROTEIN ENCODED BY GENE NO: 84

This gene is expressed in human neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as
reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions, which include, but are
25 not limited to, disorders of the inflammatory and immune systems. Similarly,
polypeptides and antibodies directed to these polypeptides are useful in providing
immunological probes for differential identification of the tissue(s) or cell type(s). For
a number of disorders of the above tissues or cells, particularly of the inflammatory and
immune systems, expression of this gene at significantly higher or lower levels may be
30 routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily
fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or
cell sample taken from an individual having such a disorder, relative to the standard
gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an
individual not having the disorder.

35 The tissue distribution indicates that the protein products of this gene are useful
for diagnosis and treatment of disorders of the immune and inflammatory systems.

FEATURES OF PROTEIN ENCODED BY GENE NO: 85

This gene is expressed in activated neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions, which include, but are
not limited to, inflammation and immune system diseases. Similarly, polypeptides and
antibodies directed to these polypeptides are useful in providing immunological probes
10 for differential identification of the tissue(s) or cell type(s). For a number of disorders
of the above tissues or cells, particularly of the immune system and inflammatory
system, expression of this gene at significantly higher or lower levels may be routinely
detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g.,
serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample
15 taken from an individual having such a disorder, relative to the standard gene
expression level, i.e., the expression level in healthy tissue or bodily fluid from an
individual not having the disorder.

The tissue distribution indicates that the protein products of this gene are useful
for diagnosis and treatment of diseases of the inflammatory and immune systems.

20 FEATURES OF PROTEIN ENCODED BY GENE NO: 86

This gene is expressed in activated neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as
reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions, which include, but are
25 not limited to, inflammation and immune system disorders. Similarly, polypeptides and
antibodies directed to these polypeptides are useful in providing immunological probes
for differential identification of the tissue(s) or cell type(s). For a number of disorders
of the above tissues or cells, particularly of the inflammatory and immune system,
expression of this gene at significantly higher or lower levels may be routinely detected
30 in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum,
plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from
an individual having such a disorder, relative to the standard gene expression level, i.e.,
the expression level in healthy tissue or bodily fluid from an individual not having the
disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID
35 NO: 319 as residues: Met-1 to Gly-6, Gly-32 to Pro-43, Leu-55 to Gln-60.

The tissue distribution indicates that the protein products of this gene are useful
for diagnosis and treatment of disorders of the immune and inflammatory system.

FEATURES OF PROTEIN ENCODED BY GENE NO: 87

In specific embodiments, polypeptides of the invention comprise the sequence:

EQVLALLWPRFELILEMNVQSVRSTDPQRLGGLDTRPHYITRRYAEFSSALVSIN
 5 QTIPNERTMQLLGQLQVEVENFVLRVAAEFSSRKEQLVFLINNYDMMLGVLME
 RAADDSEVESFQQLLNARTQEFIEELLSPFGLVAFVKEAEALIERGQAERLR
 GEEARVTQLIRGFGSSWKSSVESLSQDVMRSFTNFRNGTSIIQG (SEQ ID
 NO:541), ALLKYRFFYQFLLGNERATAKEIRDEYVETLSKIYLSYYRSYLGRMLK
 VQYEEVAEKDDLGMGVEDTAKKGFXXSKPSRSRNTIFTLGTRGSVISPTLEAPILV
 10 PHTAQR (SEQ ID NO: 542); EQRYPFALFRSQHYXLLDNSCREYLFICEFFVVS
 GPXAHDLFHAVMGRTLSMTLKHLDSYLADCYDAIAVFLCIHIVLRFRNIAAKRD
 VPALDRYW (SEQ ID NO:543), GGLDTRPHYITRRYAEFSSALVSINQ (SEQ ID
 NO:544); SRKEQLVFLINNYDMMLGVL (SEQ ID NO: 545) and/or ALLKYRFFY
 QFLLGNERATAKEIRDEYVETLSKIYLSYYRSYLGRMLKVQYEEVAEKDDLGMG
 15 VEDTAKKGFXXSKPSLSRNTIFTLGTRGSVISPTLEAPILVPHTAQRXEQRYPF
 EALFRSQHYXLLDNSCREYLFICEFFVVS GPXAHDLFHAVMGRTLSMTLKHL
 SYLADCYDAIAVFLCIHIVLRFRNIAAKRDVPALDRYWEQVLALLWPRFELILEM
 NVQSVRSTDPQRLGGLDTRPHYITRRYAEFSSALVSINQTIPNERTMQLLGQLQV
 EVENFVLRVAAEFSSRKEQLVFLINNYDMMLGVL MERAADDSEVESFQQLLN
 20 ARTQEFIEELLSPFGLVAFVKEAEALIERGQAERLRGEEARVTQLIRGFGSSW
 KSSVESLSQDVMRSFTNFRNGTS (SEQ ID NO:546). Polynucleotides encoding
 these polypeptides are also encompassed by the invention. The translation product of
 this gene shares sequence homology with suppressor of actin mutation which is thought
 to be important in mutation suppression.

25 This gene is expressed primarily in fetal liver and to a lesser extent in a variety
 of other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as
 reagents for differential identification of the tissue(s) or cell type(s) present in a
 biological sample and for diagnosis of diseases and conditions, which include, but are
 30 not limited to, liver and mutations. Similarly, polypeptides and antibodies directed to
 these polypeptides are useful in providing immunological probes for differential
 identification of the tissue(s) or cell type(s). For a number of disorders of the above
 tissues or cells, particularly of the liver or cancer, expression of this gene at
 significantly higher or lower levels may be routinely detected in certain tissues (e.g.,
 35 cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial
 fluid or spinal fluid) or another tissue or cell sample taken from an individual having
 such a disorder, relative to the standard gene expression level, i.e., the expression level

in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 320 as residues: Val-53 to Arg-60, Thr-88 to Thr-94, Ala-142 to Ser-150, Gly-188 to Glu-196, Gly-208 to Ser-214, Thr-227 to Gly-232, Lys-279 to Phe-285.

- 5 The tissue distribution and homology to suppressor of actin mutation suggest that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and of liver disorder or cancer.

FEATURES OF PROTEIN ENCODED BY GENE NO: 88

- 10 This gene maps to chromosome 9, and therefore can be used in linkage analysis as a marker for chromosome 9. In specific embodiments, polypeptides of the invention comprise the sequence:
- YEGKEFDYVFSIDVNEGGPSYKLPYNTSDDPWLTAYNFLQKNDLNPMFLDQVA
KFIIDNTKGQMLGLGNPSFSDPFTGGGRYVPGSSGSSNTLPTADPFTGAGRYV
15 PGSASMGTTMAGVDPFTGNSAYRSAASKTMNIYFPKKEAVTFDQANPTQILGK
LKLNGTAPEEKKLTEDDLILLEKILSLICNSSSEKPTVQQLQILWKAINCPEDIV
FPALDILRLSIKHPSVNENFCNEKEGAQFSSHLINLLNPKGKPANQLLALRTFC
NCFVGQAGQKLMMSQRESLMSHAIELKSGSNKNI (SEQ ID NO: 547);
HIALATLALNYSVCFHKD (SEQ ID NO: 548); HNIEGKAQCLSLISTILEVVQ
20 DLEATFRLLVALGTLISDDSNVQLAKS (SEQ ID NO:549); LGVDSQIKKYSS
VSEPAKVSECCRFILNLL (SEQ ID NO:550); and/or YEGKEFDYVFSIDVNEGGPS
YKLPYNTSDDPWLTAYNFLQKNDLNPMFLDQVAKFIIDNTKGQMLGLGNPSF
DPFTGGGRYVPGSSGSSNTLPTADPFTGAGRYVPGSASMGTTMAGVDPFTGN
SAYRSAASKTMNIYFPKKEAVTFDQANPTQILGKLKELNGTAPEEKKLTEDDLI
25 LLEKILSLICNSSSEKPTVQQLQILWKAINCPEDIVFPALDILRLSIKHPSVNENFC
NEKEGAQFSSHLINLLNPKGKPANQLLALRTFCNCFVGQAGQKLMMSQRESL
MSHAIELKSGSNKNIHIALATLALNYSVCFHKDHNIEGKAQCLSLISTILEVVQD
LEATFRLLVALGTLISDDSNVQLAKSLGVDSQIKKYSSVSEPAKVSECCRFILN
LL (SEQ ID NO:551). Polynucleotides encoding these polypeptides are also
30 encompassed by the invention. These polypeptides share significant homology with
phospholipase A2 activating protein which is thought to be important in signal
transduction (see, e.g., Wang et al., Gene 161(2):237-241 (1995)).

- 35 This gene is expressed primarily in endothelial cells, to a less extent in placenta, endometrial stromal cells, osteosarcoma, testis tumor, muscle, and infant brain that are likely to be rich in blood vessels.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a

biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, disorders in vascular system, aberrant angiogenesis, tumor angiogenesis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the vascular system or tumors, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution of this gene in endothelial cells and several potential highly vascularized tissues and its homology to phospholipase A2 activating protein suggest that this gene may be involved in transducing signals for endothelial cells in angiogenesis or vasculogenesis.

FEATURES OF PROTEIN ENCODED BY GENE NO: 89

In specific embodiments, polypeptides of the invention comprise the sequence:
 YPNQDGDILRDQVLHEHIQRLSKVVTANHRALQIPEVYLREAPWPSAQSEIRTIS
 20 AYKTPRDKVQCILRMCSTIMNLLSLANEDSVPGADDFVPVLVFLIKANPPCLL
 STVQYISSFYASCLSGEESYWWMQFTA AVE (SEQ ID NO:552); YPNQDGDILR
 DQVLHEHIQRLSKVVTANHRALQIPEVYLREAPWPSAQSEIRTISAYKTPRDKVQ
 CILRMCSTIMNLLSLANEDSVPGADDFVPVLVFLIKANPPCLLSTVQYISSFYA
 SCLSGEESYWWMQFTA AVEFIKTI (SEQ ID NO:553); YPNQDGDILRDQVL (SEQ
 25 ID NO:554); EAPWPSAQSEI (SEQ ID NO:555); PVLVFLIKANP (SEQ ID
 NO:560); SGEESYWWMQFTA AVEFIKTI (SEQ ID NO:556); ADDFVPVLV
 FLIKANPP (SEQ ID NO:557); YKTPRDKVQCIL (SEQ ID NO:558); and/or
 GADDFVPVLVFLIK (SEQ ID NO:559). The translation product of this gene shares
 sequence homology with human ras inhibitor and yeast VPS9p which is thought to be
 30 important in golgi vacuole transport.

This gene is expressed primarily in T cells and melanocytes and to a lesser extent in a variety of other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, dysfunction and disorders involving T cells and melanocytes. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing

immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to ras inhibitor indicates that polynucleotides and polypeptides corresponding to this gene are useful for regulating signal transduction; diagnosis and treatment of disorders involving T cells and melanocytes.

FEATURES OF PROTEIN ENCODED BY GENE NO: 90

This gene maps to chromosome 9 and therefore polypeptides of the invention can be used in linkage analysis as a marker for chromosome 9. The translation product of this gene shares sequence homology with neuronal olfactomedin-related ER localized protein which is thought to be important in influence the maintenance, growth, or differentiation of chemosensory cilia on the apical dendrites of olfactory neurons. In specific embodiments, polypeptides of the invention comprise the sequence: SARASTQPPAGQHGPC (SEQ ID NO:561); MPGRWRWQRDMHPARKLLSLL FLILMGTELTQD (SEQ ID NO:562); SAAPDSLRRSSKGSTRGSL (SEQ ID NO:563); AAIVIWGRGKSESRIAKTPGI (SEQ ID NO:564); FRGGGTLVLPPTHT PEWLIL (SEQ ID NO:567); PLGITLPLGAPETGGGD (SEQ ID NO:565); and/or CAAETWKGSQRAGQLCALLA (SEQ ID NO:566).

This gene is expressed in pineal gland.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neurological and endocrinological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the neurological or endocrine systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e.,

the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 323 as residues: Leu-20 to Ala-26, Arg-32 to Arg-39, Thr-104 to Gly-112.

5 The tissue distribution and homology to olfactomedin-related protein indicates that polynucleotides and polypeptides corresponding to this gene are useful for maintenance, growth, or differentiation of neuron cells in pineal gland, therefore, may be useful for diagnosis and treatment of neurological disorders in pineal gland.

FEATURES OF PROTEIN ENCODED BY GENE NO: 91

10 This gene is expressed primarily in prostate and apoptotic T cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, prostate disease and T cell dysfunction. Similarly, polypeptides and
15 antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the prostate cancer, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial
20 fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for detect abnormal activity in prostate and T cells
25 or probably treatment of this abnormality.

FEATURES OF PROTEIN ENCODED BY GENE NO: 92

This gene is expressed primarily in prostate and to a lesser extent in smooth muscle cells, fibroblasts, and placenta.

30 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, disorders in prostate or vascular system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes
35 for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the prosate or vascular system, expression of this gene at significantly higher or lower levels may be routinely detected in certain

tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for regulating function of prostate or highly vascularized tissues, e.g. placenta.

10 **FEATURES OF PROTEIN ENCODED BY GENE NO: 93**

This gene is expressed primarily in embryos and fetal tissues stage human and to a lesser extent in a wide variety of other proliferative tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, disorders in embryonic development and cell proliferation. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the embryonic tissues and proliferative cells, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis or treatment of abnormalities in developing and proliferative cells and organs.

30 **FEATURES OF PROTEIN ENCODED BY GENE NO: 94**

The translation product of this gene shares sequence homology with transformation related protein which is thought to be important in transformation.

This gene is expressed primarily in female reproductive tissues, i.e., breast cancer cells, placenta, and ovary and to a lesser extent in fetal lung.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are

not limited to, cancer or dysfunction of reproductive tissues. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproduction system,

5 expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the

10 disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 327 as residues: Ser-50 to Pro-61.

The tissue distribution and homology to transformation related protein indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of conditions caused by transformation, i.e. tumorigenesis in

15 reproductive organs, e.g. breast, placenta, and ovary.

FEATURES OF PROTEIN ENCODED BY GENE NO: 95

This gene is expressed primarily in testes, rhabdomyosarcoma, infant brain and to a lesser extent in some tumors and highly vascularized tissues.

20 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, tumorigenesis, abnormal angiogenesis, and/or neurological disorders. ,

Similarly, polypeptides and antibodies directed to these polypeptides are useful in

25 providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the tumor tissues or vascular tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or

30 another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 328 as residues: Arg-46 to Trp-54, Pro-60 to Ile-69, Asn-116 to Ala-122, Arg-147 to Lys-153, Ser-158 to Glu-170, Ile-399 to

35 Ser-405, Pro-486 to Met-499, Pro-502 to Asp-508.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for a range of disease states including treatment of

tumor or vascular disorders and the treatment of neurological disorders such as Alzheimer's Disease, Parkinson's Disease, Huntingtons Disease, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder and panic disorder.

5 FEATURES OF PROTEIN ENCODED BY GENE NO: 96

This gene maps to chromosome 7 and therefore polynucleotides of the present invention can be used in linkage analysis as a marker for chromosome 7. The translation product of this gene is homologous to the *Clostridium perfringens* enterotoxin (CPE) receptor gene product and shares sequence homology with a human ORF specific to prostate and a glycoprotein specific to oligodendrocytes both of which are tissue specific proteins. (See e.g., Katahira et al., J Cell Biol. 136(6):1239-1247 (1997). PMID: 9087440; UI: 97242441.

This gene is expressed primarily in pancreas tumor and ulcerative colitis and to a lesser extent in several tumors and normal tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, pancreatic disorder, ulcerative colitis, tumors and food poisoning. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the digestive system or tumorigenic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 329 as residues: Gly-147 to Met-152, Cys-177 to Lys-188.

The tissue distribution and homology to prostate and oligodendrocyte-specific protein indicates that polynucleotides and polypeptides corresponding to this gene are useful for marker of diagnosis or treatment of disorder in pancreas, ulcerative colitis, and tumors. Furthermore, identity to the human receptor for *Clostridium perfringens* enterotoxin indicates that the soluble portion of this receptor could be used in the treatment of food poisoning associated with *Clostridia perfringens* by blocking the activity of perfringens enterotoxin.

FEATURES OF PROTEIN ENCODED BY GENE NO: 97

The translation product of this gene shares sequence homology with ATPase which is thought to be important in metabolism.

- 5 This gene is expressed primarily in testes and several hematopoietic cells and to a lesser extent in other tissues.

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, leukemia and hematopoietic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoietic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 330 as residues: Leu-37 to Ala-42.

The tissue distribution and homology to ATPase indicates that polynucleotides and polypeptides corresponding to this gene are useful for marker of diagnosis and treatment of leukemia and other hematopoietic disorders.

25 **FEATURES OF PROTEIN ENCODED BY GENE NO: 98**

- In specific embodiments, polypeptides of the invention comprise the sequence: MRSARPSLGCLPSWAFSQUALNI (SEQ ID NO:568); LLGLKGLAPAEISAVCE KGNFN (SEQ ID NO:569); VAHGLAWSYYIGYLRILPELQARIR (SEQ ID NO:570); TYNQHYNLLRGAVSQRC (SEQ ID NO:571); ILLPLDCGVDPNLSM ADPNIRFLDKLPQQTGDRAGIKDRVYSN (SEQ ID NO:572); SIYELLENGQRAGT CVLEYATPLQTLFAMSQYSQAGFSGEDRLEQ (SEQ ID NO:573); AKLFCRTLE DILADAPESQNNCRLLIAYQEPADDSSFSLSQEVLRLRQEEKEEVTVGSLKTS AV PSTSTMSQEPELLISGMEKPLPLRTDFS (SEQ ID NO:574); and/or LLGLKGLA PAEISAVCEKGNFNVAHGLAWSYYIGYLRILPEL (SEQ ID NO:575).

- 35 Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in prostate BPH and to a lesser extent in bone marrow.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, benign prostatic hypertrophy or prostate cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the male urinary system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 331 as residues: Ile-60 to Asn-69, Leu-106 to Asp-112, Glu-130 to Gly-136, Phe-160 to Glu-167, Pro-184 to Cys-190, Glu-197 to Ser-202, Arg-215 to Glu-221, Thr-237 to Pro-242.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis or treatment of benign prostatic hypertrophy or prostate cancer.

FEATURES OF PROTEIN ENCODED BY GENE NO: 99

This gene is expressed primarily in salivary gland.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, disorders or injuries of the salivary gland. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of glandular tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment of disorders of, or injuries to the salivary gland or other glandular tissue.

FEATURES OF PROTEIN ENCODED BY GENE NO: 100

This gene maps to chromosome 15, accordingly, polynucleotides of the invention can be used in linkage analysis as a marker for chromosome 15. The translation product of this gene shares sequence homology with a *C.elegans* gene of unknown function. In specific embodiments, polypeptides of the invention comprise the sequence: DPRVRLNSLTCKHIFISLTQ (SEQ ID NO:583); TMKLLKLRNIV KLSLYRHFTN (SEQ ID NO:576); TLILAVAASIVFIWTTMKFRI (SEQ ID NO:577); VTCQSDWRELWVDDAIWRLLFMSILFVI (SEQ ID NO:578); MVLWR PSANNQRFAFSPLSEEEEEDEQ (SEQ ID NO:580); KEPMLKESFEGMKMRS TKQEPNGNSKVNKAQEDDL (SEQ ID NO:584); and/or KWVEENVPSVTDVALP ALLDSDEERMITHFERSKME (SEQ ID NO:582). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in thyroid and to a lesser extent in osteoclastoma, kidney medulla, and lung.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, thyroid dysfunction or cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the endocrine system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 333 as residues: Lys-107 to Leu-124, Glu-150 to Thr-159, Pro-173 to Asp-179, Ser-192 to Ser-201.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of thyroid dysfunction or cancer.

FEATURES OF PROTEIN ENCODED BY GENE NO: 101

This gene maps to chromosome 16, therefore polynucleotides of the invention can be used in linkage analysis as a marker for chromosome 16. In specific embodiments, polypeptides of the invention comprise the sequence:

IRHELTVLRDTRPACA (SEQ ID NO:585); and/or MDFXMALIYD (SEQ ID NO:586). Polynucleotides encoding these polypeptides are also encompassed by the invention.

5 This gene is expressed primarily in kidney cortex and to a lesser extent in adult brain, corpus colosum, hippocampus, and frontal cortex.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neurological disorders. Similarly, polypeptides and antibodies directed to
10 these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial
15 fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment or diagnosis of neurological
20 disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 102

In specific embodiments, polypeptides of the invention comprise the sequence:
MQEMMRNQDRALSNLESIPGGYNA (SEQ ID NO:587); LRRMYTDIQEPMLSA
25 AQEQF GGNPF (SEQ ID NO:588); ASLVNTSSGEGSQPSRTENRDPLPNPWAP
QT (SEQ ID NO:589); SQSSASSGTASTVGGTTGSTASGTSGQSTTAPNLVPGV
GASMFNTPG MQSLLQQITENPQLMQNMLSAPY (SEQ ID NO:590);
MRSMMQSLSQNPDLAAQMMLNNPLFAGNPQLQE QMRQQLPTFLQQ (SEQ ID
NO:591); MQNPDTLSAMSNPRAMQALLQIQQLQTLATEAPGLIPGFTPGLG
30 ALGSTGGSSGTNGSNATPSENTSPTAGT (SEQ ID NO:592); TEPGHQQFI
QQMLQALAGVNPQLQNPEVRFQQLEQLSAMGFLNREANLQALIATGGDINAA
IERLLGSQPS (SEQ ID NO:593); RNPAMMQEMMRNQDRALSNLESIPGGY
NALRRMYTDIQEPMLSAA (SEQ ID NO:594); GNPFA SLVNTSS (SEQ ID
NO:595); ENRDPLPNPWA (SEQ ID NO:595); GKILKDQDTLSQHGIHD (SEQ ID
35 NO:597); GLTVHLVIKTQNRP (SEQ ID NO:598); SELQSQMQRQLLSNPPEMM
(SEQ ID NO:599); PEISHMLNNPDIMR (SEQ ID NO:600); and/or
RQLIMANPQMQQLIQRNP (SEQ ID NO:601). Polynucleotides encoding these

polypeptides are also encompassed by the invention.

This gene is expressed primarily in breast.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, breast cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of tumor systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of some types of breast cancer.

FEATURES OF PROTEIN ENCODED BY GENE NO: 103

The translation product of this gene shares sequence homology with secreted serine proteases and lysozyme C precursor, which is thought to be important in bacteriolytic function. In specific embodiments, polypeptides of the invention comprise the sequence: NLCHVDCQDLLNP NLLAGIHCAKRIVS (SEQ ID NO:602); LDGFEGYSLSDWLCLAFVESKFN (SEQ ID NO:603); NENADGSFDYGLFQINSHYWCN (SEQ ID NO:604); and/or NLCHVDCQDLLNP NLLAGIHCAKRIVS (SEQ ID NO:605). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in testes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, infection. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or

another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 336 as residues: Ile-62 to Phe-70, Asn-78 to Asn-84.

The tissue distribution and homology to lysozyme C precursor indicates that polynucleotides and polypeptides corresponding to this gene are useful for boosting the monocyte-macrophage system and enhance the activity of immunoagents.

10 **FEATURES OF PROTEIN ENCODED BY GENE NO: 104**

This gene is expressed primarily in apoptotic T-cell.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of some immune disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 105

The translation product of this gene shares sequence homology with ARI protein of Drosophila (accession 2058299; EMBL: locus DMARIADNE, accession X98309), which is thought to be important in axonal path-finding in the central nervous system. In specific embodiments, polypeptides of the invention comprise the sequence IREVNEVIQNPAT (SEQ ID NO:606); ITRILLSHFNWDKEKLMERYF DGNLEKLFA (SEQ ID NO:607); NTRSSAQDMPCQICYLNYPNSYF (SEQ ID NO:608); TGLECGHKFCMQCWSEYLTTKIMEEGMGQTISCPAHG (SEQ ID NO:614); CDILVDDNTVMRLITDSKVKLKYQHLITNSFVECNRLWKWCPAPD CHHVVKVQYPDAKPV (SEQ ID NO:609); CDILVDDNTVMRLITDSK

VKLKYQHLITNSFVECNRLWKWCPAPDCHHVVKV (SEQ ID NO:610);
 GCNHMVCRNQNKAEFCWVCLGPWEPHGSAWYNCNRYNEDDAKAARDAQE
 RSRAALQRYL (SEQ ID NO:611); FYCNRYMNHMQSLRFEHKL YAQVKQ
 KMEEMQQHNMSWIEVQFLKKAVDVLCQCRATLMT (SEQ ID NO: 612);
 5 YVFAFYLLKKNNQSIIFENNQADLENATEVLSGYLERDISQDSLQDIKQKVQDKY
 RYCESR (SEQ ID NO:613) Polynucleotides encoding these polypeptides are also
 encompassed by the invention.

This gene is expressed primarily in adult brain, and to a lesser extent in
 endometrial tumor, melanocytes, and infant brain.

10 Therefore, polynucleotides and polypeptides of the invention are useful as
 reagents for differential identification of the tissue(s) or cell type(s) present in a
 biological sample and for diagnosis of diseases and conditions, which include, but are
 not limited to, diseases or injuries involving axonal path development. Similarly,
 polypeptides and antibodies directed to these polypeptides are useful in providing
 15 immunological probes for differential identification of the tissue(s) or cell type(s). For
 a number of disorders of the above tissues or cells, particularly of the central nervous
 system, expression of this gene at significantly higher or lower levels may be routinely
 detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g.,
 serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample
 20 taken from an individual having such a disorder, relative to the standard gene
 expression level, i.e., the expression level in healthy tissue or bodily fluid from an
 individual not having the disorder.

The tissue distribution and homology to ARI protein indicates that
 polynucleotides and polypeptides corresponding to this gene are useful for treatment of
 25 disease states or injuries involving axonal path development, including
 neurodegenerative diseases and nerve injury.

FEATURES OF PROTEIN ENCODED BY GENE NO: 106

The translation product of this gene shares sequence homology with cytochrome
 30 b561 [Sus scrofa] which is thought to be an integral membrane protein of
 neuroendocrine storage vesicles of neurotransmitters and peptide hormones.

This gene is expressed primarily in frontal cortex and to a lesser extent in
 rhabdomyosarcoma.

Therefore, polynucleotides and polypeptides of the invention are useful as
 35 reagents for differential identification of the tissue(s) or cell type(s) present in a
 biological sample and for diagnosis of diseases and conditions, which include, but are
 not limited to, neurological disorders. Similarly, polypeptides and antibodies directed to

these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 339 as residues: Ser-18 to Pro-24.

The tissue distribution and homology to cytochrome b561 [*Sus scrofa*] indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of neurological disorders. This gene may also be important in regulation of some types of cancers.

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FEATURES OF PROTEIN ENCODED BY GENE NO: 107

In specific embodiments, polypeptides of the invention comprise the sequence: MWGYLFVDAAWNFLGCLICGW (SEQ ID NO:615); MHFISSGNVSAIRSSILLRXSLSYLGNCRLRVSAIFVYFLLFLLLS (SEQ ID NO:616); and/or MDQALRGSPSEGFSTDPSPQVGRQIPSPFPWRRLVLPKASGCFLEREWLVCVFKLRTRPGAEA HAYNSSILGGRGKGIT (SEQ ID NO:617). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in pancreas tumor and to a lesser extent in cerebellum.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, pancreatic tumors. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the endocrine system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred

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epitopes include those comprising a sequence shown in SEQ ID NO: 340 as residues: Pro-22 to Phe-33.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of pancreatic tumors.

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FEATURES OF PROTEIN ENCODED BY GENE NO: 108

This gene maps to chromosome 17 and therefore polynucleotides of the invention can be used in linkage analysis as a marker for chromosome 17. In specific embodiments, polypeptides of the invention comprise the sequence:

- 10 MLPALASCCHFSPPEQAARLKKLQEQEKQQKVEFRKRMEKEVSDFIQDSGQIK
KKFQPMNKIERSILHDVVEVAGLTSFSFGEDDDCRYVMIFKKEFAPSDEELDSY
RRGEEWDPQKAEEKRNXKELAQRR (SEQ ID NO:618); EEEAAQQGPVVV
SPASDYKDKYSHLIGKGAAKDAAHMLQANKTYGCXPVANKRDTRSIEEAMNE
IRAKKRLRQSGE (SEQ ID NO:619); PPRRPAQLPLTPGAGQGAGRDKAAAIRA
15 HPGAPPLNLLP (SEQ IDNO:620); AVPQAGGKQVFDLSPLELGYVRGMCVCV
(SEQ ID NO:621) and/or MLPALASCCHFSPPEQAARLKKLQEQEKQQKVEFRK
RMEKEVSDFIQDSGQIKKKFQPMNKIERSILHDVVEVAGLTSFSFGEDDDCRYV
MIFKKEFAPSDEELDSYRRGEEWDPQKAEEKRNXKELAQRRQEEAAQQGPVVV
SPASDYKDKYSHLIGKGAAKDAAHMLQANKTYGCXPVANKRDTRSIEEAMNE
20 IRAKKRLRQSGE (SEQ ID NO:622). Polynucleotides encoding these polypeptides
are also encompassed by the invention. The translation product of this gene shares
sequence homology with FSA-1 which may play a role as a structural protein
component of the acrosome.

This gene is expressed primarily in fetal kidney and sperm.

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Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, male reproductive disorders, especially involving acrosomal dysfunction. Similarly, polypeptides and antibodies directed to these polypeptides are useful in
30 providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the male reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or
35 cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an

individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 341 as residues: Glu-8 to Asn-35.

The tissue distribution and homology to FSA-1 indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment of infertility due to
5 acrosomal disfunction of sperm.

FEATURES OF PROTEIN ENCODED BY GENE NO: 109

This gene is expressed primarily in pituitary and to a lesser extent in epididymus.

10 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, male reproductive disorders. Similarly, polypeptides and antibodies
15 directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the male reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma,
20 urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID
NO: 342 as residues: Met-1 to Trp-6.

Because the gene is found in both pituitary and epididymus, this indicates that
25 polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of male reproductive disorders. This may involve a secreted peptide produced in the pituitary targeting the epididymus.

FEATURES OF PROTEIN ENCODED BY GENE NO: 110

30 In specific embodiments, polypeptides of the invention comprise the sequence: LLCPVLNSGXSWNFPHPQSQPEYSFHGFHSTRLWI (SEQ ID NO:623); and/or PSTPWFLFLLGLTCPFSTSHPRWDSIPP (SEQ ID NO:624). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in resting T-cells. .

35 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are

not limited to, T-cell disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of certain immune disorders, especially those involving T-cells.

FEATURES OF PROTEIN ENCODED BY GENE NO: 111

This gene is expressed primarily in cerebellum and whole brain and to a lesser extent in infant brain and fetal kidney.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neurological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 344 as residues: Asp-48 to Gly-55.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of neurological disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 112

The translation product of this gene shares sequence homology with yeast mitochondrial ribosomal protein homologous to ribosomal protein s15 of E.coli which

is thought to be important in the early assembly of ribosomes (See Accession No. M38016). This gene maps to chromosome 1, and therefore, may be used as a marker in linkage analysis for chromosome 1.

This gene is expressed primarily in developmental tissues.

5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, development of cancers and tumors in addition to healing wounds. Similarly, polypeptides and antibodies directed to these polypeptides are useful in
10 providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and developmental expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or
15 another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to ribosomal protein s15 of *E. coli* indicates that polynucleotides and polypeptides corresponding to this gene are useful for
20 diseases related to the assembly of ribosomes in the mitochondria which is important in the translation of RNA into protein. Therefore, this indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and intervention of multiple tumors as well as in healing wounds which are thought to be under similar regulation as developmental tissues. Protein, as well as, antibodies directed against the
25 protein have utility as tumor markers, in addition to immunotherapy targets, for the above listed tumors and tissues.

FEATURES OF PROTEIN ENCODED BY GENE NO: 113

The translation product of this gene shares sequence homology with human
30 poliovirus receptor precursors which are thought to be important in viral binding and uptake. Preferred polypeptide fragments comprise the following amino acid sequence:
ELISISNVALADEGEYTCSTFTMPVRTAKSLVTVLGIPQKPIITGYKSSLREKDT
ATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFTVSSSVTFQVTR
EDDGASIVCSVNHESLKGADRSTSQRIVLYTPTAMIRPDPPHPREGQKLLHLC
35 EGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGS
YKAYYTLNVND (SEQ ID NO:625). Also preferred are polynucleotide fragments encoding these polypeptide fragments (See Accession No. gnl|PID|d1002627).

This gene is expressed almost exclusively in human brain tissue.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, susceptibility to viral disease and diseases of the CNS especially cancers of that system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 346 as residues: Leu-26 to Asp-37, Lys-53 to Ser-59.

The tissue distribution and homology to poliovirus receptor precursors indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and prevention of diseases that involve the binding and uptake of virus particles for infection. It might also be helpful in genetic therapy where the goal is to insert foreign DNA into infected cells. With the help of this protein, the binding and uptake of this foreign DNA might be aided. In addition, it is expected that over expression of this gene will indicate abnormalities involving the CNS, particularly cancers of that system.

FEATURES OF PROTEIN ENCODED BY GENE NO: 114

The translation product of this gene shares sequence homology with YO87_CAEEL hypothetical 28.5 KD protein ZK1236.7 in chromosome III of *Caenorhabditis elegans* in addition to alpha-1 collagen type III (See Accession No. gi537432). One embodiment for this gene is the polypeptide fragment(s) comprising the following amino acid sequence: VPELPDRVHQLHQA VQG CALGRPGFPGGPTH SGHHKSHPGPAGGDYNRCDRPGQVHLHNPRGTGRRGQLHPTAGPGVHRRA CPSQQPLPHRLGPGVPCPSPLTPVLPSWTQSWCG LPGYTSSS (SEQ ID NO:630). An additional embodiment is the polynucleotide fragment(s) encoding these polypeptide fragments

This gene is expressed primarily in brain cells and to a lesser extent in activated B and T cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neurodegeneration and immunological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the neural and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 347 as residues: Glu-34 to Glu-39, Gly-51 to Ser-72, Ala-88 to Glu-93, Gln-100 to Val-105.

The tissue distribution and homology to YO87_CAEEL hypothetical 28.5 KD protein ZK1236.7 in chromosome III of *Caenorhabditis elegans* as well as to a conserved alpha-1 collagen type III protein indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection and treatment of neurodegenerative disease states and behavioral disorders such as Alzheimer's Disease, Parkinson's Disease, Huntingtons' Disease, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder and panic disorders. Because the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, and leukemia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 115

The translation product of this gene shares sequence homology with alpha 3 type IX collagen which is thought to be important in hyaline cartilage formation via its ability to uptake inorganic sulfate by cells (See Accession No. gi975657). One embodiment of this gene is the polypeptide fragment comprising the following amino acid sequence: SLRRPRSAAXQTLTFLSSVSSASSSALPGSREPCDPRAPPPR SGSAASCCSCCCSCPRRRAPLRSPRGSKRRIRQREVVDLYNGMCLQGPAVGPRD GSPGANGIPGTPGIPGRDGFKEGKECLRESFEESWTPNYKQCSWSSLNY GIDLGKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSPG LPIEAIYLDQGSPPEMNSTINIHR TSSVEGLCEGIGAGLVDVAIWVGTCSDYPKG DASTGWNSVSRIIIIEELPK (SEQ ID NO:634). An additional embodiment are the

polynucleotide fragments encoding this polypeptide fragment.

This gene is expressed primarily in smooth muscle and to a lesser extent in synovial tissue.

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, dwarfism, spinal deformation, and specific joint abnormalities as well as chondrodysplasias i.e., spondyloepiphyseal dysplasia congenita, familial osteoarthritis, Atelosteogenesis type II, metaphyseal chondrodysplasia type Schmid and autoimmune
10 disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the skeletal system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily
15 fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to alpha 3 type IX collagen indicates that
20 polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of diseases associated with the mutation in this gene which leads to the many different types of chondrodysplasias. By the use of this product, the abnormal growth and development of bones of the limbs and spine could be routinely detected or treated in utero since the protein or muteins thereof could affect epithelial cells early in
25 development and later the chondrocytes of the developing craniofacial structure.

FEATURES OF PROTEIN ENCODED BY GENE NO: 116

The translation product of this gene shares sequence homology with retrovirus-related reverse transcriptase which is thought to be important in viral replication. One
30 embodiment for this gene is the polypeptide fragments comprising the following amino acid sequence: TKKENC RPASLMNIDTKILNKILMNQ (SEQ ID NO:640). An additional embodiment is the polynucleotide fragments encoding these polypeptide fragments (See Accession No. pirlA25313|GNHUL1).

This gene is expressed primarily in human meningioma.

35 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are

not limited to, retroviral diseases such as AIDS, and possibly certain cancers due to transactivation of latent cell division genes. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to retrovirus-related reverse transcriptase indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection and treatment of diseases and maladies associated with retroviral infection since a functional reverse transcriptase (RT) or RT-like molecule is an integral component of the retroviral life cycle.

FEATURES OF PROTEIN ENCODED BY GENE NO: 117

The translation product of this gene shares sequence homology with an unknown gene from *C. elegans*, as well as weak homolog with mammalian metaxin, a gene contiguous to both thrombospondin 3 and glucocerebrosidase, is known to be required for embryonic development. Preferred polypeptide fragments comprise the following amino acid sequence: MCNLPIKVVCRAAEYMSPSGKVPXXHVGNGQ VVSELGPIVQFVKAKGHSLSDGLEEVQKAEMKAYMELVNNMLLTAELYLQWC DEATVGXITHXRYGSPYPWPLXHILAYQKQWEVKKXKAIGWGKKTLDQVLE DVDQCCQALSQRLGTQPYFFNKQPTELD LVFGHLYTILTTQLTNDELSEKVKN YSNLLAFCRRI EQHYFEDRGKGRLS (SEQ ID NO:641); MCNLPIKVVCRAAE YMSPSGKVPXXHVGNGQVVSELGPIVQFVK (SEQ ID NO:642). Also preferred are polynucleotide fragments encoding these polypeptide fragments (See Accession No. gil1326108).

This gene is expressed primarily in fetal tissues and to a lesser extent in hematopoietic cells and tissues, including spleen, monocytes, and T cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cancer; lymphoproliferative disorders; inflammation; chondrosarcoma, and Gaucher disease. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification

of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoietic and embryonic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of cancer and other proliferative disorders. Expression in embryonic tissue and other cellular sources marked by proliferating cells indicates that this protein may play a role in the regulation or cellular division. Additionally, the expression in hematopoietic cells and tissues indicates that this protein may play a role in the proliferation, differentiation, and survival of hematopoietic cell lineages. Thus, this gene may be useful in the treatment of lymphoproliferative disorders, and in the maintenance and differentiation of various hematopoietic lineages from early hematopoietic stem and committed progenitor cells.

FEATURES OF PROTEIN ENCODED BY GENE NO: 118

The translation product of this gene shares sequence homology with reverse transcriptase which is important in the synthesis of a cDNA chain from an RNA molecule, and is a method whereby the infecting RNA chains of retroviruses are transcribed into their DNA complements. One embodiment for this gene is the polypeptide fragment comprising the following amino acid sequence:
 MXXXNSHITIFTLNVNGLNAPNERHRLANWIQSQDQVCCIQETHLTGRDTHRL
 KIKGWRKIYQANGKQKK (SEQ ID NO:647). An additional embodiment is the polynucleotide fragments comprising polynucleotides encoding these polypeptide fragments (See Accession No. gil2072964).

This gene is expressed primarily in skin and to a lesser extent in neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancer, hematopoietic disorders; inflammation; disorders of immune surveillance. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the epidermis and/or hematopoietic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and

wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

- 5 The tissue distribution and homology to reverse transcriptase indicates that polynucleotides and polypeptides corresponding to this gene are useful for cancer therapy. Expression in the skin also indicates that this gene is useful in wound healing and fibrosis. Expression by neutrophils also indicates that this gene product plays a role in inflammation and the control of immune surveillance (i.e. recognition of viral
- 10 pathogens). Reverse transcriptase family members are also useful in the detection and treatment of AIDS.

FEATURES OF PROTEIN ENCODED BY GENE NO: 119

- 15 The translation product of this gene shares sequence homology with reverse transcriptase which is important in the synthesis of a cDNA copy of an RNA molecule, and is a method whereby a retrovirus reverse-transcribes its genome into an inheritable DNA copy.

 This gene is expressed primarily in the frontal cortex of brain.

- 20 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cancer and neurodegenerative disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders
- 25 of the above tissues or cells, particularly of the CNS and peripheral nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e.,
- 30 the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

- The tissue distribution and homology to reverse transcriptase suggest that this is useful in the treatment of cancer and AIDS. The expression in brain indicates that it plays a role in neurodegenerative disorders and in neural degeneration.

FEATURES OF PROTEIN ENCODED BY GENE NO: 120

One embodiment of this gene has homology to a hypothetical protein in *Schizosaccharomyces pombe* (See Accession No. 2281980). Another embodiment for this gene is the polypeptide fragments comprising the following amino acid sequence:

5 IYHLHSWIFFHFKRAFCMCFITMKVIHAHCSKLRKCXNAQISVFCTTLTASYPT
(SEQ ID NO:651). An additional embodiment is the polynucleotide fragments encoding these polypeptide fragments. This gene maps to chromosome 18, and therefore, may be used as a marker in linkage analysis for chromosome 18.

10 This gene is expressed primarily in adult hypothalamus and to a lesser extent in infant brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neurodegenerative disorders; endocrine function; and vertigo. Similarly,
15 polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain, CNS and peripheral nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded
20 tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
25 corresponding to this gene are useful for the treatment and diagnosis of neurodegenerative disorders; diagnosis of tumors of a brain or neuronal origin; treatments involving hormonal control of the entire body and of homeostasis, behavioral disorders, such as Alzheimer's Disease, Parkinson's Disease, Huntington's Disease, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder and
30 panic disorder. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo.

FEATURES OF PROTEIN ENCODED BY GENE NO: 121

35 The translation product of this gene shares sequence homology with the human IRLB protein which is thought to be important in binding to a c-myc promoter element and thus regulating its transcription (See Accession No. gil33969). This gene maps to

chromosome 1, and therefore, may be used as a marker in linkage analysis for chromosome 1.

This gene is expressed primarily in brain and breast and to a lesser extent in a variety of hematopoietic tissues and cells.

5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cancer of the brain and breast; lymphoproliferative disorders; neurodegenerative diseases. Similarly, polypeptides and antibodies directed to these
10 polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the CNS, breast, and immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial
15 fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of cancer of the
20 brain, breast, and hematopoietic system. In addition, it may be useful for the treatment of neurodegenerative disorders, as well as disorders of the hematopoietic system, including defects in immune competency and inflammation. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and immunotherapy targets for the above listed tumors and tissues.

25

FEATURES OF PROTEIN ENCODED BY GENE NO: 122

The translation product of this gene shares sequence homology with an ATP synthase, a key component of the proton channel that is thought to be important in the translocation of protons across the membrane.

30 This gene is expressed primarily in T cell lymphoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, T cell lymphoma. Similarly, polypeptides and antibodies directed to these
35 polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or

lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to ATP synthase indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment of defects in proton transport, homeostasis, and metabolism, as well as the diagnosis and treatment of lymphoma. Because the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, and leukemia

FEATURES OF PROTEIN ENCODED BY GENE NO: 123

This gene maps to chromosome 15, and therefore, may be used as a marker in linkage analysis for chromosome 15.

This gene is expressed primarily in a variety of fetal tissues, including fetal liver, lung, and spleen, and to a lesser extent in a variety of blood cells, including eosinophils and T cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cancer (abnormal cell proliferation); T cell lymphomas; and hematopoietic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the fetus and immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of conditions involving cell proliferation. Expression of this gene in fetal tissues, as well as in a variety of blood cell lineages indicates that it may play a role in either cellular proliferation; apoptosis; or cell survival. Thus it may be useful in the management and

treatment of a variety of cancers and malignancies. In addition, its expression in blood cells suggest that it may play additional roles in hematopoietic disorders and conditions, and could be useful in treating diseases involving autoimmunity, immune modulation, immune surveillance, and inflammation..

5

FEATURES OF PROTEIN ENCODED BY GENE NO: 124

This gene is expressed primarily in placenta and to a lesser extent in pineal gland and rhabdomyosarcoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, developmental, endocrine, and female reproductive disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the [insert system where a related disease state is likely, e.g., immune], expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 357 as residues: Leu-69 to Val-76.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of disorders in development. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and immunotherapy targets for the above listed tumors and tissues.

FEATURES OF PROTEIN ENCODED BY GENE NO: 125

This gene is expressed primarily in benign prostatic hyperplasia.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of benign prostatic hyperplasia. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive

system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of benign prostatic hyperplasia. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and immunotherapy targets for the above listed tumors and tissues.

FEATURES OF PROTEIN ENCODED BY GENE NO: 126

This gene is expressed primarily in apoptotic T-cells and to a lesser extent in suppressor T cells and ulcerative colitis.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, diseases involving premature apoptosis, and immunological and gastrointestinal disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of disorders involving inappropriate levels of apoptosis, especially in immune cell lineages. Because the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases (such as AIDS), and leukemia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 127

This gene is expressed primarily in Raji cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, inflammation and T cell autoimmune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 360 as residues: Asp-23 to Gly-29.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of inflammation and T cell autoimmune disorders. Because the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases (such as AIDS), and leukemia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 128

The translation product of this gene shares sequence homology with an *C. elegans* coding region C47D12.2 of unknown function (See Accession No. gnllPIDle348986). One embodiment for this gene is the polypeptide fragments comprising the following amino acid sequence: EDDGFNRSIHEVILKNITWY SERVLTEISLGSLLLVVIRTIQYNMTRTRDKYLHTNCLAALANMSAQFRSLHQY AAQRISLFSLLSKKHNVLEQATQSLRGSLSNDVPLPDYAQDLNVIEEVIRMM LEIINSCLTNSLHHNPNLVALLYKRDLFEQFRTHPSFQDIMQNIDLVISFFSSRLL QAGS (SEQ ID NO:657); EDDGFNRSIHEVILKNITWYSERVLTEISLGSLLLVV (SEQ ID NO:658); RTIQYNMTRTRDKYLHTNCLAALANMSAQFRSLHQYAAQ RIISLFSLLSKKHNVLEQATQSLRGSLSNDVPLPDY AQD (SEQ ID NO:661); SCLTNSLHHNPNLVALLYKRDLFEQFRTHPSFQD IMQNIDLVISFFSSRLLQAGS (SEQ ID NO:660). An additional embodiment is the polynucleotide fragments encoding these polypeptide fragments. This gene maps to

chromosome 18, and therefore, may be used as a marker in linkage analysis for chromosome 18.

This gene is expressed primarily in smooth muscle and to a lesser extent in fetal liver.

5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, atherosclerosis and other cardiovascular and hepatic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing
10 immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the circulatory system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample
15 taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of circulatory system
20 disorders such as atherosclerosis, hypertension, and thrombosis. In addition, the tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection and treatment of liver disorders and cancers (e.g. hepatoblastoma, jaundice, hepatitis, liver metabolic diseases and conditions that are attributable to the differentiation of hepatocyte progenitor cells). In addition the
25 expression in fetus would suggest a useful role for the protein product in developmental abnormalities, fetal deficiencies, pre-natal disorders and various wound-healing models and/or tissue trauma.

FEATURES OF PROTEIN ENCODED BY GENE NO: 129

30 The translation product of this gene shares sequence homology with a ribosomal protein which is thought to be important in cellular metabolism, in addition to the *C.elegans* protein F40F11.1 which does not have a known function at the current time (See Accession No. gnllPIDle244552). Preferred polypeptide fragments comprise the following amino acid sequence:
35 MADIQTERAYQKQPTIFQNKRVLLGETGKEKLPRVTNKNIGLGFKDT
PRRLLRGTIDKKCPFTGNVSIRGRILSGVVTQDEDAEDHCHPPRLSALHPQVQ
PLREAPQEHVCTPVPL LQGRPDR (SEQ ID NO:662); MKMQRTIVIRRDYLH

YIRKYNRFEKRRHKNMSVHLSPCFRDVQIGDIVTVGECRPLSKTVRFNVLKVTK
 AAGTKKQFQKF (SEQ ID NO:663); MADIQTERAYQKQPTIFQNKKRVLLGET
 GK (SEQ ID NO:664); HCHPPRLSALHPQVQPLREAPQEHVCTPVPL LQGRPDR
 (SEQ ID NO:666); NIGLGFKDTPRLLRGTYIDKKCPFTGNVSIRGRILSGVVTQ
 5 (SEQ ID NO:669); MKMQRTIVIRRDYLHYIRKYNRFEKRRHKNMSVHLS (SEQ
 ID NO:667); CFRDVQIGDIVTVGECRPLSKTVRFNVLKVTKAAGTKKQFQKF
 (SEQ ID NO:668). Also preferred are polynucleotide fragments encoding these
 polypeptide fragments.

10 This gene is expressed primarily in Wilm's tumor and to a lesser extent in
 thymus and stromal cells.

Therefore, polynucleotides and polypeptides of the invention are useful as
 reagents for differential identification of the tissue(s) or cell type(s) present in a
 biological sample and for diagnosis of diseases and conditions, which include, but are
 not limited to, diseases affecting RNA translation. Similarly, polypeptides and
 15 antibodies directed to these polypeptides are useful in providing immunological probes
 for differential identification of the tissue(s) or cell type(s). For a number of disorders
 of the above tissues or cells, particularly of the Wilm's tumors, expression of this gene
 at significantly higher or lower levels may be routinely detected in certain tissues (e.g.,
 cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial
 20 fluid or spinal fluid) or another tissue or cell sample taken from an individual having
 such a disorder, relative to the standard gene expression level, i.e., the expression level
 in healthy tissue or bodily fluid from an individual not having the disorder. Preferred
 epitopes include those comprising a sequence shown in SEQ ID NO: 362 as residues:
 Thr-11 to Asp-20.

25 The tissue distribution and homology to a ribosomal protein indicates that
 polynucleotides and polypeptides corresponding to this gene are useful for diseases
 affecting RNA translation.

FEATURES OF PROTEIN ENCODED BY GENE NO: 130

30 The translation product of this gene shares sequence homology with a yeast
 DNA helicase which is thought to be important in global transcriptional regulation (See
 Accession No. gnllPIDle243594). One embodiment for this gene is the polypeptide
 fragments comprising the following amino acid sequence: IFYDSDWNPTVDQQA
 MDRAHRLGQTKQVTYRLICKGTIEERILQRAKEKSEIQRMVISG (SEQ ID
 35 NO:670); TRMIDLLEEYMVYRKHTYXRLDGSSKISERRDMVADFQNRNDI
 FVFLSTRAGGLGINLTAXDTVHF (SEQ ID NO:671); TRMIDLLEEYMVYRK
 HTYXRLDGSSKISERRDM (SEQ ID NO:674); RRDMMVADFQNRNDIFVFL

STRAGGLGINLTAXDTVHF (SEQ ID NO:675) , IFYDSDWNPTVDQQAMD
RAHRLGQTKQVTYRLICKG (SEQ ID NO:676); RLICKGTIEERILQRAK
EKSEIQRMVISG (SEQ ID NO:678). An additional embodiment is the polynucleotide
fragments encoding these polypeptide fragments.

5 This gene is expressed primarily in amygdala.

 Therefore, polynucleotides and polypeptides of the invention are useful as
reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions, which include, but are
not limited to, diseases and disorders of the brain. Similarly, polypeptides and
10 antibodies directed to these polypeptides are useful in providing immunological probes
for differential identification of the tissue(s) or cell type(s). For a number of disorders
of the above tissues or cells, particularly of the central nervous system, expression of
this gene at significantly higher or lower levels may be routinely detected in certain
tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma,
15 urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an
individual having such a disorder, relative to the standard gene expression level, i.e.,
the expression level in healthy tissue or bodily fluid from an individual not having the
disorder.

 The tissue distribution and homology to a DNA helicase indicates that
20 polynucleotides and polypeptides corresponding to this gene are useful for diseases
affecting RNA transcription, particularly developmental disorders and healing wounds
since the later are though to approximate developmental transcriptional regulation.

FEATURES OF PROTEIN ENCODED BY GENE NO: 131

25 This gene is expressed primarily in prostate and to a lesser extent in amygdala
and pancreatic tumors.

 Therefore, polynucleotides and polypeptides of the invention are useful as
reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions, which include, but are
30 not limited to, prostate enlargement and gastrointestinal disorders, particularly of the
pancreas and gall bladder. Similarly, polypeptides and antibodies directed to these
polypeptides are useful in providing immunological probes for differential identification
of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells,
particularly of the reproductive system, expression of this gene at significantly higher or
35 lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded
tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or
another tissue or cell sample taken from an individual having such a disorder, relative to

the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

5 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of prostate diseases, including benign prostatic hyperplasia and prostate cancer. In addition, the tissue distribution in tumors of the pancreas indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and intervention of these tumors, in addition to other tissues where expression has been indicated. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or
10 immunotherapy targets for the above listed tumors and tissues.

FEATURES OF PROTEIN ENCODED BY GENE NO: 132

This gene is expressed primarily in adult lung and to a lesser extent in hypothalamus.

15 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, pulmonary diseases and neurological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological
20 probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the pulmonary and respiratory systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample
25 taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of pulmonary and
30 respiratory disorders such as emphysema, pneumonia, and pulmonary edema and emboli. In addition, the tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioral disorders such as Alzheimer's Disease, Parkinson's Disease, Huntington's Disease, schizophrenia, mania, dementia, paranoia,
35 obsessive compulsive disorder and panic disorder. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental

disorders associated with the developing embryo, sexually-linked disorders, or disorders of the cardiovascular system.

FEATURES OF PROTEIN ENCODED BY GENE NO: 133

5 This gene is expressed primarily in human liver.

 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cirrhosis of the liver and other hepatic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the digestive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of liver disorders such as cirrhosis, jaundice, and Hepatitis. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

25 FEATURES OF PROTEIN ENCODED BY GENE NO: 134

 This gene is expressed primarily in fetal kidney and to a lesser extent in fetal liver and spleen.

 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, development and regeneration of liver and kidney and immunological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the digestive and excretory systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or

another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 367 as residues: Pro-70 to Arg-77, Tyr-102 to Thr-107.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of diseases of the kidney and liver, such as cirrhosis, kidney failure, kidney stones, and liver failure, hepatoblastoma, jaundice, hepatitis, liver metabolic diseases and conditions that are attributable to the differentiation of hepatocyte progenitor cells. In addition the expression in fetus would suggest a useful role for the protein product in developmental abnormalities, fetal deficiencies, pre-natal disorders and various wound-healing models and/or tissue trauma.

15 **FEATURES OF PROTEIN ENCODED BY GENE NO: 135**

This gene is expressed primarily in brain, bone marrow, and to a lesser extent in placenta, T cell, testis and neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neurodegenerative and immunological diseases and cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 368 as residues: Met-1 to His-6.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioral disorders such as Alzheimer's Disease, Parkinson's Disease, Huntingtons Disease, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder and panic disorder. In addition, the gene or gene product may also

play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, or sexually-linked disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 136

- 5 Translation product of this gene is homologous to the human WD repeat protein HAN11. Preferred polypeptide fragments comprise the following amino acid sequence:
- MSLHGKRKEIYKYEAPWTVYAMNWSVRPDKRFRLLALGSFVEEYNNKVQLVG
LDEESSEFICRNTFDHPYPTTKLMWIPDTKGVYPDLLATSGDYLRVWRVGETET
10 RLECLLNNNKNNSDFCAPLTSFDWNEVDPYLLGTSSIDTTCTIWGLETGQVLGRV
NLVSGHVKTQLIAHDKEVYDIAFSRAGGGRDMFASVGADGSVRMFDLRHLEH
STIYEDPQHHPLRLCWNKQDPNYLATMAMDGMEVVILDVRVPAHLXPGTTIE
HVSMAILGPHIHPATSALQRM TTRLSSGTSSKCPEPLRTL SWPTQLXGEINN VQ
WASTQPELSPSATT TAWRYSECSVGGAVPTRQGLLYFLPLPHPQS (SEQ ID
15 NO:679); MSLHGKRKEIYKYEAPWTVYAMNWSVRPDKRFRLLALGSFV
EEYNNKVQLVGLDEESSEFICRNTFDHPYPTTKLMWIPDTKGVYPDLLATSGDY
LRVWRVGETETRLECLLNNNKNNSDFCAPLTSFDWNEVDPYLL (SEQ ID
NO:680); SFDWNEVDPYLLGTSSIDTTCTIWGLETGQVLGRVNLVSGHVK
TQLIAHDKEVYDIAFSRAGGGRDMFASVGADGSVRMFDLRHLEHSTIYEDPQH
20 HPLLRLCWNKQDPNYLATMAMDGMEVVILDVRVPAHLXPGTTI (SEQ ID
NO:681); VGADGSVRMFDLRHLEHSTIYEDPQHHPLLRLCWNKQDPNYLA
TMAMDGMEVVILDVRVPAHLXPGTTIEHVSMAILGPHIHPATSALQRM TTRL
SGTSSKCPEPLRTL SWPTQLXGEINN VQWASTQPELSPSATT TAWRYSECSV
GAVPTRQGLLYFLPLPHPQS (SEQ ID NO:682). Also preferred are polynucleotide
25 fragments encoding these polypeptide fragments.

This gene is expressed primarily in placenta, embryo, T cell and fetal lung and to a lesser extent in endothelial, tonsil and bone marrow.

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
30 biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immunological and developmental diseases in addition to cancers. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the
35 immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or

cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 369 as residues: Gly-19 to Gln-28, Pro-36 to Phe-42.

5 The tissue distribution in tumors of colon, ovary, and breast origins indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and intervention of these tumors, in addition to other tumors where expression has been indicated. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above
10 listed tumors and tissues. Because the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, and leukemia.

15 **FEATURES OF PROTEIN ENCODED BY GENE NO: 137**

 This gene is expressed primarily in TNF and INF induced epithelial cells, T cells and kidney.

 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
20 biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, inflammatory conditions particularly inflammatory reactions in the kidney. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of renal
25 system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an
30 individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 370 as residues: Thr-67 to Gly-72, Gln-132 to Ala-145, Arg-150 to Pro-157.

 The tissue distribution indicates that the protein products of this gene are useful for treating the damage caused by inflammation of the kidney.

35

FEATURES OF PROTEIN ENCODED BY GENE NO: 138

This gene maps to chromosome 1, and therefore, may be used as a marker in linkage analysis for chromosome 1 (See Accession No. D63485).

5 This gene is expressed primarily in breast cancer and colon cancer and to a lesser extent in thymus and fetal spleen.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cancers, especially of the breast and colon tissues. Similarly,
10 polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum,
15 plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in tumors of colon and breast origins indicates that
20 polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and intervention of these tumors, in addition to other tumors where expression has been indicated. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues.

25 **FEATURES OF PROTEIN ENCODED BY GENE NO: 139**

This gene maps to chromosome 17, and therefore, can be used as a marker for linkage analysis from chromosome 17.

This gene is expressed primarily in CD34 positive cells, and to lesser extent in activated T-cells and neutrophils.

30 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immunologically related diseases and hematopoietic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing
35 immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system and hematopoietic system, expression of this gene at significantly higher or lower levels

may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in CD34, T-cell and neutrophils indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of hematopoietic disorders and immunologically related diseases, such as anemia, leukemia, inflammation, infection, allergy, immunodeficiency disorders, arthritis, asthma, immune deficiency diseases such as AIDS.

FEATURES OF PROTEIN ENCODED BY GENE NO: 140

This gene was recently cloned by another group, who called the gene KIAA0313 gene. (See Accession No. d1021609.) Preferred polypeptide fragments comprise the amino acid sequence:

LYATATVISSPSTEXLSQDQGDRA SLDAADSGRGSWTSCSSGSHDNIQTIQ
 HQRSWETLPFGHTHFDYSGDPAGLWASSSHMDQIMFSDHSTKYNRQNSRES
 LEQAQSRASWASSTGYWGEDSEGDGTIKRRGGKDV SIEAESSLT SVTTEETK
 PVPMPAHIAVASSTTKGLIARKEGRYREPPPTPPGYIGIPITDFPEGHSH PARKP
 PDYNVALQSRMVARSSDTAGPSSVQQPHGHPTSSRPVNKPQWHKXNESDPR
 L APYQSQGFSTEEDEDEQVSAV (SEQ ID NO:683); HMDQIMFSDHSTKYNRQ
 NQSRESLEQAQSRASWASSTGYWGE (SEQ ID NO:684); SVTTEETK PVPMP
 AHIAVASSTTKGLIARKEGRYREPPPTPPGYIGIPITD (SEQ ID NO:685); and
 VALQSRMVARSSDTAGPSSVQQPHGHPTSSRPVNKPQW
 HKXNESDPR L APYQSQGF (SEQ ID NO:686). Also preferred are polynucleotide
 fragments encoding these polypeptide fragments. This gene maps to chromosome 4,
 and therefore, may be used as a marker in linkage analysis for chromosome 4 (See
 Accession No. AB002311).

This gene is expressed primarily in ovarian cancer, tumors of the Testis, brain, and colon.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, ovarian, testicle, brain and colon cancers. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the male and female reproductive systems,

expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e.,
5 the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in tumors of colon, ovary, testis, and brain origins indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and intervention of these tumors, in addition to other tumors where
10 expression has been indicated. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues.

FEATURES OF PROTEIN ENCODED BY GENE NO: 141

15 This gene is expressed primarily in spleen and colon cancer.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, colon cancer and immunological disorders. Similarly, polypeptides and
20 antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the gastrointestinal tract and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g.,
25 serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in tumors of colon, ovary, and breast origins indicates
30 that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and intervention of these tumors, in addition to other tumors where expression has been indicated. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues.

35

FEATURES OF PROTEIN ENCODED BY GENE NO: 142

Translation product is homologous to T cell translocation protein, a putative zinc finger factor (See Accession No. 340454), as well as to the G-protein coupled receptor TM5 consensus polypeptide (See Accession No. R50734). Preferred polypeptide

5 fragments comprise the following amino acid sequence:

CLLFVVFVSLGMRCLFWTIVYNVLYLKHKCNTVLLCYHLCSI (SEQ ID NO:687);
ACSKLIPAFEMVMRAKDNVYHLDCFACQLCNQRXCVDKFFLKNNXXLCQT
DYEEGLMKEGYAPXVR (SEQ ID NO:688). Also preferred are polynucleotide
fragments encoding these polypeptide fragments.

10 This gene is expressed primarily in fetal brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neurological disorders including brain cancer. Similarly, polypeptides
15 and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the Central Nervous System, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum,
20 plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
25 corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioral disorders such as Alzheimer's Disease, Parkinson's Disease, Huntingtons Disease, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder and panic disorder. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with
30 the developing embryo.

FEATURES OF PROTEIN ENCODED BY GENE NO: 143

Translation product for this gene has significant homology to the Fas ligand, which is a cysteine-rich type II transmembrane protein/tumor necrosis factor receptor
35 homolog. Mutations within this protein have been shown to result in generalized lymphoproliferative disease leading to the development of lymphadenopathy and autoimmune disease (See Medline Article No. 94185175). Preferred polypeptide

fragments comprise the following amino acid sequence:

SALSEPGAPDRRRPCPESVPRRPDDEQWPPPTALCLDVAPLPPSS (SEQ ID NO:689). Also preferred are polynucleotide fragments encoding these polypeptide fragments (See Accession No. 473565).

5 This gene is expressed primarily in osteoblasts, lung, and brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, osteoblast-related, pulmonary, neurological, and immunological
10 diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the skeletal and nervous systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded
15 tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 376 as residues: Trp-33 to Thr-40, Lys-
20 45 to Ile-63.

The tissue distribution in osteoblasts, lung, and brain combined with its homology to the Fas ligand indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and intervention of these tumors, in addition to other tumors where expression has been indicated. Protein, as well as,
25 antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues. Because the Fas ligand gene is known to be expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including asthma, immune deficiency diseases such as AIDS
30 and leukemia, and various autoimmune disorders including lupus and arthritis.

FEATURES OF PROTEIN ENCODED BY GENE NO: 144

This gene shares sequence homology with a 21.5 KD transmembrane protein in the SEC15-SAP4 intergenic region of yeast. (See Accession No. 1723971.) Preferred
35 polypeptide fragments comprise the amino acid sequence:

AHASESGERWWACCGVRFGLRSIEAIGRSCCHDGPGLVANRGRFRFKWAIEL
SGPGGGSRRSDRGSGQGDSLVPVGYLDKQVPDTSVQETDRILVEKRCWDIAL

GPLKQIPMNLFIMYMAGNTISIFPTMMVCMMAWRPIQALMAISATFKMLESSSQ
 KFLQGLVYLIGNLMGLALAVYKCQSMGLLPTHASDWLAFIEPPERMEFSGG
 GLLL (SEQ ID NO:691); PVGYLDKQVPDTSVQETDRILVEKRCWDIALGPLKQ
 IPMNLFI (SEQ ID NO:693); and ATFKMLESSSQKFLQGLVYLIGNLMGLALAV
 5 YKCQSMGLLPTHASD (SEQ ID NO:692). Also preferred are polynucleotide
 fragments encoding these polypeptide fragments.

This gene is expressed primarily in osteoclastoma, hemangiopericytoma, liver,
 lung.

Therefore, polynucleotides and polypeptides of the invention are useful as
 10 reagents for differential identification of the tissue(s) or cell type(s) present in a
 biological sample and for diagnosis of diseases and conditions, which include, but are
 not limited to, osteoclastoma, hemangiopericytoma, liver and lung tumors. Similarly,
 polypeptides and antibodies directed to these polypeptides are useful in providing
 immunological probes for differential identification of the above tissue(s) or cell
 15 type(s). For a number of disorders of the above tissues or cells, particularly of the lung
 and liver systems, expression of this gene at significantly higher or lower levels may be
 routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily
 fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or
 cell sample taken from an individual having such a disorder, relative to the standard
 20 gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an
 individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
 corresponding to this gene are useful for diagnosing osteoclastoma,
 hemangiopericytoma, liver and lung tumors.

25

FEATURES OF PROTEIN ENCODED BY GENE NO: 145

Translation product of this gene shares homology with the glucagon-69 gene
 which may indicate this gene plays a role in regulating metabolism. (See Accession No.
 A60318) One embodiment for this gene is the polypeptide fragments comprising the
 30 following amino acid sequence:
 PTTKLDIMEKKKHHIQIRFPSFYHKLVDSGRMRSKRETRREDSDTKHNL (SEQ ID
 NO:694). An additional embodiment is the polynucleotide fragments encoding these
 polypeptide fragments.

This gene is expressed primarily in brain, kidney, colon, and testis.

35 Therefore, polynucleotides and polypeptides of the invention are useful as
 reagents for differential identification of the tissue(s) or cell type(s) present in a
 biological sample and for diagnosis of diseases and conditions, which include, but are

not limited to, brain, kidney, colon, and testicular cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the male reproductive system, neurological, circulatory, and gastrointestinal systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in tumors of brain, kidney, colon, and testis origins, indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and intervention of these tumors, in addition to other tumors where expression has been indicated. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues. The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioral disorders such as Alzheimer's Disease, Parkinson's Disease, Huntingtons Disease, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder and panic disorder. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, sexually-linked disorders, or disorders of the cardiovascular system.

25 FEATURES OF PROTEIN ENCODED BY GENE NO: 146

The translation product of this gene shares sequence homology with goliath protein which is thought to be important in the regulation of gene expression during development. Protein may serve as a transcription factor. One embodiment for this gene is the polypeptide fragments comprising the following amino acid sequence:

30 TEHIIAVMITELRGKDILSYLEKNISVQMTIAVGTRMPPKNFSRGS�VFVSISFIV
 LMISSAWLIFYFIQKIRYTNARDRNQRRLLGDAAKKAISKLTTRTVKKGDKETD
 PDFDHCAVCIESYKQNDVVRILPCKHVFHKSCVDPWLSEHCTCPMCKLNILKA
 LGIV (SEQ ID NO:695); TEHIIAVMITELRGKDILSYLEKNISVQMTIAVGTRMP
 PKNFSRGS�VFVSISFIVLM IISSAWLIFYF (SEQ ID NO:697); SISFIVLMISSA
 35 WLIFYFIQKIRYTNARDRNQRRLLGDAAKKAISKLTTRTVKKGDKKE (SEQ ID
 NO:698); VKKGDKETDPDFDHCAVCIESYKQNDVVRILPCKHVFHKSCVDP

WLSEHCTCPMCKLNILKALGIV (SEQ ID NO:699). An additional embodiment is the polynucleotide fragments encoding these polypeptide fragments (See Accession No. 157535). Moreover, another embodiment is the polynucleotide fragments encoding these polypeptide fragments:

- 5 MTHPGTEHIIA VMITELRGKDILSYLEKNISVQMTIAVGTRMPPKNFSRGS
LVFVSISFIVLMISSAWLIFYFIQKIRYTNARDRNQRR LGDAAKKAISKLTTRTV
KKGDKETDPDFDHCAVCIESYKQNDVVRILPCKHV FHKSCVDPWLSEHCTCP
MCKLNILKALGIVPNLPCTDNVAFDMERLRTQAVNRRSALGDLAGDNSLGL
PLRTSGISPLPQDGELTPRTGEINIAVTKEWFIIASFGLLSALTLCYMIIRATASLN
10 ANEVEWF (SEQ ID NO:696); MTHPGTEHIIA VMITELRGKDILSYLEKNISVQM
TIAVGTRMPPKNFSRGS LVFVSISFIVLMISSAWLIFYFIQKIRYTNARDRNQRR
LGDAAKKAISKLTTRT (SEQ ID NO:700); AAKKAISKLTTRTVKKGDKE
TDPDFDHCAVCIESYKQNDVVRILPCKHV FHKSCVDPWLSEHCTCPMCKLNIL
KALGIVPNLPC (SEQ ID NO:701); TQAVNRRSALGDLAGDNSLGLPLRTSGI
15 SPLPQDGELTPRTGEINIAVTKEWFIIASFGLLSALTLCYMIIRATASLNANEVEW
F (SEQ ID NO:702); PLHGVADHLGCDPQTRFFVPPNIKQWIAL LQRGNCTF
KEKISRAAFHNAVAVVIYNNKSKEEPVTMTHPGTEHIIA VMITELRGKDILSYLE
KNISVQMTIAVGTRMPPKNFSRGS LVFVSISFIVLMISSAWLIFYFIQKIRYTN
ARDRNQRR LGDAAKKAISKLTTRTVKKGDKETDPDFDHCAVCIESYKQNDVVR
20 LPCKHV FHKSCVDPWLSEHCTCPMCKLNILKALGIVPNLPCTDNVAFDMERLT
RTQAVNRRSALGDLAGDNSLGLPLRTSGISPLPQDGELTPRTGEINIAVTKEW
FIIASFGLLSALTLCYMIIRATASLNANEVEWF (SEQ ID NO:703); and
HGVADHLGCDPQTRFFVPPNIKQWIAL LQRGNCTFKEKISRAAFHNAVAVVIY
NNKSKEE (SEQ ID NO:704). An additional embodiment is the polynucleotide
25 fragments encoding these polypeptide fragments. When tested against Jurkat cell lines,
supernatants removed from cells containing this gene activated the GAS pathway.
Thus, it is likely that this gene activates immune cells through the JAKS/STAT signal
transduction pathway.

- 30 This gene is expressed primarily in macrophage, breast, kidney and to a lesser
extent in synovium, hypothalamus and rhabdomyosarcoma.

- Therefore, polynucleotides and polypeptides of the invention are useful as
reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions, which include, but are
not limited to, schizophrenia and cancer. Similarly, polypeptides and antibodies directed
35 to these polypeptides are useful in providing immunological probes for differential
identification of the tissue(s) or cell type(s). For a number of disorders of the above
tissues or cells, particularly of the immune and neural system, expression of this gene at

significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to zinc finger protein indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment of schizophrenia, kidney disease and other cancers. The tissue distribution in macrophage, breast, and kidney origins indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and intervention of tumors within these tissues, in addition to other tumors where expression has been indicated. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues. Because the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, and leukemia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 147

The translation product of this gene shares sequence homology with HNP36 protein, an equilibrative nucleoside transporter, which is thought to be important in gene transcription as well as serving as an important component of the nucleoside transport apparatus (See Accession No. 1845345). One embodiment for this gene is the polypeptide fragments comprising the following amino acid sequence:

MSGQGLAGFFASVAMICAIASGSELSESAFGYFITACAVIILTIICYLGLPRLEFYR
 YYQQLKLEGPGEQETKLDLISKGEEPRAGKEESGVSVSNSQPTNESHSHKAILK
 NISVLAFSVCFTITIGMFPAVTVEVKSSIAGSSTWERYFIPVSCFLT FNIFDWLG
 RSLTAVFMWPGKDSRWLPSWXLARLVFVPLLLLCNIKPRRYLTVVFEHDAWFI
 FFMAAFASNGYLASLCMCFGPKKVKPAEAETAEPSPSSCVVWHWGLFS
 PSCSGQLCDKGWTEGLPASLPVCLLPARGDPEWSGGFFF (SEQ ID
 NO:705); MSGQGLAGFFASVAMICAIASGSELSESAFGYFITACAVIILTIIC
 YLGLPRLEFYRYYQQLKLE GPGEQETKLDLISKGEEPRAGKEESGVSVSNSQ
 PTNESHSH (SEQ ID NO:706); SGVSVSNSQPTNESHSHKAILKNISVLAFSVCFT
 FTITIGMFPAVTVEVKSSIAGSSTWERYFIPVSCFLT FNIFDWLGRS (SEQ ID
 NO:707), TIGMFPAVTVEVKSSIAGSSTWERYFIPVSCFLT FNIFDWLGRSLTAVF
 MWPGKDSRWLPSWXLARLVFVPLLLLCNIK PRRYLTVVFEHDA (SEQ ID
 NO:708); FGPKKVKPAEAETAEPSPSSCVVWHWGLFSPSCSGQLCDK

GWTEGLPASLPVCLLPSPARGDPEWSSGGFFF (SEQ ID NO:709). An additional embodiment is the polynucleotide fragments encoding these polypeptide fragments.

This gene is expressed primarily in eosinophils and aortic endothelium and to a lesser extent in umbilical vein endothelial cell and thymus.

5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, hematopoietic disease. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential
10 identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the circular system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having
15 such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to HNP36 protein indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment of blood neoplasias and other hematopoietic disease.

20

FEATURES OF PROTEIN ENCODED BY GENE NO: 148

This gene is expressed primarily in breast cancer cell lines, thymus stromal cells, and ovary.

Therefore, polynucleotides and polypeptides of the invention are useful as
25 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, endocrine and female reproductive system diseases including breast cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell
30 type(s). For a number of disorders of the above tissues or cells, particularly of the endocrine system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard
35 gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of endocrine disorders. In addition, the tissue distribution in tumors of thymus, ovary, and breast origins indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and intervention of these tumors, in addition to other tumors where expression has been indicated. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues

10 **FEATURES OF PROTEIN ENCODED BY GENE NO: 149**

Translation product of this gene has homology to pmt1 and pmt 2, two conserved schizosaccharomyces pombe genes. One embodiment for this gene is the polypeptide fragments comprising the following amino acid sequence:
 DDDGFEIVPIEDPAKHRILDPEGLALGAVIASSKKAKRDLIDNSFNRYTFNEDEG
 15 ELPEWFVQEEKQHRIRQLPVGKKEVEHYRKRWREINARPIXXXXXXXXXXXXX
 XXXXXXLEQTRKKAEEAVVNTVDIXRTRES (SEQ ID NO:710);
 DDDGFEIVPIEDPAKHRILDPEGLALGAVIASSKKAKRDLIDNSFNRYTF (SEQ
 ID NO:711); KRWREINARPIXXXXXXXXXXXXXXXXXXXXLEQTRKKAEE
 AVVNTVDIXRTRES (SEQ ID NO:712). An additional embodiment is the
 20 polynucleotide fragments encoding these polypeptide fragments (See Accession No.
 e1216734).

This gene is expressed primarily in retina and ovary and to a lesser extent in breast cancer cell, epididymus and osteosarcoma.

Therefore, polynucleotides and polypeptides of the invention are useful as
 25 reagents for differential identification of the tissue(s) or cell type(s) present in a
 biological sample and for diagnosis of diseases and conditions, which include, but are
 not limited to, neuronal growth disorders, cancer and reproductive system disorders.
 Similarly, polypeptides and antibodies directed to these polypeptides are useful in
 providing immunological probes for differential identification of the tissue(s) or cell
 30 type(s). For a number of disorders of the above tissues or cells, particularly of the
 neural and reproductive system, expression of this gene at significantly higher or lower
 levels may be routinely detected in certain tissues (e.g., cancerous and wounded
 tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or
 another tissue or cell sample taken from an individual having such a disorder, relative to
 35 the standard gene expression level, i.e., the expression level in healthy tissue or bodily
 fluid from an individual not having the disorder. Preferred epitopes include those
 comprising a sequence shown in SEQ ID NO: 382 as residues: Met-1 to Gly-7.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis or treatment of reproductive system disease and cancers.

5 FEATURES OF PROTEIN ENCODED BY GENE NO: 150

One embodiment for this gene is the polypeptide fragments comprising the following amino acid sequence:

MIKDKGRARTALTSSQPAHLCPENPLLHLKAAVKEKKRNKKKKTIGSPKRIQS
 PLNNKLLNSPAKTLPGACGSPQKLIDGFLKHEGPPAEKPLEELSASTSGVPGLS
 10 SLQSDPAGCVRPPAPNLAGAVEFNDVKTLLREWITTISDPM EEDILQVVKYCTD
 LIEEKDLEKLDLVIKYMKRLMQQSVE SVWNMAFD FILDNVQVVLQQTYGSTLK
 VT (SEQ ID NO:713); MIKDKGRARTALTSSQPAHLCPENPLLHLKAAVKE
 KKRNNKKKTIGSPKRIQ (SEQ ID NO:714); KRIQSPLNNKLLNSPAKT
 LPGACGSPQKLIDGFLKHEGPPAEKPLEELSASTSGVPGLSSLQSDPAGCVRPP
 15 APNLAGAVEFNDVKTLLREWITTISDPM (SEQ ID NO:715);
 TISDPM EEDILQVVKYCTDLIEEKDLEKLDLVIKYMKRLMQQSVE
 SVWNMAFD FILDNVQVVLQQTYGSTLKVT (SEQ ID NO:716). An additional
 embodiment is the polynucleotide fragments encoding these polypeptide fragments.

This gene is expressed primarily in 12 week embryo and to a lesser extent in
 20 hemangiopericytoma and frontal cortex.

Therefore, polynucleotides and polypeptides of the invention are useful as
 reagents for differential identification of the tissue(s) or cell type(s) present in a
 biological sample and for diagnosis of diseases and conditions, which include, but are
 not limited to, growth disorders and hemangiopericytoma. Similarly, polypeptides and
 25 antibodies directed to these polypeptides are useful in providing immunological probes
 for differential identification of the tissue(s) or cell type(s). For a number of disorders
 of the above tissues or cells, particularly of the circular and neural system, expression
 of this gene at significantly higher or lower levels may be routinely detected in certain
 tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma,
 30 urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an
 individual having such a disorder, relative to the standard gene expression level, i.e.,
 the expression level in healthy tissue or bodily fluid from an individual not having the
 disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID
 NO: 383 as residues: Leu-4 to Lys-11.

35 The tissue distribution indicates that polynucleotides and polypeptides
 corresponding to this gene are useful for the treatment of growth disorders,
 hemangiopericytoma and other soft tissue tumors.

FEATURES OF PROTEIN ENCODED BY GENE NO: 151

The translation product of this gene has been found to have homology to a human DNA mismatch repair protein PMS3. Preferred polypeptide fragments comprise the following amino acid sequence: FCHDCKFPEASPAMNCEP (SEQ ID NO:717).
5 Also preferred are polynucleotide fragments encoding these polypeptide fragments (See Accession No. R95250).

This gene is expressed primarily in neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as
10 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, lymphoma, immunodeficiency diseases, and cancers resulting from genetic instability. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the
15 tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to
20 the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 384 as residues: Met-1 to Lys-6.

The tissue distribution in neutrophils and the sequence homology indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis of
25 Hodgkin's lymphoma, since the elevated expression and secretion by the tumor mass may be indicative of tumors of this type. Additionally the gene product may be used as a target in the immunotherapy of the cancer. Because the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including
30 arthritis, asthma, immune deficiency diseases such as AIDS, and leukemia. Furthermore, its homology to a known DNA repair protein would suggest gene may be useful in establishing cancer predisposition and prevention in gene therapy applications.

FEATURES OF PROTEIN ENCODED BY GENE NO: 152

35 This gene is expressed primarily in neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a

biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, infectious diseases and lymphoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment of inflammation and infectious diseases.

15 **FEATURES OF PROTEIN ENCODED BY GENE NO: 153**

One embodiment for this gene is the polypeptide fragments comprising the following amino acid sequence:

MASSVPAGGHTRAGGIFLIGKLDLEASLFKSFQWLPFVLRKKC

NFFCWDSSAHSPLHPLSASCSAPACHASDTHLLYPSTRALCPSIFAWLVAPHS

20 VFRTNAPGPTPSSQSSPVFPVFPVSFMALIVCXLVCC (SEQ ID NO:720);

MASSVPAGGHTRAGGIFLIGKLDLEASLFKSFQWLPFVLRKKCNFFCWDSSAH

SLPLHPLSASCSAPACHA (SEQ ID NO:721);FAWL VAPHSVFRTNAPGPTPS

SQSSPVFPVFPVSFMALIVCXLVCC (SEQ ID NO:722). An additional embodiment is the polynucleotide fragments encoding these polypeptide fragments.

25 This gene is expressed primarily in neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, inflammation and infectious disease. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred

epitopes include those comprising a sequence shown in SEQ ID NO: 386 as residues: Ser-11 to Pro-17.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment of infectious diseases and inflammation.

FEATURES OF PROTEIN ENCODED BY GENE NO: 154

This gene is expressed in multiple tissues including ovary, uterus, adipose tissue, brain, and the liver.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, uterine, ovarian, brain, and liver cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the female reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution of this gene indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnostic or therapeutic uses in the treatment of the female reproductive system, obesity, and liver disorders, particularly cancer in the above tissues.

FEATURES OF PROTEIN ENCODED BY GENE NO: 155

This gene maps to chromosome 3, and therefore, may be used as a marker in linkage analysis for chromosome 3 (See Accession No. D87452).

This gene is expressed in multiple tissues including brain, aortic endothelial cells, smooth muscle, pituitary, testis, melanocytes, spleen, neutrophils, and placenta.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immunological disorders including immunodeficiencies, cancers of the brain and the female reproductive system, as well as cardiovascular disorders, such as

atherosclerosis and stroke. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous and immune systems, expression of this gene at

5 significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

10 The tissue distribution suggest that polynucleotides and polypeptides corresponding to this gene are useful in treatment/detection of disorders in the nervous system, including schizophrenia, neurodegeneration, neoplasia, brain cancer as well as cardiovascular and female reproductive disorders including cancer within the above tissues.

15

FEATURES OF PROTEIN ENCODED BY GENE NO: 156

The translation product of this gene shares sequence homology with the human gene encoding cytochrome b561 (See Accession No. P10897). Cytochrome b561 is a transmembrane electron transport protein that is specific to a subset of secretory vesicles

20 containing catecholamines and amidated peptides. This protein is thought to supply reducing equivalents to the intravesicular enzymes dopamine-beta-hydroxylase and alpha-peptide amidase. Preferred polypeptides of the invention comprise the amino acid sequence:

MAMEGYWRFLALLGSALLVGFLSVIFALVWVLHYREGLGWDGSALEFNWHP

25 VLMVTGFVFIQGIAIVYRLPWTWKCSKLLMKSIHAGLNAVAAILAIISVVAVFE
NHNVNNIANMYSLHSWVGLIAVICYLLQLLSGFSVFLLPWAPLSLRAFLMPIHV
YSGIVIFGTVIATALMGLTEKLIFSLRDPAYSTFPPEGVFVNTLGLLILVFGALIF
WIVTRPQWKRPKEPNSTILHPNGGTEQGARGSMPAYSGNNMDKSDSEL
NSEVAARKRNLALDEAGQRSTM (SEQ ID NO:724); as well as antigenic fragments

30 of at least 20 amino acids of this gene and/or biologically active fragments. Also preferred are polynucleotide fragments encoding these polypeptide fragments.

This gene is expressed primarily in anergic T-cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a

35 biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune system and metabolism related diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological

probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, 5 urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product or RNA of this gene is 10 useful for treatment or diagnosis of immune system and metabolic diseases or conditions including Tay-Sachs disease, phenylketonuria, galactosemia, various porphyrias, and Hurler's syndrome.

FEATURES OF PROTEIN ENCODED BY GENE NO: 157

15 The translation product of this gene shares sequence homology with collagen which is important in mammalian development. This gene also shows sequence homology with bcl-2. (See Accession No. P80988.) Preferred polypeptide fragments comprise the amino acid sequence: PGRAGPSPGLSLQLPAEPGHPAGNLAPL 20 TSRPQPLCRIPAVPG (SEQ ID NO:725). Also preferred are polynucleotide sequences encoding this polypeptide fragment.

This gene is expressed primarily in HL-60 tissue culture cells and to a lesser extent in liver, breast, and uterus.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a 25 biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immunological diseases, hereditary disorders involving the MHC class of immune molecules, as well as developmental disorders and reproductive disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell 30 type(s). For a number of disorders of the above tissues or cells, particularly of the immune and reproductive system expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to 35 the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those

comprising a sequence shown in SEQ ID NO: 390 as residues: Ser-39 to Gly-46, Leu-49 to Ala-62.

The tissue distribution and homology to collagen indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of hereditary MHC disorders and particularly autoimmune disorders including rheumatoid arthritis, lupus, scleroderma, and dermatomyositis, as well as many reproductive disorders, including cancer of the uterus, and breast tissues.

FEATURES OF PROTEIN ENCODED BY GENE NO: 158

10 This gene is expressed primarily in the amygdala region of the brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, a variety of brain disorders, particularly those effecting mood and personality. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain and central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and/or diagnosis of a variety of brain disorders, particularly bipolar disorder, unipolar depression, and dementia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 159

This gene is expressed in a variety of tissues and cell types including brain, smooth muscle, kidney, salivary gland and T-cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cancers of a variety of organs including brain, smooth muscle, kidney, salivary gland and T-cells and cardiovascular disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders

of the above tissues or cells, particularly of the central nervous, urinary, salivary, digestive, and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or
5 another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in brain, smooth muscle, and T-cells indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis of
10 various neurological, and cardiovascular disorders, but not limited to cancer within the above tissues. Additionally the gene product may be used as a target in the immunotherapy of the cancer. Because the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma,
15 immune deficiency diseases such as AIDS, and leukemia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 160

The translation product of this gene shares sequence homology with collagen which is thought to be important in cellular interactions, extracellular matrix formation,
20 and has been found to be an identifying determinant in autoimmune disorders. Moreover, this gene shows sequence homology with the yeast protein, Sls1p, an endoplasmic reticulum component, involved in the protein translocation process in Yeast *Yarrowia lipolytica*. (See Accession No. 1052828; see also J. Biol. Chem. 271, 11668-11675 (1996).) With mouse, this same region shows sequence homology with
25 the heavy chain of kinesin. (See Accession No. 2062607.) Recently, suppression of the heavy chain of kinesin was shown to inhibit insulin secretion from primary cultures of mouse beta-cells. (See Endocrinology 138 (5), 1979-1987 (1997).) Moreover, kinesin was found associated with drug resistance and cell immortalization. (See 468355.) Thus, it is likely that this gene also act as a genetic suppressor elements.

30 This gene is expressed primarily in the greater omentum and to a lesser extent in a variety of organs and cell types including gall bladder, stromal bone marrow cells, lymph node, liver, testes, pituitary, and thymus.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
35 biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, disorders of the endocrine, gastrointestinal, and immunological systems, including autoimmune disorders and cancers in a variety of organs and cell types.

Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and gastrointestinal systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 393 as residues: Asn-27 to Leu-47, Gln-81 to Lys-88, Asp-93 to Lys-102, Asn-107 to Leu-116, Met-129 to Glu-141, Glu-150 to Asp-157, Lys-176 to Glu-185, Glu-333 to Tyr-349, Cys-393 to Leu-403, Gln-423 to Gly-429.

The tissue distribution in within various endocrine and immunological tissues combined with the sequence homology to a conserved collagen motif indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis of various autoimmune disorders including, but not limited to, rheumatoid arthritis, lupus erythematosus, scleroderma, dermatomyositis. Because the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, and leukemia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 161

This gene has homology to the tissue inhibitor of metalloproteinase 2. Such inhibitors are vital to proper regulation of metalloproteins such as collagenases (See Accession No. P16368). In addition, this gene maps to chromosome 17, and therefore, may be used as a marker in linkage analysis for chromosome 17 (See Accession No. P16368).

This gene is expressed primarily in several types of cancer including osteoclastoma, chondrosarcoma, and rhabdomyosarcoma and to a lesser extent in several non-malignant tissues including synovium, amygdala, testes, placenta.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, various types of cancer, particularly cancers of bone and cartilage, as well as various autoimmune disorders. Similarly, polypeptides and antibodies directed

to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the musculoskeletal system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in various cancers and the sequence homology to a collagenase inhibitor indicates that polynucleotides and polypeptides corresponding to this gene are useful for detection of various autoimmune disorders such as rheumatoid arthritis, lupus, scleroderma, and dermatomyositis. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, and leukemia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 162

This gene is homologous to the mitochondrial ATP6 gene and therefore is likely a homolog of this gene family (See Accession No. X76197).

This gene is expressed primarily in brain tissue.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, a variety of brain disorders, including Down's syndrome, depression, Schizophrenia, and epilepsy. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in brain tissue indicates this gene is useful for diagnosis of various neurological disorders including, but not limited to, brain cancer.

Additionally the gene product may be used as a target in the immunotherapy of cancer in the brain as well as for the diagnosis of metabolic disorders such as obesity Tay-Sachs disease, phenylketonuria and Hurler's Syndrome.

FEATURES OF PROTEIN ENCODED BY GENE NO: 163

This gene is expressed primarily in placenta, neutrophils, and microvascular endothelial cells and to a lesser extent in multiple tissues including brain, prostate, spleen, thymus, and bone.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neutropenia and other diseases of the immune system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in placenta indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis various female reproductive disorders. Additionally the gene product may be used as a target in the immunotherapy of various cancers. Because the gene is expressed in some cells of lymphoid and endocrine origin, the natural gene product may be involved in immune functions and metabolism regulation, respectively. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, and leukemia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 164

This gene is expressed primarily in neutrophils, monocytes, bone marrow, and fetal liver.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune system disorders including, but not limited to, autoimmune disorders such as lupus, and immunodeficiency disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders

of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having
 5 such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in various immune system tissue indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis of various immunological disorders such as Hodgkin's lymphoma, arthritis,
 10 asthma, immune deficiency diseases such as AIDS, and leukemia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 165

The translation product of this gene shares sequence homology with dystrophin which is thought to be defective in both Duchene and Becker Muscular Dystrophy.
 15 Preferred polypeptide fragments comprise the following amino acid sequence:
 MKLLGECSSSIDSVKRLEHKLKEEEESLPGFVNLHSTETQTAGVIDRWELLQAAQ
 ALSKELRMKQNLQKWQQFNSDLNSIWAUWLGDTTEELEQLQRLELSTDIQTIELQ
 IKKLKELQKAVDHRKAILLSINLCSPEFTQADSKESRDLQDRLXQMNGRWDRV
 CSLLEEWGRLLQDALMQCQGFHEMSHGLLLMLENIDRRKNEIVPIDSNLDAEIL
 20 QDHHKQLMQIKHELLESQLRVASLQDMSCQLLVNAEGTDCLEAKEKVHVIGNR
 LKLLLKEVSRHIKELEKLLDVSSSQQLSSWSSADELDTSGSVSPXSGRSTPNR
 QKTPRGKCSLSQPGPSVSSPHSRSTKGGSDSSLSEXPGRSGRGFLFRVLRAA
 LPLQLLLLLLIGLACL VPMSEEDYSCALSNNFARSFHPMLRYTNGPPPL (SEQ ID
 NO:726); MKLLGECSSSIDSVKRLEHKLKEEEESLPGFVNLHSTETQTAGVIDR
 25 WELLQAQALSKELRMKQNLQKWQQFNSDLNSIWAUWLGDTTEELEQLQRLELS
 TDIQTIELQIK (SEQ ID NO:727); KLKELQKAVDHRKAILLSINLCSPEFTQADSK
 ESRDLQDRLXQMNGRWDRVCSLLEEWGRLLQDALMQCQGFHEMSHGLLLML
 ENIDRRKNEIVPIDSNLDAEILQDHHKQLMQIKHELLESQLRVASLQDMSCQL
 (SEQ ID NO:728); QDMSCQLLVNAEGTDCLEAKEKVHVIGNRLKLLLKEVS
 30 RHIKELEKLLDVSSSQQLSSWSSADELDTSGSVSPXSGRSTPNRQKTPRGKCS
 LSQPGPSVSSPHS (SEQ ID NO:729); DSSLSEXPGRSGRGFLFRVLRAAL
 PLQLLLLLLIGLACL VPMSEEDYSCALSNNFARSFHPMLRYTNGPPPL (SEQ ID
 NO:730). Also preferred are polynucleotide fragments encoding these polypeptide
 fragments. Furthermore, this gene maps to chromosome 6, and therefore, may be used
 35 as a marker in linkage analysis for chromosome 6 (See Accession No. N62896).

This gene is expressed in numerous tissues including the heart, kidney, and brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, musculoskeletal disorders including Muscular Dystrophy and cardiovascular diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the muscle tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to dystrophin indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of Muscular Dystrophy and other muscle disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 166

This gene is expressed primarily in human cerebellum.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, diseases of the central nervous system, including Alzheimer's Disease, Parkinson's Disease, ALS, and mental illnesses. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 399 as residues: Pro-20 to Gly-26, Leu-37 to Pro-42, His-57 to Gly-63.

The tissue distribution indicates that the protein products of this gene are useful for treatment/diagnosis of diseases of the central nervous system and may protect or

enhance survival of neuronal cells by slowing progression of neurodegenerative diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 167

5 Preferred polypeptides encoded by this gene comprise the following amino acid sequence:

MKLLICGNYLAPSHSESSRRCCLLCFYPLCLEINFGMKVFLSMPFLVLFQ

SLIQED (SEQ ID NO:731). Polynucleotides encoding such polypeptides are also provided. This gene is believed to reside on chromosome 15. Therefore polynucleotides
10 derived from this gene are useful in linkage analysis as chromosome 15 markers.

This gene is expressed primarily in human testes tumor and to a lesser extent in normal human testes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
15 biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, diseases of the testes, particularly cancer, and other reproductive disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of
20 the male reproductive tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily
25 fluid from an individual not having the disorder.

The tissue distribution indicates that the protein products of this gene are useful for treatment/diagnosis of testicular diseases including cancers.

FEATURES OF PROTEIN ENCODED BY GENE NO: 168

30 This gene is expressed primarily in fetal liver.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, conditions affecting hematopoietic development and metabolic diseases.
35 Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the

hepatic system, and fetal hematopoietic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 401 as residues: His-7 to Trp-17, Leu-19 to Lys-27, Pro-33 to Gly-44, Lys-68 to Gly-74, Lys-85 to Cys-95.

The tissue distribution indicates that the protein products of this gene are useful for treatment/diagnosis of diseases of the developing liver and hematopoietic system, and act as a growth differentiation factor for hematopoietic stem cells.

FEATURES OF PROTEIN ENCODED BY GENE NO: 169

The polypeptide encoded by this gene is believed to be a membrane bound receptor. The extracellular domain of which is expected to consist of the following amino acid sequence:

RILLVKYSANEENKYDYLPPTTVNVCSELVKLVFCVLVSFCVIKKDHQSRNLKY
 ASWKEFSDFMKWSIPAFLYFLDNLIVFYVLSYLPAMAVIFS NFSIITALLFRIV
 LKXRLNWIQWASLLTLFLSIVALTAGTKTLQHNLAGRGFHHD AFFSPSNSCLL
 FRNECPRKD NCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISSMANI
 YNEKILKEGNQLTEXIFIQNSKL YFFGILFNGLTLGLQRSNRDQIKNCGFFYGH
 S (SEQ ID NO:732). Thus, preferred polypeptides encoded by this gene comprise the extracellular domain as shown above. It will be recognized, however, that deletions of either end of the extracellular domain up to the first cysteine from the N-terminus and the first cysteine of the C-terminus, is expected to retain the biological functions of the full-length extracellular domain because the cysteines are thought to be responsible for providing secondary structure to the molecule. Thus, deletions of one or more amino acids from either end (or both ends) of the extracellular domain are contemplated. Of course, further deletions including the cysteines are also contemplated as useful as such polypeptides is expected to have immunological properties such as the ability to evoke and immune response. Polynucleotides encoding all of the foregoing polypeptides are provided.

This gene is expressed primarily in human osteoclastoma and to a lesser extent in hippocampus and chondrosarcoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are

not limited to, cancers, particularly those of the bone and connective tissues. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the skeletal system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 402 as residues: Met-1 to Cys-6, Ala-41 to Tyr-49, Lys-76 to Lys-84.

The tissue distribution indicates that the protein products of this gene are useful for diagnosis of cancers of the bone and connective tissues, and may act as growth factors for cells involved in bone or connective tissue growth.

FEATURES OF PROTEIN ENCODED BY GENE NO: 170

Preferred polypeptides encoded by this gene comprising the following amino acid sequence:

NSVPNLQTLAVLTEAIGPEPAIPRXPREPPVATSTPATPSAGPQPLPTGTV

LVPGGPAPPCLGEAWALLPPCRPSLTSCFWSPRPSPWKETGV (SEQ ID NO:733). Polynucleotides encoding such polypeptides are also provided herein.

This gene is expressed primarily in hematopoietic progenitor cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, diseases of the blood including cancer and autoimmune disorders.

Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the blood/circulatory system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 403 as residues: Gln-4 to His-10, Pro-25 to His-32.

The tissue distribution indicates that the protein products of this gene are useful for diagnosis of diseases involving growth differentiation of hematopoietic cells.

FEATURES OF PROTEIN ENCODED BY GENE NO: 171

5 Preferred polypeptides encoded by this gene comprise the following amino acid sequences: ALQLAFYPDAVEEWLEENVHPSLQRLQXLLQDLSEVSAPP (SEQ ID NO:734); and/or CHPPALAGTLLRTPEGRAHARGLLLEAGGA (SEQ ID NO:735). Polynucleotides encoding such polypeptides are also provided. The protein product of this gene shares sequence homology with metallothionines. Thus, polypeptide encoded
10 by this gene are expected to have metallothionine activity, such activities are known in the art and described elsewhere herein.

This gene is expressed primarily in kidney cortex.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
15 biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, diseases of the kidney including cancer and renal dysfunction. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the renal system, expression of this gene at significantly higher or lower levels may be routinely detected
20 in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID
25 NO: 404 as residues: Ser-47 to Gln-52.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/diagnosis of diseases of the kidney including kidney failure.

30

FEATURES OF PROTEIN ENCODED BY GENE NO: 172

This gene is expressed primarily in 12 week old early stage human.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
35 biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, developmental abnormalities. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for

differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the developing embryo, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 405 as residues: Gln-31 to Thr-43, Gly-51 to Ser-58, Pro-65 to Pro-72.

10 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/diagnosis of developmental problems with fetal tissue. The gene may be involved in vital organ development in the early stage, especially hematopoiesis, cardiovascular system, and neural development.

15 **FEATURES OF PROTEIN ENCODED BY GENE NO: 173**

 The translation product of this gene shares sequence homology with TGN38, an integral membrane protein previously shown to be predominantly localized to the trans-Golgi network (TGN) of cells.

20 This gene is expressed primarily in developing embryo and to a lesser extent in cancer tissues including lymphoma, endometrial, prostate and colon.

 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, developmental abnormalities and cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the developing fetus, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 406 as residues: His-65 to Ser-72, Pro-82 to Gly-91, Pro-98 to Glu-118, Ser-126 to Gly-166, Pro-180 to Asp-188, Tyr-209 to Lys-214, Gln-220 to Leu-228.

35 The tissue distribution and homology to an integral membrane protein indicates that polynucleotides and polypeptides corresponding to this gene are useful for

diagnosis of cancers and developmental abnormalities where aberrant expression relates to an abnormality.

FEATURES OF PROTEIN ENCODED BY GENE NO: 174

5 The translation product of this gene shares sequence homology with a dnaJ heat shock protein from *E. coli* which is allelic to sec63, a gene that affects transit of nascent secretory proteins across the endoplasmic reticulum in yeast.

 This gene is expressed primarily in Hodgkin's lymphoma and to a lesser extent in testes.

10 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification
15 of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to
20 the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 407 as residues: Thr-13 to Trp-21, Arg-74 to Asp-81.

 The tissue distribution and homology to dnaJ indicates that polynucleotides and polypeptides corresponding to this gene are useful as a diagnostic for cancer including
25 Hodgkin's lymphoma.

FEATURES OF PROTEIN ENCODED BY GENE NO: 175

 This gene is expressed primarily in endothelial cells and to a lesser extent in
30 bone marrow stromal cells.

 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, diseases involving angiogenic abnormalities including diabetic
35 retinopathy, macular degeneration, and other diseases including arteriosclerosis and cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell

type(s). For a number of disorders of the above tissues or cells, particularly of the vascular system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein products of this gene are useful for treating diseases where an increase or decrease in angiogenesis is indicated and as a factor in the wound healing process.

FEATURES OF PROTEIN ENCODED BY GENE NO: 176

The translation product of this gene shares sequence homology with MAT8 (mouse) which is thought to be important in regulating chloride conductance in cells (particularly in the breast) by modulating the response mediated by cAMP and protein kinase C to extracellular signals.

This gene is expressed primarily in amniotic cells and hematopoietic cells including macrophages, Neutrophils, T cells, TNF induced aortic endothelium and to a lesser extent in testes, TNF induced epithelial cells, and smooth muscle.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, inflammatory responses mediated by T cells, macrophages, and/or neutrophils particularly those involving TNF, and also cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 409 as residues: Thr-19 to Ala-33, Leu-54 to Asp-82, Pro-89 to Ala-97, Pro-100 to Lys-125, Ser-127 to Phe-135, Gly-164 to Leu-169, Cys-173 to Arg-178.

The tissue distribution and homology to mat-8 indicates that polynucleotides and polypeptides corresponding to this gene are useful for modifying inflammatory

responses to cytokines such as TNF and thus modifying the duration and/or severity of inflammation. Polynucleotides and polypeptides derived from this gene are thought to be useful in the diagnosis and treatment of cancer.

5 FEATURES OF PROTEIN ENCODED BY GENE NO: 177

This gene is expressed primarily in endothelial cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, vascular restenosis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the vascular system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating diseases associated with vascular response to injury such as vascular restenosis following angioplasty..

FEATURES OF PROTEIN ENCODED BY GENE NO: 178

One embodiment of the claimed invention comprises:

MRPDWKAGAGPGGPPQKPAPSSQRKPPARPSAAAAAIAVAAEEERRLRQRN
RLRLEEDKPAVERCLEELVFGDVENDEALLRRLRGPRVQEHEDSGDSEVENEAKGNFPPQKKPVWVDEEDEDEEMVDMMNFRKDMMKNAESKLSKDNLKK
RLKEEFQHAMGGVPAWAETTKRKTSSDDESEEDDLLQRTGNFISTSTSLPRG
ILKMKNQCQHANAERPTVARISICAVPSRCTDCDGCWD (SEQ ID NO:737); or
CLEELVFGDVENDEALLRRLRGPRVQEHEDSGDSEVENEAKGNFPPQKKPV
WVDEEDEDEEMVDMMNFRKDMMKNAESKLSKDNLKKRLKEEFQHAMG
GVPAWAETTKRKTSSDDESEEDDLLQRTGNFISTSTSLPRGILKMKNQCQHA
NAERPTVARISICAVPSRCTDCDGC (SEQ ID NO: 738). LKEKIVRSFEVSPDGS
FLLINGIAGYLHLLAMKTKELIGSMKINGRVAASTFSSDSKKVYASSGDGEVYV
WDVNSRKCLNRFVDEGSLYGLSIATSRNGQYVACGSNCGVVNIYNQDSCLQE
TNPPIKAIMNLVTGVTSLTFTNPTTEILAIASEKMKEAVRLVHLPSCTVFSNFPVI
KNKNISHVHTMDFSPRSGYFALGNEKGKALMYRLHHYSDF (SEQ ID NO:739);

and/or KINGRVAASTFSSDSKKVYASSGDGEVYVWDVNSRKCLNRFVDEGSL
YGLSIATSRNGQYVACGSNCGVVNIYNQDSCLQETNPKPIKAIMNLVTGVTSLT
FNPTTEILAIASEKMKEAVRLVHLPSCTVFSNFPVIKNKNISHVHTMDFSPRSG
YFALGNEKGKAL (SEQ ID NO:740).

5 This gene is expressed primarily in epididymus and endometrial tumors and to a lesser extent in T cell lymphoma and cell lines derived from colon cancer.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, tumors of the reproductive organs including testis and endometrial cells. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 411 as residues: Ser-67 to Lys-72, Val-87 to Leu-93, Tyr-128 to Pro-141, Asp-204 to Gly-210.

The tissue distribution indicates that the protein products of this gene are useful for treating tumors of the endometrium or epithelial tumors of the reproductive system.

25 **FEATURES OF PROTEIN ENCODED BY GENE NO: 179**

Preferred polypeptides encoded by this gene comprise the following amino acid sequence:

MRILQLILLALATGLVGGETRIIKGFECKLHSQPWQAALFEKTRLLCGATLIAPR
WLLTAAHCLKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDH
30 RNDIMLVKMASPV SITWAVRPLTLSSRCV TAGTSCSFPAGAARPDPSYACLTPC
DAPTSPSLSTRSVRTP TPATSQTPWCVPACRKGARTPARVTPGALWSVTSLFKA
LSPGARIRVRSPESLVSTRKSANMWTGSRRR (SEQ ID NO:741); ETRIIKGFEC
KLHSQPWQAALFEKTRLLCGATLIAPRWLLTAAHCLKPRYIVHLGQHNLQKEE
GCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPV SITWAVRPLTLSSR
35 CVTAGTSCSFPAGAARPDPSYACLTPCDAPTSPSLSTRSVRTP TPATSQTPWCVP
ACRKGARTPARVTPGALWSVTSLFKALSPGARIRVRSPESLVSTRKSANMWTG

SRRR (SEQ ID NO:742); or CKLHSQPWQAALFEKTRLLCGATLIAPRWLLT
AAHCLKPRYIVHLGQHNQKEEGCEQTRTATESFPHPGFNS

(SEQ ID NO:743). The translation product of this gene shares sequence homology
with neuropsin a novel serine protease which is thought to be important in modulating
5 extracellular signaling pathways in the brain. Owing to the structural similarity to other
serine proteases the protein products of this gene are expected to have serine protease
activity which may be assayed by methods known in the art and described elsewhere
herein.

This gene is expressed primarily in endometrial tumor and to a lesser extent in
10 colon cancer, benign hypertrophic prostate, and thymus.

Therefore, polynucleotides and polypeptides of the invention are useful as
reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions, which include, but are
not limited to, cancers of the endometrium or colon and benign hypertrophy of the
15 prostate. Similarly, polypeptides and antibodies directed to these polypeptides are
useful in providing immunological probes for differential identification of the tissue(s)
or cell type(s). For a number of disorders of the above tissues or cells, particularly of
the urogenital or reproductive systems, expression of this gene at significantly higher or
lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded
20 tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or
another tissue or cell sample taken from an individual having such a disorder, relative to
the standard gene expression level, i.e., the expression level in healthy tissue or bodily
fluid from an individual not having the disorder. Preferred epitopes include those
comprising a sequence shown in SEQ ID NO: 412 as residues: Gly-12 to Ser-22, Pro-
25 34 to Ser-53.

The tissue distribution and homology to serine proteases indicates that
polynucleotides and polypeptides corresponding to this gene are useful for diagnosing
or treating hyperproliferative disorders such as cancer of the endometrium or colon and
hyperplasia of the prostate.

30

FEATURES OF PROTEIN ENCODED BY GENE NO: 180

Preferred polypeptide encoded by this gene comprise the following amino acid
sequence: VLQGRYFSPILEMRRLRPEGXXNLPGGSRAQKEPRQDLTLVLWPHC
PHFAMTRSYPVKQCMVQGSFYCIFKGPVQNWC (SEQ ID NO:744).

35 Polynucleotides encoding such polypeptide are also provided.

This gene is expressed primarily in fetal brain

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, identifying and expanding stem cells in the CNS. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein products of this gene are useful for detecting and expanding stem cell populations in the (or of the) central nervous system.

FEATURES OF PROTEIN ENCODED BY GENE NO: 181

This gene is expressed primarily in early stage human brain and a stromal cell line.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, developmental abnormalities of the CNS. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 414 as residues: Gln-42 to Gln-47, Gln-54 to Pro-60.

The tissue distribution indicates that the protein products of this gene play a role in the development of the central nervous system. Therefore this gene and its products

are useful for diagnosing or treating developmental abnormalities of the central nervous system.

FEATURES OF PROTEIN ENCODED BY GENE NO: 182

5 Preferred polypeptides encoded by this gene comprise the following amino acid sequence:

MPIIDQVNPELHDFMQSAEVGTIFALSWLITWFGHVLSDFRHVVRLYDF
 FLACHPLMPIYFAAVIVLYREQEVLDCDCDMASVHHLLSQIPQDLPYETLISRXE
 TFLFSFHPNLLGRPLNSKLRGRQPLLSKTLSTWHQPSRGLIWCCGSGXRGLL
 10 RPEDRTKDVLTKPRTNRFVKLA VMGLTVALGAAALAVVKSALWAPKFQLQL
 FP (SEQ ID NO:745); or CPEFFIPATLPCPFVFAFTSEASSRAYLTQRGPGGLAQ
 NLMPLPVGFWMGSLPPPWCWRKWVSEACSCFC (SEQ ID NO:746) These

polypeptides are structurally similar to various TGF-beta family members. Thus, this polypeptide is expected to have a variety of activities in the modulation of cell growth
 15 and proliferation.

This gene is expressed primarily in osteoclastoma, microvascular endothelium, and bone marrow derived cell lines.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
 20 biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, hematological diseases particularly involving aberrant proliferation of stem cells. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of
 25 the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an
 30 individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 415 as residues: Ser-33 to Ala-39.

The tissue distribution indicates that the protein products of this gene is useful for treating disorders of the progenitors of the immune system. Applications include in vivo expansion of progenitor cells, ex vivo expansion of progenitor cells, or the
 35 treatment of tumors of the circulatory system, such as lymphomas.

FEATURES OF PROTEIN ENCODED BY GENE NO: 183

This gene maps to chromosome 17 and therefore, polynucleotides of the invention can be used in linkage analysis as a marker for chromosome 17. In specific embodiments, polypeptides of the invention comprise the sequence:

- 5 GFGSVSAAGRSGGTWQPVQ (SEQ ID NO:747); PGGLAVGSRWWSRSLT (SEQ ID NO:748); LEPSRQRRPRRRGGTSRPETDQRAKCWRQL (SEQ ID NO:749); and/or VCLRCQNRMEN (SEQ ID NO:750). In further specific embodiments, polypeptides of the invention comprise the sequence: MAACTARRPGR GQPLVVPVADXGPVAKAALCAAXAGAFSPASTTTTTRHLSSNRNPEGKVLETV
 10 GVFEVVPKQNGKYETGQLFLHSIFGYRGVVLFPWQARLXDRDVASAAPEKAEN PAGHGSKEVKGKTHTYYQVLIDARDCPHISQRSQTEAVTFLANHDDSRALYAIP GLDYVSHEDILPYTSTDQVPIQHELFLFYDQTKAPPFVARETLRAWQEKNH PWLELSDVHRETTENIRVTVIPFYMGMREAQNSHVYWWRYCIRLENLSDSDVVQ LRERHWRIFSLSGTLETVRGRGVVGREPVLSEKQPAFQYSSHVSLQASSGHMW
 15 GTFRFERPDGSHFDVRIPPFSLSENKDEKTPPSGLHW (SEQ ID NO:751); MAACTARRPGRGQPLVVPVADXGPVAKAALCAA (SEQ ID NO:752); VLETVG VFEVVPKQNGKYETGQLFLHSIFGYRGVVL (SEQ ID NO:757); GLDYVSHEDILPYTST (SEQ ID NO:758); DVHRETTENIRVTVIPFYM (SEQ ID NO:759); WWRYCIRLENLSDSDVQLRER (SEQ ID NO:760); and/or PAFQYSS
 20 HVSLQASSGHMWGTFRFER (SEQ ID NO:761). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in gall bladder, prostate, and fetal brain, and to a lesser extent in a few tumor and fetal tissues.

- 25 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, growth related disorders such as cancers. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders
 30 of the above tissues or cells, particularly of the prostate, gall bladder, and fetal brain, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e.,
 35 the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of growth-related disorders, such cancers.

5 FEATURES OF PROTEIN ENCODED BY GENE NO: 184

In specific embodiments, polypeptides of the invention comprise the sequence:SLCCPEGAEGC (SEQ ID NO:762) and/or QLKKTTHYDRPCP (SEQ ID NO:763). Polynucleotides encoding these polypeptides are also encompassed by the invention.

- 10 This gene is expressed primarily in stromal cell, tonsil, and glioblastoma and to a lesser extent in some other tissues.

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune and inflammatory disorders and glioblastoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the stromal cells, tonsil, and glioblastoma expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Additionally, it is believed that the product of this gene regulates pancreatic cell differentiation into beta cells. Accordingly, polynucleotides and polypeptides of the invention are useful in the treatment of insulin-dependent diabetes mellitus and associated conditions e.g. pancreatic hypofunction and the prevention, as well as the treatment of undifferentiated type pancreatic cancers. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 417 as residues: Pro-27 to Ala-32.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of immune and inflammatory disorders and glioblastoma.

35 FEATURES OF PROTEIN ENCODED BY GENE NO: 185

This gene is expressed primarily in hepatocellular carcinoma and to a lesser extent in other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, liver diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the liver, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 418 as residues: Gly-32 to Lys-39.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of liver diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 186

This gene is expressed primarily in hippocampus and to a lesser extent in other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neuronal disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hippocampus, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of neuronal disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 187

This gene is expressed primarily in bone cancer and hippocampus and to a lesser extent in osteoclastoma and other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, bone-related disorders and neuronal diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the bone, osteoclast, and hippocampus, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of bone-related disorders and neuronal diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 188

This gene maps to chromosome 4 and therefore polynucleotides of the invention can be used in linkage analysis as a marker for chromosome 4.

This gene is expressed primarily in neuronal tissues such as hippocampus, spinal cord, and hypothalamus and to a lesser extent in a few other tissues such as ovary.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neuronal diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the neuronal tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of neuronal disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 189

This gene maps to chromosome 10, therefore, polynucleotides of the invention can be used in linkage analysis as a marker for chromosome 10.

5 This gene is expressed primarily in neuronal tissues and immune tissues, and to a lesser extent in a few other tissues such as skin tumor, lung etc.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neuronal and immune-related disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the neuronal and immune-related tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 422 as residues: Pro-19 to Asp-25.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of neuronal and immune-related disorders.

25 FEATURES OF PROTEIN ENCODED BY GENE NO: 190

The translation product of this gene shares sequence homology with human N33, a gene located in a homozygously deleted region of human metastatic prostate cancer which is thought to be important in prevention of prostate cancer. In specific embodiments, polypeptides of the invention comprise the sequence:

30 AQRKKEMVLSEKVSQLEWTKRVPVIRMNGDKFRRLVKAPPRNYSVIVMFTA
LQLHRQCVVCKQADEEFQILANSWRYSSAFTNRIFFAMVDFDEGSDVFQMLNM
NSAPTFINFPKKGPKRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNMA
ARWRFWCVSVT (SEQ ID NO:765); MVVALLIVCDVPSAS (SEQ ID NO:766);
AQRKKEMVLSEKVSQLEWTKRVPVIRMNGDKF (SEQ
35 ID:768); RRLVKAPPRNYSVIVMFTALQLHRQCVVCKQADEEFQILANSWRY
SSAFTNRIFFA (SEQ ID NO:769); MVDFDEGSDVFQMLNMNSAPTFINFPK
GKP (SEQ ID NO:770); KRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPN

(SEQ ID NO:771); and/or YAGPLMLGLLLA VIGGLVYLRRVIWNFSLIKLDGLLQL CVLCLL (SEQ ID NO:772). Polynucleotides encoding these polypeptides are also encompassed by the invention.

5 This gene is expressed primarily in infant adrenal gland prostate cell line and to a lesser extent in a few other tissues like liver, smooth muscle etc.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, prostate cancer and endocrine disorders. Similarly, polypeptides and
10 antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the prostate and adrenal gland, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma,
15 urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 423 as residues: Pro-34 to Gly-43, Arg-113 to Pro-120.

20 The tissue distribution and homology to N33 indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment for prostate cancer and endocrine disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 191

25 This gene is expressed primarily in T cell and to a lesser extent in fetal lung.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune disorders. Similarly, polypeptides and antibodies directed to
30 these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal
35 fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue

or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 424 as residues: Trp-3 to Phe-9.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of immune disorders.

5

FEATURES OF PROTEIN ENCODED BY GENE NO: 192

This gene maps to chromosome 6, therefore, polynucleotides of the invention can be used in linkage analysis as a marker for chromosome 6. Neural activity and neurotrophins induce synaptic remodeling in part by altering gene expression. This gene is believed to be a glycosylphosphatidylinositol-anchored protein encoded by a hippocampal gene and to possess neural activity. This molecule is believed to be expressed in postmitotic-differentiating neurons of the developing nervous system and neuronal structures associated with plasticity in the adult. Message of this gene is believed to be induced by neuronal activity and by the activity-regulated neurotrophins BDNF and NT-3. The product of this gene is believed to stimulate neurite outgrowth and arborization in primary embryonic hippocampal and cortical cultures and to act as a downstream effector of activity-induced neurite outgrowth. In specific embodiments, polypeptides of the invention comprise the sequence: DAVFKGFSDCLLKLGD (SEQ ID NO:773); CQEGAKDMWDKLRKESKNLN (SEQ ID NO:774); VLLVLSAALATWLSF (SEQ ID NO:775); MGLKLNGRYISLILAVQIAYLVQAVR AAGKCD VFKGFSDCLLKLGD (SEQ ID NO:776); PAAWDDKTNIKTVC TYW EDFHSCTVTALTDCQEGAKDMWDKLRKESKNLN IQGSLFELCGSGNGAAGSL LPAFPVLLVLSAALATWLSF (SEQ ID NO:777); and/or MGLKLNGRYISLILAVQIAYLVQAVRAAGKCD VFKGFSDCLLKLGD SXXXXXPAAWDDKTNIKTVC TYW EDFHSCTVTALTDCQEGAKDMWDKLRKESKNLN IQGSLFELCGSGNGAAGSL LPAFPVLLVLSAALATWLSF (SEQ ID NO:778). Polynucleotides encoding this polypeptide are also encompassed by the invention.

This gene is expressed primarily in human placenta, endometrial tumor and tissues of the central nervous system (CNS).

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, relating to reproductive disorders, cancers and neurological diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive and neurological disorders, expression of this gene at significantly higher

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or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue
5 or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 425 as residues: Asp-47 to Asp-63, His-75 to Tyr-80, Pro-83 to Tyr-89.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of reproductive
10 disorders such as endometrial tumors. Expression of this gene in tissues of the CNS and its strong homology to Neuritin suggest that the protein product from this gene may also be used in the treatment and diagnosis of neurological disorders and in the regeneration of neural tissues, e.g., following injury.

15 **FEATURES OF PROTEIN ENCODED BY GENE NO: 193**

The translation product of this gene shares sequence homology with tenascin which is thought to be important in development. The translation product of this gene is believed to be a ligand of the fibroblast growth factor family. FGF ligand activity is known in the art and can be assayed by methods known in the art and disclosed
20 elsewhere herein.

This gene is expressed primarily in endometrial tumors, and other types of tumors.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
25 biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cancers. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the cancer tissues, expression of this gene at significantly higher or lower
30 levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those
35 comprising a sequence shown in SEQ ID NO: 426 as residues: Gly-29 to Glu-34, Arg-71 to Arg-76, Thr-176 to Cys-182, Gly-184 to Glu-199.

The tissue distribution and homology to tenascin indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of cancers.

5 **FEATURES OF PROTEIN ENCODED BY GENE NO: 194**

In specific embodiments, polypeptides of the invention comprise the sequence: MNSAAGFSHLDRRERVLKLGESFEKQPRCASTLC (SEQ ID NO:779).

Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in fetal human lung and neutrophils.

10 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, lung development and respiratory disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes
15 for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the respiratory system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual
20 having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

 The tissue distribution in fetal lung and neutrophils indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis
25 and treatment of lung and immunity related diseases, for example, lung cancer, viral, fungal or bacterial infections (e.g. lesions caused by tuberculosis), inflammation (e.g. pneumonia), metabolic lesions etc.

FEATURES OF PROTEIN ENCODED BY GENE NO: 195

30 This gene is expressed primarily in breast lymph node.

 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immunal disorders. Similarly, polypeptides and antibodies directed to
35 these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at

significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of immunal disorders.

10 **FEATURES OF PROTEIN ENCODED BY GENE NO: 196**

This gene maps to chromosome 5 and accordingly, polynucleotides of the invention can be used in linkage analysis as a marker for chromosome 5. The translation product of this gene shares sequence homology with human M-phase phosphoprotein 4 which is thought to be important in phosphorylation and signal transduction processes. In specific embodiments, polypeptides of the invention comprise the sequence: TIYPTEELQAVQKIVSITERALKLVSD (SEQ ID NO:780); RALKGVLRV GVLAKGLLLRGDRNVNLVLLC (SEQ ID NO:781); ALAALRHAKWFQARAN GLQSCVIIIRILDLCQRVPTWS (SEQ ID NO:782); GDALRRVFECISSGIL (SEQ ID NO:783); LAFRQIHKVLGMDPLP (SEQ ID NO:784); and/or TIYPTEELQAVQ KIVSITERALKLVSDSLSEHEKNKNKEGDDKKEGGKDRALKGVLRVGVLAGG LLLRGDRNVNLVLLCSEKPSKTLLSRIAENLPKQLAVISPEKYDIKCAVSEAAIIL NSCVEPKMQVTITLTSPPIREENMREGDVTSGMVKDPPDVLDRQKCLDALAALR HAKWFQARANGLQSCVIIIRILDLCQRVPTWSDFPSWAMELLVEKAISSASSP QSPGDALRRVFECISSGILKGSPGLLDPEKDPFDTLATMTDQQREDITSSAQFA LRLLAFRQIHKVLGMDPLPQMSQRFNIHNNRKRRRSDSGVDGFEEAGKKDKK DYDNF (SEQ ID NO:785). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in Human Hippocampus and to a lesser extent in Prostate, Human Frontal Cortex.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, disorders related to reproductive system and nervous system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive system and nervous system, expression of this gene at significantly higher or lower

levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to human M-phase phosphoprotein 4 indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of reproductive and nervous system disorders.

10 **FEATURES OF PROTEIN ENCODED BY GENE NO: 197**

In specific embodiments, polypeptides of the invention comprise the sequence: MGSQHSAAARPSSCRRKQEDDRDG (SEQ ID NO:786); LLAEREQEEAIAQFPYVEFTGRDSITCLTC (SEQ ID NO:787); and/or QGTGYIPTEQVNELVALIPHSDQRLRPQRTKQYV (SEQ ID NO:788).

15 Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in Human Primary Breast Cancer and to a lesser extent in Human Adult Spleen, Hodgkin's Lymphoma I, Salivary Gland.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cancer and immunal disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the cancer and immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 430 as residues: Ser-126 to Gly-138.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of cancer and immunal disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 198

This gene is expressed primarily in monocytes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, blood cell disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of blood cell disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 199

This gene is expressed primarily in Human Ovary and Synovia and to a lesser extent in Human 8 Week Whole Embryo.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, reproductive and developmental disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive and developmental system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of reproductive and developmental disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 200

This gene maps to chromosome 8 and therefore polynucleotides of the invention can be used in linkage analysis as a marker for chromosome 8. The translation product of this gene shares limited sequence homology with collagen proline rich domain.

This gene is expressed primarily in CNS.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neurological diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 433 as residues: Pro-35 to Asp-41.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of neurological diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 201

Translation product of this gene shares homology with a mammalian histone H1a protein. One embodiment for this gene is the polypeptide fragments comprising the following amino acid sequence: ARLNVGRESLKREMLKSQGVKVSSEPMGAR HSSWPEGAAFCCKKVQGAQMFPFRR (SEQ ID NO:789); ARLNVGRESLKR EML (SEQ ID NO:790); LKSQGVKVSSEPMGARHSSW (SEQ ID NO:791); AFCKKVQGAQMFPFRR (SEQ ID NO:792). An additional embodiment is the polynucleotide fragments encoding these polypeptide (See Accession No. pirlS24178) fragments.

This gene is expressed primarily in neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are

not limited to, immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at

5 significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

10 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of immune disorders. Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in vital immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such

15 as AIDS, and leukemia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 202

This gene is expressed primarily in neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as

20 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential

25 identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level

30 in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of immune disorders. Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for

35 immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, and leukemia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 203

This gene is expressed primarily in Neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions, which include, but are
not limited to, infectious disorders, immune disorders, and cancers. Similarly,
polypeptides and antibodies directed to these polypeptides are useful in providing
immunological probes for differential identification of the tissue(s) or cell type(s). For
10 a number of disorders of the above tissues or cells, particularly of the immune system,
expression of this gene at significantly higher or lower levels may be routinely detected
in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum,
plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from
an individual having such a disorder, relative to the standard gene expression level, i.e.,
15 the expression level in healthy tissue or bodily fluid from an individual not having the
disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID
NO: 436 as residues: Thr-31 to Lys-36.

The tissue distribution indicates that polynucleotides and polypeptides
corresponding to this gene are useful for diagnosis and treatment of infectious
20 disorders, immune disorders, and cancers. Since the gene is expressed in cells of
lymphoid origin, the natural gene product may be involved in immune functions.
Therefore it may be also used as an agent for immunological disorders including
arthritis, asthma, immune deficiency diseases such as AIDS, and leukemia. Protein, as
well as, antibodies directed against the protein may show utility as a tumor marker
25 and/or immunotherapy targets for the above listed tumors and tissues.

FEATURES OF PROTEIN ENCODED BY GENE NO: 204

This gene maps to chromosome 16 and therefore polynucleotides of the
invention can be used in linkage analysis as markers for chromosome 16. The
30 translation product of this gene shares sequence homology with lactate dehydrogenase
which is thought to be important in lactate metabolism.

This gene is expressed primarily in human tonsils and to a lesser extent in
Spleen, and Neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as
35 reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions, which include, but are
not limited to, immune disorders, infectious disorders, and cancers. Similarly,

polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune disorders, infectious disorders, and cancers, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 437 as residues: Gly-7 to Ser-12.

The tissue distribution and homology to lactate dehydrogenase gene indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of immune disorders, infectious disorders, and cancers.

15 **FEATURES OF PROTEIN ENCODED BY GENE NO: 205**

The translation product of this gene shares sequence homology with Gcap1 protein which is developmentally regulated in brain.

This gene is expressed primarily in placenta and endometrial tumor and to a lesser extent in several other tumors.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, vasculogenesis/angiogenesis and tumorigenesis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the vascular system and tumors, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to Gcap1 protein indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of disorder or dysfunction of vascular system of tumorigenesis.

FEATURES OF PROTEIN ENCODED BY GENE NO: 206

In specific embodiments, polypeptides of the invention comprise the sequence
 MPYAQWLAENDRFEEAQKAFHKAGRQREA (SEQ ID NO:799);
 VQVLEQLTNNAVAESRFNDAAYYYWMLSMQCLDIAQD (SEQ ID NO:794);
 5 PAQKDTMLGKFYHFQRLAELYHGYHAIHRHTEDP (SEQ ID NO: 795);
 FSVHRPETLFNISRFLHSLPKDTPSGISKVKILFT (SEQ ID NO:800);
 LAKQSKALGAYRLARHAYDKLRGLYIP (SEQ ID NO:796); ARFQKSIELG
 TLTIRAKPFHDSEELVPLCYRCSTNN (SEQ ID NO: 797); and/or PLLNNLGNCV
 INCRQPFIFSASSYDVLHLVEFYLEEGITDEEAISLIDLEVLRPKRDDRQLEICKQQ
 10 LPDSCG (SEQ ID NO:798). Polynucleotides encoding these polypeptides are also
 encompassed by the invention.

This gene is expressed primarily in testes.

Therefore, polynucleotides and polypeptides of the invention are useful as
 reagents for differential identification of the tissue(s) or cell type(s) present in a
 15 biological sample and for diagnosis of diseases and conditions, which include, but are
 not limited to, male reproductive and endocrine disorders. Similarly, polypeptides and
 antibodies directed to these polypeptides are useful in providing immunological probes
 for differential identification of the tissue(s) or cell type(s). For a number of disorders
 of the above tissues or cells, particularly of the reproductive and endocrine systems,
 20 expression of this gene at significantly higher or lower levels may be routinely detected
 in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum,
 plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from
 an individual having such a disorder, relative to the standard gene expression level, i.e.,
 the expression level in healthy tissue or bodily fluid from an individual not having the
 25 disorder.

The tissue distribution indicates that polynucleotides and polypeptides
 corresponding to this gene are useful for treatment of male reproductive and endocrine
 disorders.

30 FEATURES OF PROTEIN ENCODED BY GENE NO: 207

This gene is expressed in fetal lung.

Therefore, polynucleotides and polypeptides of the invention are useful as
 reagents for differential identification of the tissue(s) or cell type(s) present in a
 biological sample and for diagnosis of diseases and conditions, which include, but are
 35 not limited to, lung diseases such as cystic fibrosis. Similarly, polypeptides and
 antibodies directed to these polypeptides are useful in providing immunological probes
 for differential identification of the tissue(s) or cell type(s). For a number of disorders

of the above tissues or cells, particularly of the respiratory system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual
5 having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 440 as residues: Tyr-49 to Cys-54.

The tissue distribution indicates that polynucleotides and polypeptides
10 corresponding to this gene are useful for detection and treatment of disorders associated with developing lungs particularly in premature infants where the lungs are the last tissues to develop. The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and intervention of lung tumors since the gene may be involved in the regulation of cell division,
15 particularly since it is expressed in fetal tissue. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and immunotherapy targets for the above listed tumors and tissues.

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
1	HLHDS67	97979 03/27/97	Uni-ZAP XR	11	2526	427	2526	458	458	234	1	30	31	30
2	HLHDZ58	97979 03/27/97	Uni-ZAP XR	12	1131	1	1131	129	129	235	1	14	15	115
3	HLMMJ13	97979 03/27/97	Lambda ZAP II	13	941	39	941	62	62	236	1	44	45	102
3	HLMMJ13	97979 03/27/97	Lambda ZAP II	218	941	39	941	245	245	441	1	35	36	41
4	HLTEI25	97979 03/27/97	Uni-ZAP XR	14	843	1	843	155	155	237	1	19	20	42
5	HMSJX24	97979 03/27/97	Uni-ZAP XR	15	1018	1	1018	90	90	238	1	18	19	36
6	HNFE65	97979 03/27/97	Uni-ZAP XR	16	661	1	661	76	76	239	1	28	29	127
7	HNHDX07	97979 03/27/97	Uni-ZAP XR	17	553	1	553	106	106	240	1	23	24	66
8	HNHGC82	97979 03/27/97	Uni-ZAP XR	18	869	1	869	101	101	241	1	21	22	68
9	HNHGO09	97979 03/27/97	Uni-ZAP XR	19	959	1	959	176	176	242	1	21	22	44
10	HOUBE18	97979 03/27/97	Uni-ZAP XR	20	1446	1	1446	101	101	243	1	27	28	50
11	HOUDL69	97979 03/27/97	Uni-ZAP XR	21	1471	579	1460	692	692	244	1	31	32	42

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
12	HPMF171	97979 03/27/97	Uni-ZAP XR	22	1402	242	1402	401	401	245	1	32	33	60
13	HPMGQ55	97979 03/27/97	Uni-ZAP XR	23	1047	1	1047	164	164	246	1	26	27	35
14	HPQAC69	97979 03/27/97	Lambda ZAP II	24	990	1	988	82	82	247	1	20	21	37
15	HPTBB03	97979 03/27/97	Uni-ZAP XR	25	1208	350	1173	398	398	248	1	29	30	210
16	HPTWA66	97979 03/27/97	pBluescript	26	1922	1381	1922	24	24	249	1	33	34	547
16	HPTWA66	97979 03/27/97	pBluescript	219	575	1	575	148	148	442	1	22	23	65
17	HPTWC08	97979 03/27/97	pBluescript	27	1951	1422	1874	219	219	250	1	19	20	299
18	HRGCZ46	97979 03/27/97	Uni-ZAP XR	28	3989	2635	3989		2748	251	1	16	17	39
19	HSADV34	97979 03/27/97	Uni-ZAP XR	29	3735	2966	3735	272	272	252	1	30	31	594
19	HSADV34	97979 03/27/97	Uni-ZAP XR	220	3018	1929	3018	26	26	443	1	1	2	156
20	HSDFW61	97974 04/04/97 209080 05/29/97	Uni-ZAP XR	30	1667	59	1625	138	138	253	1	32	33	130
21	HSDGP60	97974 04/04/97	Uni-ZAP XR	31	1408	1	1408	285	285	254	1			20

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of NT Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
		209080 05/29/97												
22	HSOAI55	97974 04/04/97 209080 05/29/97	Uni-ZAP XR	32	2031	1273	2031	1285	1285	255	1	29	30	30
23	HSQEO84	97974 04/04/97 209080 05/29/97	Uni-ZAP XR	33	971	13	971	91	91	256	1	19	20	218
23	HSQEO84	97974 04/04/97 209080 05/29/97	Uni-ZAP XR	221	968	8	968	86	86	444	1	20	21	56
24	HSXAM05	97974 04/04/97 209080 05/29/97	Uni-ZAP XR	34	1792	369	1792	470	470	257	1	26	27	49
25	HSXAS67	97974 04/04/97 209080 05/29/97	Uni-ZAP XR	35	896	1	896	96	96	258	1	32	33	121
26	HTDAF28	97974 04/04/97 209080 05/29/97	pSport1	36	912	1	912	38	38	259	1	22	23	87
27	HTEGQ64	97974	Uni-ZAP XR	37	1382	67	1382	271	271	260	1			25

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
		04/04/97 209080 05/29/97												
28	HTGEU09	97974 04/04/97 209080 05/29/97	Uni-ZAP XR	38	872	1	872	74	74	261	1	18	19	28
29	HTOAM21	97974 04/04/97 209080 05/29/97	Uni-ZAP XR	39	812	1	812	41	41	262	1	30	31	43
30	HTPBW79	209511 12/03/97	Uni-ZAP XR	40	1515	118	1507	302	302	263	1	24	25	362
30	HTSEV09	97974 04/04/97 209080 05/29/97	pBluescript	222	1404	1	1265	92	92	445	1	19	20	415
31	HJPCD40	97974 04/04/97 209080 05/29/97	Uni-ZAP XR	41	704	22	704		117	264	1	18	19	127
32	HTWBY48	97974 04/04/97 209080 05/29/97	pSport1	42	1094	1	1094	32	32	265	1	34	35	53
33	HTWC146	97974 04/04/97	pSport1	43	1821	892	1647	56	56	266	1	26	27	28

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
		209080 05/29/97												
34	HTXGI75	97974 04/04/97 209080 05/29/97	Uni-ZAP XR	44	1024	30	1024		167	267	1	20	21	25
35	HWTFBF59	97974 04/04/97 209080 05/29/97	Uni-ZAP XR	45	983	779	983	85	85	268	1	30	31	221
35	HWTFBF59	97974 04/04/97 209080 05/29/97	Uni-ZAP XR	223	707	488	707	514	514	446	1	41	42	64
36	HADAE74	97974 04/04/97 209080 05/29/97	pSport1	46	2421	664	1587	710	710	269	1			2
37	HAGFB60	97974 04/04/97 209080 05/29/97	Uni-ZAP XR	47	840	1	840	97	97	270	1	30	31	48
38	HATEF60	97974 04/04/97 209080 05/29/97	Uni-ZAP XR	48	2432	1193	2246	1491	1491	271	1	17	18	51
39	HBMSN25	97974	Uni-ZAP XR	49	1742	1165	1742	1207	1207	272	1	23	24	31

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
		04/04/97 209080 05/29/97												
40	HCDAR68	97974 04/04/97 209080 05/29/97	Uni-ZAP XR	50	1487	181	1455	325	325	273	1	35	36	56
41	HCE3J79	97974 04/04/97 209080 05/29/97	Uni-ZAP XR	51	1328	251	1328	525	525	274	1			21
42	HMDAN54	97974 04/04/97 209080 05/29/97	Uni-ZAP XR	52	1856	725	1853	928	928	275	1	33	34	50
43	HCECA49	97974 04/04/97 209080 05/29/97	Uni-ZAP XR	53	1558	310	1408	393	393	276	1			1
44	HCEEC15	97974 04/04/97 209080 05/29/97	Uni-ZAP XR	54	948	1	948	9	9	277	1	23	24	65
45	HCESF40	97974 04/04/97 209080 05/29/97	pBluescript	55	990	99	990	193	193	278	1	32	33	256

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
45	HCESF40	97974 04/04/97 209080 05/29/97	pBluescript	224	1384	99	1384	193	193	447	1	32	33	205
46	HCFMV39	97974 04/04/97 209080 05/29/97	pSport I	56	1603	1	1296	96	96	279	1	29	30	102
47	HCM SX86	97975 04/04/97 209081 05/29/97	Uni-ZAP XR	57	1052	5	786	12	12	280	1	28	29	32
48	HCNAP62	97975 04/04/97 209081 05/29/97	Lambda ZAP II	58	814	1	558	93	93	281	1	22	23	42
49	HCRAF32	97975 04/04/97 209081 05/29/97	Uni-ZAP XR	59	1215	257	1215		356	282	1	19	20	20
50	HCUDC07	97975 04/04/97 209081 05/29/97	ZAP Express	60	478	1	478	147	147	283	1	36	37	69
51	HCWBB42	97975 04/04/97 209081	ZAP Express	61	618	1	618	212	212	284	1	35	36	74

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of NT Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
52	HDTAB05	97975 04/04/97 209081 05/29/97	PCMVSport 2.0	62	751	1	751	257	257	285	1	21	22	32
53	HE2AV74	97975 04/04/97 209081 05/29/97	Uni-ZAP XR	63	780	283	780		433	286	1			16
54	HE2AY71	97975 04/04/97 209081 05/29/97	Uni-ZAP XR	64	588	21	588	169	169	287	1			16
55	HE2GS36	97975 04/04/97 209081 05/29/97	Uni-ZAP XR	65	774	272	774	445	445	288	1			37
56	HE2OF09	97975 04/04/97 209081 05/29/97	Uni-ZAP XR	66	1866	1313	1866	1596	1596	289	1			11
57	HE6EU50	97975 04/04/97 209081 05/29/97	Uni-ZAP XR	67	1152	117	686	237	237	290	1	20	21	34
58	HE9HU17	97975 04/04/97	Uni-ZAP XR	68	2483	1577	2448	1620	1620	291	1			14

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
		209081 05/29/97											
59	HE9ND48	97975 04/04/97 209081	Uni-ZAP XR	69	536	1	536	83	83	292	1	36	43
		05/29/97											
60	HEBBW11	97975 04/04/97 209081	Uni-ZAP XR	70	865	647	865		388	293	1	30	135
		05/29/97											
61	HELDY74	97975 04/04/97 209081	Uni-ZAP XR	71	932	1	932	201	201	294	1	17	33
		05/29/97											
62	HEMAE80	97975 04/04/97 209081	Uni-ZAP XR	72	996	1	945	12	12	295	1	24	136
		05/29/97											
63	HFEBA88	97975 04/04/97 209081	Uni-ZAP XR	73	785	464	785	356	356	296	1	29	57
		05/29/97											
64	HFGAB89	97975 04/04/97 209081	Uni-ZAP XR	74	1069	196	1047	295	295	297	1	32	34
		05/29/97											
65	HFVHY45	97975	pBluescript	75	831	1	831		89	298	1	30	76

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
		04/04/97 209081 05/29/97												
66	HGBAJ93	97975 04/04/97 209081 05/29/97	Uni-ZAP XR	76	590	1	590	233	233	299	1	38	39	94
67	HGBBQ69	97975 04/04/97 209081 05/29/97	Uni-ZAP XR	77	1274	1	1273	105	105	300	1	24	25	43
68	HHFCF08	97975 04/04/97 209081 05/29/97	Uni-ZAP XR	78	1133	4	1042	175	175	301	1	23	24	30
69	HHFHJ59	97975 04/04/97 209081 05/29/97	Uni-ZAP XR	79	661	1	661	192	192	302	1	29	30	112
70	HHFHR32	97975 04/04/97 209081 05/29/97	Uni-ZAP XR	80	1378	1	1378		358	303	1			13
71	HHGCN69	97975 04/04/97 209081 05/29/97	Lambda ZAP II	81	1440	298	1440	532	532	304	1	23	24	34

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
72	HHGDO13	97975 04/04/97 209081 05/29/97	Lambda ZAP II	82	1381	766	1371	993	993	305	1	23	24	34
73	HHFED63	97975 04/04/97 209081 05/29/97	Uni-ZAP XR	83	1706	182	1644	257	257	306	1	24	25	81
74	HHSEG23	97976 04/04/97	Uni-ZAP XR	84	573	1	573	160	160	307	1	18	19	71
75	HJPAV06	97976 04/04/97	Uni-ZAP XR	85	684	199	684	323	323	308	1	27	28	33
76	HKIXL73	97976 04/04/97	pBluescript	86	1036	591	1036	690	690	309	1	32	33	114
77	HKMNC43	97976 04/04/97	pBluescript	87	908	1	908	139	139	310	1	18	19	108
78	HMEIE31	97976 04/04/97	Lambda ZAP II	88	655	1	655	165	165	311	1	33	34	64
79	HMSKS35	97976 04/04/97	Uni-ZAP XR	89	1102	1	1102	228	228	312	1	26	27	49
80	HNF AE54	97976 04/04/97	Uni-ZAP XR	90	1533	665	1518	347	347	313	1	26	27	293
81	HNFJH45	97976 04/04/97	Uni-ZAP XR	91	575	1	575	275	275	314	1	30	31	67
82	HNGBT31	97976 04/04/97	Uni-ZAP XR	92	639	1	639	224	224	315	1	28	29	104

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
83	HNGIN60	97976 04/04/97	Uni-ZAP XR	93	744	1	744	225	225	316	1	43	44	70
84	HNGJG84	97976 04/04/97	Uni-ZAP XR	94	526	1	526	268	268	317	1	29	30	38
85	HNHDW42	97976 04/04/97	Uni-ZAP XR	95	426	1	426	168	168	318	1	28	29	71
86	HNHFL57	97976 04/04/97	Uni-ZAP XR	96	844	1	844	98	98	319	1	25	26	61
87	HOGAR52	97977 04/04/97 209082 05/29/97	pCMVSPORT 2.0	97	1985	453	1985	533	533	320	1	17	18	285
88	HOSBZ55	97977 04/04/97 209082 05/29/97	Uni-ZAP XR	98	1416	69	1416	246	246	321	1	32	33	54
89	HOSD192	97977 04/04/97 209082 05/29/97	Uni-ZAP XR	99	1935	141	772		274	322	1	20	21	58
90	HPBCU51	97977 04/04/97 209082 05/29/97	pBluescript SK-	100	599	1	599	86	86	323	1	27	28	119
91	HPCAL49	97977 04/04/97 209082	Uni-ZAP XR	101	784	1	784		280	324	1	18	19	43

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of NT Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
92	HPFCR13	97977 04/04/97 209082 05/29/97	Uni-ZAP XR	102	1035	602	1035	859	859	325	1	32	33	58
93	HPHAC83	97977 04/04/97 209082 05/29/97	Uni-ZAP XR	103	2218	840	2182	1035	1035	326	1	17	18	17
94	HPMBQ32	97977 04/04/97 209082 05/29/97	Uni-ZAP XR	104	1351	1	1351	18	18	327	1	23	24	86
95	HPWAN23	97977 04/04/97 209082 05/29/97	Uni-ZAP XR	105	2066	51	2052	270	270	328	1	29	30	537
95	HPWAN23	97977 04/04/97 209082 05/29/97	Uni-ZAP XR	226	2057	1	1954	220	220	449	1	29	30	315
96	HRDFB85	97977 04/04/97 209082 05/29/97	Uni-ZAP XR	106	1705	23	1697	233	233	329	1	21	22	201
97	HRGBR28	97977 04/04/97	Uni-ZAP XR	107	1167	611	1167	53	53	330	1	1	2	263

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
		209082 05/29/97												
98	HSKGN81	97977 04/04/97 209082 05/29/97	pBluescript	108	1907	151	1432	353	353	331	1	23	24	260
98	HSKGN81	97977 04/04/97 209082 05/29/97	pBluescript	227	2084	335	2084	537	537	450	1	19	20	23
99	HSPA56	97977 04/04/97 209082 05/29/97	pSport1	109	611	1	576	229	229	332	1	25	26	47
100	HE8EU04	209746 04/07/98	Uni-ZAP XR	110	2632	294	2632	337	337	333	1	25	26	333
100	HSXBT86	97977 04/04/97 209082 05/29/97	Uni-ZAP XR	228	2143	53	1096	235	235	451	1			9
101	HSXCS62	97977 04/04/97 209082 05/29/97	Uni-ZAP XR	111	2249	1	1953	90	90	334	1	18	19	199
102	HTEFU09	97977 04/04/97 209082	Uni-ZAP XR	112	2198	228	2158	400	400	335	1			23

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
103	HTKEM35	97977 04/04/97 209082	Uni-ZAP XR	113	1043	40	1043	320	320	336	1	20	21	142
		05/29/97												
104	HTGEP89	97977 04/04/97 209082	Uni-ZAP XR	114	703	1	703	285	285	337	1	29	30	94
		05/29/97												
105	HTGEW91	97977 04/04/97 209082	Uni-ZAP XR	115	3684	526	1338	584	584	338	1	24	25	37
		05/29/97												
106	HTOEY16	97977 04/04/97 209082	Uni-ZAP XR	116	1965	127	1915	202	202	339	1	27	28	38
		05/29/97												
107	HTPCN79	97977 04/04/97 209082	Uni-ZAP XR	117	503	1	503		1	340	1	7	8	70
		05/29/97												
108	HTSGM54	97977 04/04/97 209082	pBluescript	118	1133	316	1069		423	341	1	12	13	84
		05/29/97												
109	HTSHE40	97977 04/04/97	pBluescript	119	1101	118	956	218	218	342	1	31	32	89

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
		209082 05/29/97												
110	HTWAF58	97/977 04/04/97 209082	Lambda ZAP II	120	282	1	282	137	137	343	1	25	26	48
		05/29/97												
111	HTWBY29	97/977 04/04/97 209082	pSport1	121	2635	1593	2489	1654	1654	344	1	25	26	55
		05/29/97												
112	HUKFC71	209007 04/28/97 209083	Lambda ZAP II	122	994	1	932		272	345	1	15	16	221
		05/29/97												
113	HCE3Q10	209007 04/28/97 209083	Uni-ZAP XR	123	1542	1	1542	143	143	346	1	25	26	63
		05/29/97												
114	HCEVR60	209007 04/28/97 209083	Uni-ZAP XR	124	1390	82	1390	127	127	347	1	32	33	153
		05/29/97												
115	HDTAW95	209007 04/28/97 209083	pCMVSPORT 2.0	125	1288	412	1288	571	571	348	1			16
		05/29/97												
116	HE6EL90	209007	Uni-ZAP XR	126	1517	1	1452	243	243	349	1			9

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
		04/28/97 209083 05/29/97												
117	HELB029	209007 04/28/97 209083 05/29/97	Uni-ZAP XR	127	1073	198	1073		776	350	1			13
118	HERAH36	209007 04/28/97 209083 05/29/97	Uni-ZAP XR	128	300	155	300	202	202	351	1			17
119	HFXBW82	209007 04/28/97 209083 05/29/97	Lambda ZAP II	129	1275	1	1275	56	56	352	1	23	24	61
120	HHPD20	209007 04/28/97 209083 05/29/97	Uni-ZAP XR	130	472	51	472		243	353	1			32
121	HIBED17	209007 04/28/97 209083 05/29/97	Other	131	1950	284	1927	395	395	354	1	72	73	245
122	HLTER03	209007 04/28/97 209083 05/29/97	Uni-ZAP XR	132	990	1	990	78	78	355	1	22	23	34

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
123	HOABL56	209007 04/28/97 209083 05/29/97	Uni-ZAP XR	133	1720	565	1720	660	660	356	1	18	19	21
124	HPMCJ92	209007 04/28/97 209083 05/29/97	Uni-ZAP XR	134	705	28	705	106	106	357	1	28	29	98
125	HPWAZ95	209007 04/28/97 209083 05/29/97	Uni-ZAP XR	135	323	1	323	88	88	358	1	27	28	78
126	HRGBR18	209007 04/28/97 209083 05/29/97	Uni-ZAP XR	136	582	1	582		16	359	1	17	18	30
127	HSUBW09	209007 04/28/97 209083 05/29/97	Uni-ZAP XR	137	1021	1	1021	153	153	360	1	32	33	56
128	HUKCO64	209007 04/28/97 209083 05/29/97	Lambda ZAP II	138	1777	439	1777		521	361	1			2
129	H6EAA53	209007 04/28/97 209083	Uni-ZAP XR	139	643	303	643		313	362	1	7	8	31

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
130	HAGAI11	209007 04/28/97 209083 05/29/97	Uni-ZAP XR	140	1220	1	1220		127	363	1	16	17	27
131	HAGA039	209007 04/28/97 209083 05/29/97	Uni-ZAP XR	141	721	1	721		415	364	1			14
132	HALSK07	209007 04/28/97 209083 05/29/97	Uni-ZAP XR	142	1468	125	1468	210	210	365	1	29	30	33
133	HALSQ59	209007 04/28/97 209083 05/29/97	Uni-ZAP XR	143	300	4	300	101	101	366	1	22	23	66
134	HAIBP89	unknown 05/18/98	Uni-ZAP XR	144	2243	173	2243	311	311	367	1	27	28	317
134	HBCGB91	209007 04/28/97 209083 05/29/97	Uni-ZAP XR	229	1025	409	1025	624	624	452	1	20	21	25
135	HBM7D81	209008 04/28/97 209084 05/29/97	Uni-ZAP XR	145	1082	163	1082	357	357	368	1			30

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO. X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO. Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
136	HBXGK12	209008 04/28/97 209084 05/29/97	ZAP Express	146	4313	1153	4313	1313	1313	369	1	18	19	42
137	HFKFJ07	209010 04/28/97 209085 05/29/97	Uni-ZAP XR	147	1183	1	1183	149	149	370	1	41	42	254
138	HCQA140	209008 04/28/97 209084 05/29/97	Lambda ZAP II	148	734	1	734	285	285	371	1			19
139	HCWHZ24	209008 04/28/97 209084 05/29/97	ZAP Express	149	1405	1	1405	108	108	372	1	34	35	63
140	HE2GT20	209008 04/28/97 209084 05/29/97	Uni-ZAP XR	150	2890	1178	2890	1178	1178	373	1	31	32	39
141	HE8EY43	209008 04/28/97 209084 05/29/97	Uni-ZAP XR	151	2399	1181	2399	1265	1265	374	1	30	31	34
142	HFCEB37	209008 04/28/97 209084	Uni-ZAP XR	152	802	352	802		487	375	1			10

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
143	HFTCT67	209008 04/28/97	Uni-ZAP XR	153	461	24	461	145	145	376	1	37	38	63
		209084 05/29/97												
144	HGLAM46	209008 04/28/97	Uni-ZAP XR	154	2388	818	2388	648	648	377	1			18
		209084 05/29/97												
145	HHGBR15	209008 04/28/97	Lambda ZAP II	155	642	322	642	400	400	378	1			4
		209084 05/29/97												
146	HJAAU36	209008 04/28/97	pBluescript SK-	156	1251	583	1251		933	379	1	16	17	16
		209084 05/29/97												
147	HUSIT49	209008 04/28/97	pSport I	157	2127	247	2127	383	383	380	1	47	48	83
		209084 05/29/97												
148	HKLAB16	209008 04/28/97	Lambda ZAP II	158	1625	817	1625	1012	1012	381	1	18	19	20
		209084 05/29/97												
149	HLMMU76	209008 04/28/97	Lambda ZAP II	159	1687	1307	1687	1296	1296	382	1	28	29	28

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
150	HMSKQ35	209008 04/28/97 209084 05/29/97	Uni-ZAP XR	160	1842	172	1463	319	319	383	1	30	31	33
151	HNHED86	209008 04/28/97 209084 05/29/97	Uni-ZAP XR	161	770	1	770	30	30	384	1	31	32	46
152	HNHEJ88	209008 04/28/97 209084 05/29/97	Uni-ZAP XR	162	519	1	519	242	242	385	1	17	18	24
153	HNHFQ63	209008 04/28/97 209084 05/29/97	Uni-ZAP XR	163	753	1	753	164	164	386	1	17	18	67
154	HOECU83	209009 04/28/97	Uni-ZAP XR	164	1400	189	1400		508	387	1	22	23	33
155	HPTRC15	209009 04/28/97	pBluescript	165	2153	594	2153		611	388	1			13
156	HSKCP69	209009 04/28/97	Uni-ZAP XR	166	1251	219	1120			389	1			
156	HSKCP69	209009 04/28/97	Uni-ZAP XR	230	1250	223	1250	393	393	453	1	32	33	171
157	H6EAE26	209009	Uni-ZAP XR	167	882	48	882	155	155	390	1	33	34	153

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
158	HAGBX03	209009 04/28/97	Uni-ZAP XR	168	1208	1	1208	182	182	391	1			8
159	HAGDQ47	209009 04/28/97	Uni-ZAP XR	169	1307	1	1307	44	44	392	1	22	23	60
160	HAICP19	209009 04/28/97	Uni-ZAP XR	170	1624	89	1483	128	128	393	1	18	19	446
161	HAUA83	209009 04/28/97	Uni-ZAP XR	171	2003	889	2003	1080	1080	394	1			23
162	HBHAD12	209009 04/28/97	Uni-ZAP XR	172	786	1	786		176	395	1	17	18	23
163	HBMTY28	209009 04/28/97	Uni-ZAP XR	173	1758	962	1758	1184	1184	396	1	27	28	34
164	HBMP04	209009 04/28/97	Uni-ZAP XR	174	888	330	862		546	397	1			2
165	HCDD878	209009 04/28/97	Uni-ZAP XR	175	2379	750	2379	901	901	398	1	18	19	24
166	HCEQA68	209010 04/28/97 209085 05/29/97	Uni-ZAP XR	176	1348	1	1348	12	12	399	1	28	29	78
167	HCEZS40	209010 04/28/97 209085 05/29/97	Uni-ZAP XR	177	1502	178	1502	315	315	400	1			20
168	HCFNF11	209010	pSport1	178	1637	26	1607	152	152	401	1	44	45	257

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
		04/28/97 209085 05/29/97												
169	HCRBL20	209010 04/28/97 209085 05/29/97	Uni-ZAP XR	179	2911	1103	2858	192	192	402	1	32	33	424
169	HCRBL20	209010 04/28/97 209085 05/29/97	Uni-ZAP XR	231	1811	20	1811	93	93	454	1	36	37	95
170	HCUBL62	209010 04/28/97 209085 05/29/97	ZAP Express	180	519	1	519	57	57	403	1	28	29	32
171	HDSAP81	209010 04/28/97 209085 05/29/97	Uni-ZAP XR	181	968	320	968	476	476	404	1	27	28	79
172	HE2CT29	209010 04/28/97 209085 05/29/97	Uni-ZAP XR	182	1128	1	1128	111	111	405	1	26	27	94
173	HE8MG65	209010 04/28/97 209085 05/29/97	Uni-ZAP XR	183	2276	48	2276	88	88	406	1	37	38	257

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
173	HE8MG65	209010 04/28/97 209085 05/29/97	Uni-ZAP XR	232	2271	56	2232	79	79	455	1	43	44	170
174	HE9FB42	209010 04/28/97 209085 05/29/97	Uni-ZAP XR	184	2500	76	1693	518	518	407	1	1	2	623
175	HEMAM41	209010 04/28/97 209085 05/29/97	Uni-ZAP XR	185	1337	60	1328	175	175	408	1	39	40	190
175	HEMAM41	209010 04/28/97 209085 05/29/97	Uni-ZAP XR	233	1338	33	1327	175	175	456	1	32	33	91
176	HEMCV19	209010 04/28/97 209085 05/29/97	Uni-ZAP XR	186	941	33	931	79	79	409	1	23	24	178
177	HEMDX17	209010 04/28/97 209085 05/29/97	Uni-ZAP XR	187	654	1	654	137	137	410	1			13
178	HETAR54	209010 04/28/97 209085	Uni-ZAP XR	188	1848	454	1848	948	948	411	1	14	15	232

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO. X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO. Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
179	HETBX14	209010 04/28/97 209085 05/29/97	Uni-ZAP XR	189	1146	157	1146		74	412	1	14	15	53
180	HFGAB48	209010 04/28/97 209085 05/29/97	Uni-ZAP XR	190	906	156	906	245	245	413	1	30	31	32
181	HFKF140	209010 04/28/97 209085 05/29/97	Uni-ZAP XR	191	1941	120	1002	213	213	414	1	18	19	218
182	HFXHN68	209010 04/28/97 209085 05/29/97	Lambda ZAP II	192	2118	777	2118	966	966	415	1	23	24	50
183	HGBFO79	209011 04/28/97	Uni-ZAP XR	193	1538	259	1538	273	273	416	1	23	24	49
184	HGLAM56	209011 04/28/97	Uni-ZAP XR	194	1098	68	1098		185	417	1	28	29	69
185	HHLBA89	209011 04/28/97	pBluescript SK-	195	1001	1	1001	324	324	418	1	25	26	39
186	HHPDW05	209011 04/28/97	Uni-ZAP XR	196	1443	1	1443	246	246	419	1	21	22	21
187	HHPSD37	209011 04/28/97	pBluescript	197	1282	66	1282	171	171	420	1	19	20	37

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
188	HHPST70	209011 04/28/97	pBluescript	198	951	26	951		162	421	1	16	17	34
189	HHSK25	209011 04/28/97	Uni-ZAP XR	199	1740	1390	1740	1534	1534	422	1	19	20	31
190	HLASB53	209011 04/28/97	pBluescript	200	1707	401	1195	652	652	423	1	26	27	126
191	HJABZ65	209011 04/28/97	pBluescript SK-	201	779	1	779	23	23	424	1	26	27	68
192	HJPBB39	209011 04/28/97	Uni-ZAP XR	202	1617	188	1605	182	182	425	1	28	29	91
193	HLHSK94	209011 04/28/97	pBluescript	203	1974	1	1794	112	112	426	1	26	27	379
194	HLHTC70	209011 04/28/97	pBluescript	204	1057	229	1057	365	365	427	1	23	24	22
195	HLMIW92	209011 04/28/97	Lambda ZAP II	205	721	1	721	244	244	428	1	25	26	46
196	HLTCY93	209011 04/28/97	Uni-ZAP XR	206	2465	988	2465	1225	1225	429	1			4
197	HLTDB65	209011 04/28/97	Uni-ZAP XR	207	1480	1	1480		371	430	1	15	16	143
198	HMSHM43	209011 04/28/97	Uni-ZAP XR	208	872	1	872	35	35	431	1	18	19	36
199	HMSHQ24	209011 04/28/97	Uni-ZAP XR	209	1779	16	1779	148	148	432	1	24	25	36
200	HNEFAH08	209011 04/28/97	Uni-ZAP XR	210	2110	592	2110	611	611	433	1	18	19	191

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of NT Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
201	HNGAO10	209011 04/28/97	Uni-ZAP XR	211	938	1	938	107	107	434	1	27	28	30
202	HNGBE45	209011 04/28/97	Uni-ZAP XR	212	1551	1	1551	114	114	435	1	21	22	100
203	HNHAZ16	209011 04/28/97	Uni-ZAP XR	213	997	1	997	202	202	436	1	24	25	36
204	HNHCM59	209011 04/28/97	Uni-ZAP XR	214	1496	1	1132		165	437	1	28	29	41
205	HOSFM22	97977 04/04/97 209082 05/29/97	Uni-ZAP XR	215	1308	501	1308		809	438	1			1
206	HPHAC88	97977 04/04/97 209082 05/29/97	Uni-ZAP XR	216	1705	384	1705	549	549	439	1	23	24	24
207	HCDEO95	209007 04/28/97 209083 05/29/97	Uni-ZAP XR	217	999	608	999	273	273	440	1	22	23	54

Table 1 summarizes the information corresponding to each "Gene No." described above. The nucleotide sequence identified as "NT SEQ ID NO:X" was assembled from partially homologous ("overlapping") sequences obtained from the "cDNA clone ID" identified in Table 1 and, in some cases, from additional related DNA clones. The overlapping sequences were assembled into a single contiguous sequence of high redundancy (usually three to five overlapping sequences at each nucleotide position), resulting in a final sequence identified as SEQ ID NO:X.

The cDNA Clone ID was deposited on the date and given the corresponding deposit number listed in "ATCC Deposit No:Z and Date." Some of the deposits contain multiple different clones corresponding to the same gene. "Vector" refers to the type of vector contained in the cDNA Clone ID.

"Total NT Seq." refers to the total number of nucleotides in the contig identified by "Gene No." The deposited clone may contain all or most of these sequences, reflected by the nucleotide position indicated as "5' NT of Clone Seq." and the "3' NT of Clone Seq." of SEQ ID NO:X. The nucleotide position of SEQ ID NO:X of the putative start codon (methionine) is identified as "5' NT of Start Codon." Similarly, the nucleotide position of SEQ ID NO:X of the predicted signal sequence is identified as "5' NT of First AA of Signal Pep."

The translated amino acid sequence, beginning with the methionine, is identified as "AA SEQ ID NO:Y," although other reading frames can also be easily translated using known molecular biology techniques. The polypeptides produced by these alternative open reading frames are specifically contemplated by the present invention.

The first and last amino acid position of SEQ ID NO:Y of the predicted signal peptide is identified as "First AA of Sig Pep" and "Last AA of Sig Pep." The predicted first amino acid position of SEQ ID NO:Y of the secreted portion is identified as "Predicted First AA of Secreted Portion." Finally, the amino acid position of SEQ ID NO:Y of the last amino acid in the open reading frame is identified as "Last AA of ORF."

SEQ ID NO:X and the translated SEQ ID NO:Y are sufficiently accurate and otherwise suitable for a variety of uses well known in the art and described further below. For instance, SEQ ID NO:X is useful for designing nucleic acid hybridization probes that will detect nucleic acid sequences contained in SEQ ID NO:X or the cDNA contained in the deposited clone. These probes will also hybridize to nucleic acid molecules in biological samples, thereby enabling a variety of forensic and diagnostic methods of the invention. Similarly, polypeptides identified from SEQ ID NO:Y may be used to generate antibodies which bind specifically to the secreted proteins encoded by the cDNA clones identified in Table 1.

Nevertheless, DNA sequences generated by sequencing reactions can contain sequencing errors. The errors exist as misidentified nucleotides, or as insertions or deletions of nucleotides in the generated DNA sequence. The erroneously inserted or deleted nucleotides cause frame shifts in the reading frames of the predicted amino acid sequence. In these cases, the predicted amino acid sequence diverges from the actual amino acid sequence, even though the generated DNA sequence may be greater than 99.9% identical to the actual DNA sequence (for example, one base insertion or deletion in an open reading frame of over 1000 bases).

Accordingly, for those applications requiring precision in the nucleotide sequence or the amino acid sequence, the present invention provides not only the generated nucleotide sequence identified as SEQ ID NO:X and the predicted translated amino acid sequence identified as SEQ ID NO:Y, but also a sample of plasmid DNA containing a human cDNA of the invention deposited with the ATCC, as set forth in Table 1. The nucleotide sequence of each deposited clone can readily be determined by sequencing the deposited clone in accordance with known methods. The predicted amino acid sequence can then be verified from such deposits. Moreover, the amino acid sequence of the protein encoded by a particular clone can also be directly determined by peptide sequencing or by expressing the protein in a suitable host cell containing the deposited human cDNA, collecting the protein, and determining its sequence.

The present invention also relates to the genes corresponding to SEQ ID NO:X, SEQ ID NO:Y, or the deposited clone. The corresponding gene can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include preparing probes or primers from the disclosed sequence and identifying or amplifying the corresponding gene from appropriate sources of genomic material.

Also provided in the present invention are species homologs. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source for the desired homologue.

The polypeptides of the invention can be prepared in any suitable manner. Such polypeptides include isolated naturally occurring polypeptides, recombinantly produced polypeptides, synthetically produced polypeptides, or polypeptides produced by a combination of these methods. Means for preparing such polypeptides are well understood in the art.

The polypeptides may be in the form of the secreted protein, including the mature form, or may be a part of a larger protein, such as a fusion protein (see below).

It is often advantageous to include an additional amino acid sequence which contains secretory or leader sequences, pro-sequences, sequences which aid in purification, such as multiple histidine residues, or an additional sequence for stability during recombinant production.

- 5 The polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of a polypeptide, including the secreted polypeptide, can be substantially purified by the one-step method described in Smith and Johnson, *Gene* 67:31-40 (1988). Polypeptides of the invention also can be purified from natural or recombinant sources
10 using antibodies of the invention raised against the secreted protein in methods which are well known in the art.

Signal Sequences

- Methods for predicting whether a protein has a signal sequence, as well as the
15 cleavage point for that sequence, are available. For instance, the method of McGeoch, *Virus Res.* 3:271-286 (1985), uses the information from a short N-terminal charged region and a subsequent uncharged region of the complete (uncleaved) protein. The method of von Heinje, *Nucleic Acids Res.* 14:4683-4690 (1986) uses the information from the residues surrounding the cleavage site, typically residues -13 to +2, where +1
20 indicates the amino terminus of the secreted protein. The accuracy of predicting the cleavage points of known mammalian secretory proteins for each of these methods is in the range of 75-80%. (von Heinje, *supra*.) However, the two methods do not always produce the same predicted cleavage point(s) for a given protein.

- In the present case, the deduced amino acid sequence of the secreted polypeptide
25 was analyzed by a computer program called SignalP (Henrik Nielsen et al., *Protein Engineering* 10:1-6 (1997)), which predicts the cellular location of a protein based on the amino acid sequence. As part of this computational prediction of localization, the methods of McGeoch and von Heinje are incorporated. The analysis of the amino acid sequences of the secreted proteins described herein by this program provided the results
30 shown in Table 1.

- As one of ordinary skill would appreciate, however, cleavage sites sometimes vary from organism to organism and cannot be predicted with absolute certainty. Accordingly, the present invention provides secreted polypeptides having a sequence shown in SEQ ID NO:Y which have an N-terminus beginning within 5 residues (i.e., +
35 or - 5 residues) of the predicted cleavage point. Similarly, it is also recognized that in some cases, cleavage of the signal sequence from a secreted protein is not entirely

uniform, resulting in more than one secreted species. These polypeptides, and the polynucleotides encoding such polypeptides, are contemplated by the present invention.

Moreover, the signal sequence identified by the above analysis may not necessarily predict the naturally occurring signal sequence. For example, the naturally occurring signal sequence may be further upstream from the predicted signal sequence. However, it is likely that the predicted signal sequence will be capable of directing the secreted protein to the ER. These polypeptides, and the polynucleotides encoding such polypeptides, are contemplated by the present invention.

10 **Polynucleotide and Polypeptide Variants**

"Variant" refers to a polynucleotide or polypeptide differing from the polynucleotide or polypeptide of the present invention, but retaining essential properties thereof. Generally, variants are overall closely similar, and, in many regions, identical to the polynucleotide or polypeptide of the present invention.

By a polynucleotide having a nucleotide sequence at least, for example, 95% "identical" to a reference nucleotide sequence of the present invention, it is intended that the nucleotide sequence of the polynucleotide is identical to the reference sequence except that the polynucleotide sequence may include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence encoding the polypeptide. In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted or substituted with another nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the reference sequence may be inserted into the reference sequence. The query sequence may be an entire sequence shown in Table 1, the ORF (open reading frame), or any fragment specified as described herein.

As a practical matter, whether any particular nucleic acid molecule or polypeptide is at least 90%, 95%, 96%, 97%, 98% or 99% identical to a nucleotide sequence of the present invention can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci. (1990) 6:237-245). In a sequence alignment the query and subject sequences are both DNA sequences. An RNA sequence can be compared by converting U's to T's. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB alignment of DNA sequences to calculate percent identity are: Matrix=Unitary, k-tuple=4, Mismatch Penalty=1, Joining Penalty=30, Randomization

Group Length=0, Cutoff Score=1, Gap Penalty=5, Gap Size Penalty 0.05, Window Size=500 or the length of the subject nucleotide sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence because of 5' or 3' deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for 5' and 3' truncations of the subject sequence when calculating percent identity. For subject sequences truncated at the 5' or 3' ends, relative to the query sequence, the percent identity is corrected by calculating the number of bases of the query sequence that are 5' and 3' of the subject sequence, which are not matched/aligned, as a percent of the total bases of the query sequence. Whether a nucleotide is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This corrected score is what is used for the purposes of the present invention. Only bases outside the 5' and 3' bases of the subject sequence, as displayed by the FASTDB alignment, which are not matched/aligned with the query sequence, are calculated for the purposes of manually adjusting the percent identity score.

For example, a 90 base subject sequence is aligned to a 100 base query sequence to determine percent identity. The deletions occur at the 5' end of the subject sequence and therefore, the FASTDB alignment does not show a matched/alignment of the first 10 bases at 5' end. The 10 unpaired bases represent 10% of the sequence (number of bases at the 5' and 3' ends not matched/total number of bases in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 bases were perfectly matched the final percent identity would be 90%. In another example, a 90 base subject sequence is compared with a 100 base query sequence. This time the deletions are internal deletions so that there are no bases on the 5' or 3' of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only bases 5' and 3' of the subject sequence which are not matched/aligned with the query sequence are manually corrected for. No other manual corrections are to be made for the purposes of the present invention.

By a polypeptide having an amino acid sequence at least, for example, 95% "identical" to a query amino acid sequence of the present invention, it is intended that the amino acid sequence of the subject polypeptide is identical to the query sequence except that the subject polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the query amino acid sequence. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a query

amino acid sequence, up to 5% of the amino acid residues in the subject sequence may be inserted, deleted, (indels) or substituted with another amino acid. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions,

- 5 interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

As a practical matter, whether any particular polypeptide is at least 90%, 95%, 96%, 97%, 98% or 99% identical to, for instance, the amino acid sequences shown in Table 1 or to the amino acid sequence encoded by deposited DNA clone can be
10 determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci. (1990) 6:237-245). In a sequence alignment the query and
15 subject sequences are either both nucleotide sequences or both amino acid sequences. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB amino acid alignment are: Matrix=PAM 0, k-tuple=2, Mismatch Penalty=1, Joining Penalty=20, Randomization Group Length=0, Cutoff Score=1, Window Size=sequence length, Gap Penalty=5, Gap Size Penalty=0.05, Window
20 Size=500 or the length of the subject amino acid sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence due to N- or C-terminal deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for N- and C-terminal truncations of the subject sequence when calculating global percent identity.
25 For subject sequences truncated at the N- and C-termini, relative to the the query sequence, the percent identity is corrected by calculating the number of residues of the query sequence that are N- and C-terminal of the subject sequence, which are not matched/aligned with a corresponding subject residue, as a percent of the total bases of the query sequence. Whether a residue is matched/aligned is determined by results of
30 the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This final percent identity score is what is used for the purposes of the present invention. Only residues to the N- and C-termini of the subject sequence, which are not matched/aligned with the query sequence, are
35 considered for the purposes of manually adjusting the percent identity score. That is, only query residue positions outside the farthest N- and C-terminal residues of the subject sequence.

For example, a 90 amino acid residue subject sequence is aligned with a 100 residue query sequence to determine percent identity. The deletion occurs at the N-terminus of the subject sequence and therefore, the FASTDB alignment does not show a matching/alignment of the first 10 residues at the N-terminus. The 10 unpaired
5 residues represent 10% of the sequence (number of residues at the N- and C- termini not matched/total number of residues in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 residues were perfectly matched the final percent identity would be 90%. In another example, a 90 residue subject sequence is compared with a 100 residue query sequence.
10 This time the deletions are internal deletions so there are no residues at the N- or C-termini of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only residue positions outside the N- and C-terminal ends of the subject sequence, as displayed in the FASTDB alignment, which are not matched/aligned with the query
15 sequence are manually corrected for. No other manual corrections are to be made for the purposes of the present invention.

The variants may contain alterations in the coding regions, non-coding regions, or both. Especially preferred are polynucleotide variants containing alterations which produce silent substitutions, additions, or deletions, but do not alter the properties or
20 activities of the encoded polypeptide. Nucleotide variants produced by silent substitutions due to the degeneracy of the genetic code are preferred. Moreover, variants in which 5-10, 1-5, or 1-2 amino acids are substituted, deleted, or added in any combination are also preferred. Polynucleotide variants can be produced for a variety of reasons, e.g., to optimize codon expression for a particular host (change codons in
25 the human mRNA to those preferred by a bacterial host such as *E. coli*).

Naturally occurring variants are called "allelic variants," and refer to one of several alternate forms of a gene occupying a given locus on a chromosome of an organism. (Genes II, Lewin, B., ed., John Wiley & Sons, New York (1985).) These allelic variants can vary at either the polynucleotide and/or polypeptide level.
30 Alternatively, non-naturally occurring variants may be produced by mutagenesis techniques or by direct synthesis.

Using known methods of protein engineering and recombinant DNA technology, variants may be generated to improve or alter the characteristics of the polypeptides of the present invention. For instance, one or more amino acids can be
35 deleted from the N-terminus or C-terminus of the secreted protein without substantial loss of biological function. The authors of Ron et al., *J. Biol. Chem.* 268: 2984-2988 (1993), reported variant KGF proteins having heparin binding activity even after

deleting 3, 8, or 27 amino-terminal amino acid residues. Similarly, Interferon gamma exhibited up to ten times higher activity after deleting 8-10 amino acid residues from the carboxy terminus of this protein. (Dobeli et al., J. Biotechnology 7:199-216 (1988).)

Moreover, ample evidence demonstrates that variants often retain a biological activity similar to that of the naturally occurring protein. For example, Gayle and coworkers (J. Biol. Chem 268:22105-22111 (1993)) conducted extensive mutational analysis of human cytokine IL-1a. They used random mutagenesis to generate over 3,500 individual IL-1a mutants that averaged 2.5 amino acid changes per variant over the entire length of the molecule. Multiple mutations were examined at every possible amino acid position. The investigators found that "[m]ost of the molecule could be altered with little effect on either [binding or biological activity]." (See, Abstract.) In fact, only 23 unique amino acid sequences, out of more than 3,500 nucleotide sequences examined, produced a protein that significantly differed in activity from wild-type.

Furthermore, even if deleting one or more amino acids from the N-terminus or C-terminus of a polypeptide results in modification or loss of one or more biological functions, other biological activities may still be retained. For example, the ability of a deletion variant to induce and/or to bind antibodies which recognize the secreted form will likely be retained when less than the majority of the residues of the secreted form are removed from the N-terminus or C-terminus. Whether a particular polypeptide lacking N- or C-terminal residues of a protein retains such immunogenic activities can readily be determined by routine methods described herein and otherwise known in the art.

Thus, the invention further includes polypeptide variants which show substantial biological activity. Such variants include deletions, insertions, inversions, repeats, and substitutions selected according to general rules known in the art so as have little effect on activity. For example, guidance concerning how to make phenotypically silent amino acid substitutions is provided in Bowie, J. U. et al., Science 247:1306-1310 (1990), wherein the authors indicate that there are two main strategies for studying the tolerance of an amino acid sequence to change.

The first strategy exploits the tolerance of amino acid substitutions by natural selection during the process of evolution. By comparing amino acid sequences in different species, conserved amino acids can be identified. These conserved amino acids are likely important for protein function. In contrast, the amino acid positions where substitutions have been tolerated by natural selection indicates that these positions are not critical for protein function. Thus, positions tolerating amino acid substitution could be modified while still maintaining biological activity of the protein.

The second strategy uses genetic engineering to introduce amino acid changes at specific positions of a cloned gene to identify regions critical for protein function. For example, site directed mutagenesis or alanine-scanning mutagenesis (introduction of single alanine mutations at every residue in the molecule) can be used. (Cunningham and Wells, Science 244:1081-1085 (1989).) The resulting mutant molecules can then be tested for biological activity.

As the authors state, these two strategies have revealed that proteins are surprisingly tolerant of amino acid substitutions. The authors further indicate which amino acid changes are likely to be permissive at certain amino acid positions in the protein. For example, most buried (within the tertiary structure of the protein) amino acid residues require nonpolar side chains, whereas few features of surface side chains are generally conserved. Moreover, tolerated conservative amino acid substitutions involve replacement of the aliphatic or hydrophobic amino acids Ala, Val, Leu and Ile; replacement of the hydroxyl residues Ser and Thr; replacement of the acidic residues Asp and Glu; replacement of the amide residues Asn and Gln, replacement of the basic residues Lys, Arg, and His; replacement of the aromatic residues Phe, Tyr, and Trp, and replacement of the small-sized amino acids Ala, Ser, Thr, Met, and Gly.

Besides conservative amino acid substitution, variants of the present invention include (i) substitutions with one or more of the non-conserved amino acid residues, where the substituted amino acid residues may or may not be one encoded by the genetic code, or (ii) substitution with one or more of amino acid residues having a substituent group, or (iii) fusion of the mature polypeptide with another compound, such as a compound to increase the stability and/or solubility of the polypeptide (for example, polyethylene glycol), or (iv) fusion of the polypeptide with additional amino acids, such as an IgG Fc fusion region peptide, or leader or secretory sequence, or a sequence facilitating purification. Such variant polypeptides are deemed to be within the scope of those skilled in the art from the teachings herein.

For example, polypeptide variants containing amino acid substitutions of charged amino acids with other charged or neutral amino acids may produce proteins with improved characteristics, such as less aggregation. Aggregation of pharmaceutical formulations both reduces activity and increases clearance due to the aggregate's immunogenic activity. (Pinckard et al., Clin. Exp. Immunol. 2:331-340 (1967); Robbins et al., Diabetes 36: 838-845 (1987); Cleland et al., Crit. Rev. Therapeutic Drug Carrier Systems 10:307-377 (1993).)

Polynucleotide and Polypeptide Fragments

In the present invention, a "polynucleotide fragment" refers to a short polynucleotide having a nucleic acid sequence contained in the deposited clone or shown in SEQ ID NO:X. The short nucleotide fragments are preferably at least about 15 nt, and more preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably, at least about 40 nt in length. A fragment "at least 20 nt in length," for example, is intended to include 20 or more contiguous bases from the cDNA sequence contained in the deposited clone or the nucleotide sequence shown in SEQ ID NO:X. These nucleotide fragments are useful as diagnostic probes and primers as discussed herein. Of course, larger fragments (e.g., 50, 150, 500, 600, 2000 nucleotides) are preferred.

Moreover, representative examples of polynucleotide fragments of the invention, include, for example, fragments having a sequence from about nucleotide number 1-50, 51-100, 101-150, 151-200, 201-250, 251-300, 301-350, 351-400, 401-450, 451-500, 501-550, 551-600, 651-700, 701-750, 751-800, 800-850, 851-900, 901-950, 951-1000, 1001-1050, 1051-1100, 1101-1150, 1151-1200, 1201-1250, 1251-1300, 1301-1350, 1351-1400, 1401-1450, 1451-1500, 1501-1550, 1551-1600, 1601-1650, 1651-1700, 1701-1750, 1751-1800, 1801-1850, 1851-1900, 1901-1950, 1951-2000, or 2001 to the end of SEQ ID NO:X or the cDNA contained in the deposited clone. In this context "about" includes the particularly recited ranges, larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. Preferably, these fragments encode a polypeptide which has biological activity. More preferably, these polynucleotides can be used as probes or primers as discussed herein.

In the present invention, a "polypeptide fragment" refers to a short amino acid sequence contained in SEQ ID NO:Y or encoded by the cDNA contained in the deposited clone. Protein fragments may be "free-standing," or comprised within a larger polypeptide of which the fragment forms a part or region, most preferably as a single continuous region. Representative examples of polypeptide fragments of the invention, include, for example, fragments from about amino acid number 1-20, 21-40, 41-60, 61-80, 81-100, 102-120, 121-140, 141-160, or 161 to the end of the coding region. Moreover, polypeptide fragments can be about 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, or 150 amino acids in length. In this context "about" includes the particularly recited ranges, larger or smaller by several (5, 4, 3, 2, or 1) amino acids, at either extreme or at both extremes.

Preferred polypeptide fragments include the secreted protein as well as the mature form. Further preferred polypeptide fragments include the secreted protein or the mature form having a continuous series of deleted residues from the amino or the

carboxy terminus, or both. For example, any number of amino acids, ranging from 1-60, can be deleted from the amino terminus of either the secreted polypeptide or the mature form. Similarly, any number of amino acids, ranging from 1-30, can be deleted from the carboxy terminus of the secreted protein or mature form. Furthermore, any combination of the above amino and carboxy terminus deletions are preferred. Similarly, polynucleotide fragments encoding these polypeptide fragments are also preferred.

Particularly, N-terminal deletions of the polypeptide of the present invention can be described by the general formula m-p, where p is the total number of amino acids in the polypeptide and m is an integer from 2 to (p-1), and where both of these integers (m & p) correspond to the position of the amino acid residue identified in SEQ ID NO:Y.

Moreover, C-terminal deletions of the polypeptide of the present invention can also be described by the general formula 1-n, where n is an integer from 2 to (p-1), and again where these integers (n & p) correspond to the position of the amino acid residue identified in SEQ ID NO:Y.

The invention also provides polypeptides having one or more amino acids deleted from both the amino and the carboxyl termini, which may be described generally as having residues m-n of SEQ ID NO:Y, where m and n are integers as described above.

Also preferred are polypeptide and polynucleotide fragments characterized by structural or functional domains, such as fragments that comprise alpha-helix and alpha-helix forming regions, beta-sheet and beta-sheet-forming regions, turn and turn-forming regions, coil and coil-forming regions, hydrophilic regions, hydrophobic regions, alpha amphipathic regions, beta amphipathic regions, flexible regions, surface-forming regions, substrate binding region, and high antigenic index regions. Polypeptide fragments of SEQ ID NO:Y falling within conserved domains are specifically contemplated by the present invention. Moreover, polynucleotide fragments encoding these domains are also contemplated.

Other preferred fragments are biologically active fragments. Biologically active fragments are those exhibiting activity similar, but not necessarily identical, to an activity of the polypeptide of the present invention. The biological activity of the fragments may include an improved desired activity, or a decreased undesirable activity.

Epitopes & Antibodies

In the present invention, "epitopes" refer to polypeptide fragments having antigenic or immunogenic activity in an animal, especially in a human. A preferred embodiment of the present invention relates to a polypeptide fragment comprising an

epitope, as well as the polynucleotide encoding this fragment. A region of a protein molecule to which an antibody can bind is defined as an "antigenic epitope." In contrast, an "immunogenic epitope" is defined as a part of a protein that elicits an antibody response. (See, for instance, Geysen et al., Proc. Natl. Acad. Sci. USA 81:3998-4002 (1983).)

Fragments which function as epitopes may be produced by any conventional means. (See, e.g., Houghten, R. A., Proc. Natl. Acad. Sci. USA 82:5131-5135 (1985) further described in U.S. Patent No. 4,631,211.)

In the present invention, antigenic epitopes preferably contain a sequence of at least seven, more preferably at least nine, and most preferably between about 15 to about 30 amino acids. Antigenic epitopes are useful to raise antibodies, including monoclonal antibodies, that specifically bind the epitope. (See, for instance, Wilson et al., Cell 37:767-778 (1984); Sutcliffe, J. G. et al., Science 219:660-666 (1983).)

Similarly, immunogenic epitopes can be used to induce antibodies according to methods well known in the art. (See, for instance, Sutcliffe et al., supra; Wilson et al., supra; Chow, M. et al., Proc. Natl. Acad. Sci. USA 82:910-914; and Bittle, F. J. et al., J. Gen. Virol. 66:2347-2354 (1985).) A preferred immunogenic epitope includes the secreted protein. The immunogenic epitopes may be presented together with a carrier protein, such as an albumin, to an animal system (such as rabbit or mouse) or, if it is long enough (at least about 25 amino acids), without a carrier. However, immunogenic epitopes comprising as few as 8 to 10 amino acids have been shown to be sufficient to raise antibodies capable of binding to, at the very least, linear epitopes in a denatured polypeptide (e.g., in Western blotting.)

As used herein, the term "antibody" (Ab) or "monoclonal antibody" (Mab) is meant to include intact molecules as well as antibody fragments (such as, for example, Fab and F(ab')₂ fragments) which are capable of specifically binding to protein. Fab and F(ab')₂ fragments lack the Fc fragment of intact antibody, clear more rapidly from the circulation, and may have less non-specific tissue binding than an intact antibody. (Wahl et al., J. Nucl. Med. 24:316-325 (1983).) Thus, these fragments are preferred, as well as the products of a FAB or other immunoglobulin expression library. Moreover, antibodies of the present invention include chimeric, single chain, and humanized antibodies.

Fusion Proteins

Any polypeptide of the present invention can be used to generate fusion proteins. For example, the polypeptide of the present invention, when fused to a second protein, can be used as an antigenic tag. Antibodies raised against the

polypeptide of the present invention can be used to indirectly detect the second protein by binding to the polypeptide. Moreover, because secreted proteins target cellular locations based on trafficking signals, the polypeptides of the present invention can be used as targeting molecules once fused to other proteins.

5 Examples of domains that can be fused to polypeptides of the present invention include not only heterologous signal sequences, but also other heterologous functional regions. The fusion does not necessarily need to be direct, but may occur through linker sequences.

10 Moreover, fusion proteins may also be engineered to improve characteristics of the polypeptide of the present invention. For instance, a region of additional amino acids, particularly charged amino acids, may be added to the N-terminus of the polypeptide to improve stability and persistence during purification from the host cell or subsequent handling and storage. Also, peptide moieties may be added to the polypeptide to facilitate purification. Such regions may be removed prior to final
15 preparation of the polypeptide. The addition of peptide moieties to facilitate handling of polypeptides are familiar and routine techniques in the art.

 Moreover, polypeptides of the present invention, including fragments, and specifically epitopes, can be combined with parts of the constant domain of immunoglobulins (IgG), resulting in chimeric polypeptides. These fusion proteins
20 facilitate purification and show an increased half-life in vivo. One reported example describes chimeric proteins consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of mammalian immunoglobulins. (EP A 394,827; Traunecker et al., Nature 331:84-86 (1988).) Fusion proteins having disulfide-linked dimeric structures (due to the IgG)
25 can also be more efficient in binding and neutralizing other molecules, than the monomeric secreted protein or protein fragment alone. (Fountoulakis et al., J. Biochem. 270:3958-3964 (1995).)

 Similarly, EP-A-O 464 533 (Canadian counterpart 2045869) discloses fusion proteins comprising various portions of constant region of immunoglobulin molecules
30 together with another human protein or part thereof. In many cases, the Fc part in a fusion protein is beneficial in therapy and diagnosis, and thus can result in, for example, improved pharmacokinetic properties. (EP-A 0232 262.) Alternatively, deleting the Fc part after the fusion protein has been expressed, detected, and purified, would be desired. For example, the Fc portion may hinder therapy and diagnosis if the
35 fusion protein is used as an antigen for immunizations. In drug discovery, for example, human proteins, such as hIL-5, have been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists of hIL-5. (See, D.

Bennett et al., J. Molecular Recognition 8:52-58 (1995); K. Johanson et al., J. Biol. Chem. 270:9459-9471 (1995).)

Moreover, the polypeptides of the present invention can be fused to marker sequences, such as a peptide which facilitates purification of the fused polypeptide. In preferred embodiments, the marker amino acid sequence is a hexa-histidine peptide, such as the tag provided in a pQE vector (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311), among others, many of which are commercially available. As described in Gentz et al., Proc. Natl. Acad. Sci. USA 86:821-824 (1989), for instance, hexa-histidine provides for convenient purification of the fusion protein.

Another peptide tag useful for purification, the "HA" tag, corresponds to an epitope derived from the influenza hemagglutinin protein. (Wilson et al., Cell 37:767 (1984).)

Thus, any of these above fusions can be engineered using the polynucleotides or the polypeptides of the present invention.

15 **Vectors, Host Cells, and Protein Production**

The present invention also relates to vectors containing the polynucleotide of the present invention, host cells, and the production of polypeptides by recombinant techniques. The vector may be, for example, a phage, plasmid, viral, or retroviral vector. Retroviral vectors may be replication competent or replication defective. In the latter case, viral propagation generally will occur only in complementing host cells.

The polynucleotides may be joined to a vector containing a selectable marker for propagation in a host. Generally, a plasmid vector is introduced in a precipitate, such as a calcium phosphate precipitate, or in a complex with a charged lipid. If the vector is a virus, it may be packaged in vitro using an appropriate packaging cell line and then transduced into host cells.

The polynucleotide insert should be operatively linked to an appropriate promoter, such as the phage lambda PL promoter, the E. coli lac, trp, phoA and tac promoters, the SV40 early and late promoters and promoters of retroviral LTRs, to name a few. Other suitable promoters will be known to the skilled artisan. The expression constructs will further contain sites for transcription initiation, termination, and, in the transcribed region, a ribosome binding site for translation. The coding portion of the transcripts expressed by the constructs will preferably include a translation initiating codon at the beginning and a termination codon (UAA, UGA or UAG) appropriately positioned at the end of the polypeptide to be translated.

As indicated, the expression vectors will preferably include at least one selectable marker. Such markers include dihydrofolate reductase, G418 or neomycin resistance for eukaryotic cell culture and tetracycline, kanamycin or ampicillin resistance

genes for culturing in *E. coli* and other bacteria. Representative examples of appropriate hosts include, but are not limited to, bacterial cells, such as *E. coli*, *Streptomyces* and *Salmonella typhimurium* cells; fungal cells, such as yeast cells; insect cells such as *Drosophila* S2 and *Spodoptera Sf9* cells; animal cells such as CHO, COS, 293, and Bowes melanoma cells; and plant cells. Appropriate culture mediums and conditions for the above-described host cells are known in the art.

Among vectors preferred for use in bacteria include pQE70, pQE60 and pQE-9, available from QIAGEN, Inc.; pBluescript vectors, Phagescript vectors, pNH8A, pNH16a, pNH18A, pNH46A, available from Stratagene Cloning Systems, Inc.; and ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 available from Pharmacia Biotech, Inc. Among preferred eukaryotic vectors are pWLNEO, pSV2CAT, pOG44, pXT1 and pSG available from Stratagene; and pSVK3, pBPV, pMSG and pSVL available from Pharmacia. Other suitable vectors will be readily apparent to the skilled artisan.

Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-dextran mediated transfection, cationic lipid-mediated transfection, electroporation, transduction, infection, or other methods. Such methods are described in many standard laboratory manuals, such as Davis et al., *Basic Methods In Molecular Biology* (1986). It is specifically contemplated that the polypeptides of the present invention may in fact be expressed by a host cell lacking a recombinant vector.

A polypeptide of this invention can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Most preferably, high performance liquid chromatography ("HPLC") is employed for purification.

Polypeptides of the present invention, and preferably the secreted form, can also be recovered from: products purified from natural sources, including bodily fluids, tissues and cells, whether directly isolated or cultured; products of chemical synthetic procedures; and products produced by recombinant techniques from a prokaryotic or eukaryotic host, including, for example, bacterial, yeast, higher plant, insect, and mammalian cells. Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be glycosylated or may be non-glycosylated. In addition, polypeptides of the invention may also include an initial modified methionine residue, in some cases as a result of host-mediated processes. Thus, it is well known in the art that the N-terminal methionine encoded by the translation initiation codon generally is removed with high efficiency from any protein

after translation in all eukaryotic cells. While the N-terminal methionine on most proteins also is efficiently removed in most prokaryotes, for some proteins, this prokaryotic removal process is inefficient, depending on the nature of the amino acid to which the N-terminal methionine is covalently linked.

5

Uses of the Polynucleotides

Each of the polynucleotides identified herein can be used in numerous ways as reagents. The following description should be considered exemplary and utilizes known techniques.

10

The polynucleotides of the present invention are useful for chromosome identification. There exists an ongoing need to identify new chromosome markers, since few chromosome marking reagents, based on actual sequence data (repeat polymorphisms), are presently available. Each polynucleotide of the present invention can be used as a chromosome marker.

15

Briefly, sequences can be mapped to chromosomes by preparing PCR primers (preferably 15-25 bp) from the sequences shown in SEQ ID NO:X. Primers can be selected using computer analysis so that primers do not span more than one predicted exon in the genomic DNA. These primers are then used for PCR screening of somatic cell hybrids containing individual human chromosomes. Only those hybrids containing the human gene corresponding to the SEQ ID NO:X will yield an amplified fragment.

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Similarly, somatic hybrids provide a rapid method of PCR mapping the polynucleotides to particular chromosomes. Three or more clones can be assigned per day using a single thermal cycler. Moreover, sublocalization of the polynucleotides can be achieved with panels of specific chromosome fragments. Other gene mapping strategies that can be used include in situ hybridization, prescreening with labeled flow-sorted chromosomes, and preselection by hybridization to construct chromosome specific-cDNA libraries.

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Precise chromosomal location of the polynucleotides can also be achieved using fluorescence in situ hybridization (FISH) of a metaphase chromosomal spread. This technique uses polynucleotides as short as 500 or 600 bases; however, polynucleotides 2,000-4,000 bp are preferred. For a review of this technique, see Verma et al., "Human Chromosomes: a Manual of Basic Techniques," Pergamon Press, New York (1988).

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For chromosome mapping, the polynucleotides can be used individually (to mark a single chromosome or a single site on that chromosome) or in panels (for marking multiple sites and/or multiple chromosomes). Preferred polynucleotides correspond to the noncoding regions of the cDNAs because the coding sequences are

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more likely conserved within gene families, thus increasing the chance of cross hybridization during chromosomal mapping.

Once a polynucleotide has been mapped to a precise chromosomal location, the physical position of the polynucleotide can be used in linkage analysis. Linkage analysis establishes coinheritance between a chromosomal location and presentation of a particular disease. (Disease mapping data are found, for example, in V. McKusick, Mendelian Inheritance in Man (available on line through Johns Hopkins University Welch Medical Library) .) Assuming 1 megabase mapping resolution and one gene per 20 kb, a cDNA precisely localized to a chromosomal region associated with the disease could be one of 50-500 potential causative genes.

Thus, once coinheritance is established, differences in the polynucleotide and the corresponding gene between affected and unaffected individuals can be examined. First, visible structural alterations in the chromosomes, such as deletions or translocations, are examined in chromosome spreads or by PCR. If no structural alterations exist, the presence of point mutations are ascertained. Mutations observed in some or all affected individuals, but not in normal individuals, indicates that the mutation may cause the disease. However, complete sequencing of the polypeptide and the corresponding gene from several normal individuals is required to distinguish the mutation from a polymorphism. If a new polymorphism is identified, this polymorphic polypeptide can be used for further linkage analysis.

Furthermore, increased or decreased expression of the gene in affected individuals as compared to unaffected individuals can be assessed using polynucleotides of the present invention. Any of these alterations (altered expression, chromosomal rearrangement, or mutation) can be used as a diagnostic or prognostic marker.

In addition to the foregoing, a polynucleotide can be used to control gene expression through triple helix formation or antisense DNA or RNA. Both methods rely on binding of the polynucleotide to DNA or RNA. For these techniques, preferred polynucleotides are usually 20 to 40 bases in length and complementary to either the region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxy-nucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988).) Triple helix formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques are effective in model

systems, and the information disclosed herein can be used to design antisense or triple helix polynucleotides in an effort to treat disease.

Polynucleotides of the present invention are also useful in gene therapy. One goal of gene therapy is to insert a normal gene into an organism having a defective gene, in an effort to correct the genetic defect. The polynucleotides disclosed in the present invention offer a means of targeting such genetic defects in a highly accurate manner. Another goal is to insert a new gene that was not present in the host genome, thereby producing a new trait in the host cell.

The polynucleotides are also useful for identifying individuals from minute biological samples. The United States military, for example, is considering the use of restriction fragment length polymorphism (RFLP) for identification of its personnel. In this technique, an individual's genomic DNA is digested with one or more restriction enzymes, and probed on a Southern blot to yield unique bands for identifying personnel. This method does not suffer from the current limitations of "Dog Tags" which can be lost, switched, or stolen, making positive identification difficult. The polynucleotides of the present invention can be used as additional DNA markers for RFLP.

The polynucleotides of the present invention can also be used as an alternative to RFLP, by determining the actual base-by-base DNA sequence of selected portions of an individual's genome. These sequences can be used to prepare PCR primers for amplifying and isolating such selected DNA, which can then be sequenced. Using this technique, individuals can be identified because each individual will have a unique set of DNA sequences. Once an unique ID database is established for an individual, positive identification of that individual, living or dead, can be made from extremely small tissue samples.

Forensic biology also benefits from using DNA-based identification techniques as disclosed herein. DNA sequences taken from very small biological samples such as tissues, e.g., hair or skin, or body fluids, e.g., blood, saliva, semen, etc., can be amplified using PCR. In one prior art technique, gene sequences amplified from polymorphic loci, such as DQa class II HLA gene, are used in forensic biology to identify individuals. (Erlich, H., PCR Technology, Freeman and Co. (1992).) Once these specific polymorphic loci are amplified, they are digested with one or more restriction enzymes, yielding an identifying set of bands on a Southern blot probed with DNA corresponding to the DQa class II HLA gene. Similarly, polynucleotides of the present invention can be used as polymorphic markers for forensic purposes.

There is also a need for reagents capable of identifying the source of a particular tissue. Such need arises, for example, in forensics when presented with tissue of

unknown origin. Appropriate reagents can comprise, for example, DNA probes or primers specific to particular tissue prepared from the sequences of the present invention. Panels of such reagents can identify tissue by species and/or by organ type. In a similar fashion, these reagents can be used to screen tissue cultures for contamination.

In the very least, the polynucleotides of the present invention can be used as molecular weight markers on Southern gels, as diagnostic probes for the presence of a specific mRNA in a particular cell type, as a probe to "subtract-out" known sequences in the process of discovering novel polynucleotides, for selecting and making oligomers for attachment to a "gene chip" or other support, to raise anti-DNA antibodies using DNA immunization techniques, and as an antigen to elicit an immune response.

Uses of the Polypeptides

Each of the polypeptides identified herein can be used in numerous ways. The following description should be considered exemplary and utilizes known techniques.

A polypeptide of the present invention can be used to assay protein levels in a biological sample using antibody-based techniques. For example, protein expression in tissues can be studied with classical immunohistological methods. (Jalkanen, M., et al., J. Cell. Biol. 101:976-985 (1985); Jalkanen, M., et al., J. Cell . Biol. 105:3087-3096 (1987).) Other antibody-based methods useful for detecting protein gene expression include immunoassays, such as the enzyme linked immunosorbent assay (ELISA) and the radioimmunoassay (RIA). Suitable antibody assay labels are known in the art and include enzyme labels, such as, glucose oxidase, and radioisotopes, such as iodine (^{125}I , ^{121}I), carbon (^{14}C), sulfur (^{35}S), tritium (^3H), indium (^{112}In), and technetium ($^{99\text{m}}\text{Tc}$), and fluorescent labels, such as fluorescein and rhodamine, and biotin.

In addition to assaying secreted protein levels in a biological sample, proteins can also be detected in vivo by imaging. Antibody labels or markers for in vivo imaging of protein include those detectable by X-radiography, NMR or ESR. For X-radiography, suitable labels include radioisotopes such as barium or cesium, which emit detectable radiation but are not overtly harmful to the subject. Suitable markers for NMR and ESR include those with a detectable characteristic spin, such as deuterium, which may be incorporated into the antibody by labeling of nutrients for the relevant hybridoma.

A protein-specific antibody or antibody fragment which has been labeled with an appropriate detectable imaging moiety, such as a radioisotope (for example, ^{131}I , ^{112}In , $^{99\text{m}}\text{Tc}$), a radio-opaque substance, or a material detectable by nuclear magnetic

resonance, is introduced (for example, parenterally, subcutaneously, or intraperitoneally) into the mammal. It will be understood in the art that the size of the subject and the imaging system used will determine the quantity of imaging moiety needed to produce diagnostic images. In the case of a radioisotope moiety, for a human
5 subject, the quantity of radioactivity injected will normally range from about 5 to 20 millicuries of ^{99m}Tc. The labeled antibody or antibody fragment will then preferentially accumulate at the location of cells which contain the specific protein. In vivo tumor imaging is described in S.W. Burchiel et al., "Immunopharmacokinetics of Radiolabeled Antibodies and Their Fragments." (Chapter 13 in Tumor Imaging: The
10 Radiochemical Detection of Cancer, S.W. Burchiel and B. A. Rhodes, eds., Masson Publishing Inc. (1982).)

Thus, the invention provides a diagnostic method of a disorder, which involves (a) assaying the expression of a polypeptide of the present invention in cells or body fluid of an individual; (b) comparing the level of gene expression with a standard gene
15 expression level, whereby an increase or decrease in the assayed polypeptide gene expression level compared to the standard expression level is indicative of a disorder.

Moreover, polypeptides of the present invention can be used to treat disease. For example, patients can be administered a polypeptide of the present invention in an effort to replace absent or decreased levels of the polypeptide (e.g., insulin), to
20 supplement absent or decreased levels of a different polypeptide (e.g., hemoglobin S for hemoglobin B), to inhibit the activity of a polypeptide (e.g., an oncogene), to activate the activity of a polypeptide (e.g., by binding to a receptor), to reduce the activity of a membrane bound receptor by competing with it for free ligand (e.g., soluble TNF receptors used in reducing inflammation), or to bring about a desired
25 response (e.g., blood vessel growth).

Similarly, antibodies directed to a polypeptide of the present invention can also be used to treat disease. For example, administration of an antibody directed to a polypeptide of the present invention can bind and reduce overproduction of the polypeptide. Similarly, administration of an antibody can activate the polypeptide, such
30 as by binding to a polypeptide bound to a membrane (receptor).

At the very least, the polypeptides of the present invention can be used as molecular weight markers on SDS-PAGE gels or on molecular sieve gel filtration columns using methods well known to those of skill in the art. Polypeptides can also be used to raise antibodies, which in turn are used to measure protein expression from a
35 recombinant cell, as a way of assessing transformation of the host cell. Moreover, the polypeptides of the present invention can be used to test the following biological activities.

Biological Activities

The polynucleotides and polypeptides of the present invention can be used in assays to test for one or more biological activities. If these polynucleotides and polypeptides do exhibit activity in a particular assay, it is likely that these molecules may be involved in the diseases associated with the biological activity. Thus, the polynucleotides and polypeptides could be used to treat the associated disease.

Immune Activity

A polypeptide or polynucleotide of the present invention may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, or mobilization (chemotaxis) of immune cells. Immune cells develop through a process called hematopoiesis, producing myeloid (platelets, red blood cells, neutrophils, and macrophages) and lymphoid (B and T lymphocytes) cells from pluripotent stem cells. The etiology of these immune deficiencies or disorders may be genetic, somatic, such as cancer or some autoimmune disorders, acquired (e.g., by chemotherapy or toxins), or infectious. Moreover, a polynucleotide or polypeptide of the present invention can be used as a marker or detector of a particular immune system disease or disorder.

A polynucleotide or polypeptide of the present invention may be useful in treating or detecting deficiencies or disorders of hematopoietic cells. A polypeptide or polynucleotide of the present invention could be used to increase differentiation and proliferation of hematopoietic cells, including the pluripotent stem cells, in an effort to treat those disorders associated with a decrease in certain (or many) types hematopoietic cells. Examples of immunologic deficiency syndromes include, but are not limited to: blood protein disorders (e.g. agammaglobulinemia, dysgammaglobulinemia), ataxia telangiectasia, common variable immunodeficiency, Digeorge Syndrome, HIV infection, HTLV-BLV infection, leukocyte adhesion deficiency syndrome, lymphopenia, phagocyte bactericidal dysfunction, severe combined immunodeficiency (SCIDs), Wiskott-Aldrich Disorder, anemia, thrombocytopenia, or hemoglobinuria.

Moreover, a polypeptide or polynucleotide of the present invention could also be used to modulate hemostatic (the stopping of bleeding) or thrombolytic activity (clot formation). For example, by increasing hemostatic or thrombolytic activity, a polynucleotide or polypeptide of the present invention could be used to treat blood coagulation disorders (e.g., afibrinogenemia, factor deficiencies), blood platelet disorders (e.g. thrombocytopenia), or wounds resulting from trauma, surgery, or other causes. Alternatively, a polynucleotide or polypeptide of the present invention that can

decrease hemostatic or thrombolytic activity could be used to inhibit or dissolve clotting. These molecules could be important in the treatment of heart attacks (infarction), strokes, or scarring.

5 A polynucleotide or polypeptide of the present invention may also be useful in treating or detecting autoimmune disorders. Many autoimmune disorders result from inappropriate recognition of self as foreign material by immune cells. This inappropriate recognition results in an immune response leading to the destruction of the host tissue. Therefore, the administration of a polypeptide or polynucleotide of the present invention that inhibits an immune response, particularly the proliferation, 10 differentiation, or chemotaxis of T-cells, may be an effective therapy in preventing autoimmune disorders.

Examples of autoimmune disorders that can be treated or detected by the present invention include, but are not limited to: Addison's Disease, hemolytic anemia, antiphospholipid syndrome, rheumatoid arthritis, dermatitis, allergic encephalomyelitis, 15 glomerulonephritis, Goodpasture's Syndrome, Graves' Disease, Multiple Sclerosis, Myasthenia Gravis, Neuritis, Ophthalmia, Bullous Pemphigoid, Pemphigus, Polyendocrinopathies, Purpura, Reiter's Disease, Stiff-Man Syndrome, Autoimmune Thyroiditis, Systemic Lupus Erythematosus, Autoimmune Pulmonary Inflammation, Guillain-Barre Syndrome, insulin dependent diabetes mellitus, and autoimmune 20 inflammatory eye disease.

Similarly, allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems, may also be treated by a polypeptide or polynucleotide of the present invention. Moreover, these molecules can be used to treat anaphylaxis, hypersensitivity to an antigenic molecule, or blood group incompatibility.

25 A polynucleotide or polypeptide of the present invention may also be used to treat and/or prevent organ rejection or graft-versus-host disease (GVHD). Organ rejection occurs by host immune cell destruction of the transplanted tissue through an immune response. Similarly, an immune response is also involved in GVHD, but, in this case, the foreign transplanted immune cells destroy the host tissues. The 30 administration of a polypeptide or polynucleotide of the present invention that inhibits an immune response, particularly the proliferation, differentiation, or chemotaxis of T-cells, may be an effective therapy in preventing organ rejection or GVHD.

Similarly, a polypeptide or polynucleotide of the present invention may also be used to modulate inflammation. For example, the polypeptide or polynucleotide may 35 inhibit the proliferation and differentiation of cells involved in an inflammatory response. These molecules can be used to treat inflammatory conditions, both chronic and acute conditions, including inflammation associated with infection (e.g., septic

shock, sepsis, or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine induced lung injury, inflammatory bowel disease, Crohn's disease, or resulting from over production of cytokines (e.g., TNF or IL-1.)

Hyperproliferative Disorders

A polypeptide or polynucleotide can be used to treat or detect hyperproliferative disorders, including neoplasms. A polypeptide or polynucleotide of the present invention may inhibit the proliferation of the disorder through direct or indirect interactions. Alternatively, a polypeptide or polynucleotide of the present invention may proliferate other cells which can inhibit the hyperproliferative disorder.

For example, by increasing an immune response, particularly increasing antigenic qualities of the hyperproliferative disorder or by proliferating, differentiating, or mobilizing T-cells, hyperproliferative disorders can be treated. This immune response may be increased by either enhancing an existing immune response, or by initiating a new immune response. Alternatively, decreasing an immune response may also be a method of treating hyperproliferative disorders, such as a chemotherapeutic agent.

Examples of hyperproliferative disorders that can be treated or detected by a polynucleotide or polypeptide of the present invention include, but are not limited to neoplasms located in the: abdomen, bone, breast, digestive system, liver, pancreas, peritoneum, endocrine glands (adrenal, parathyroid, pituitary, testicles, ovary, thymus, thyroid), eye, head and neck, nervous (central and peripheral), lymphatic system, pelvic, skin, soft tissue, spleen, thoracic, and urogenital.

Similarly, other hyperproliferative disorders can also be treated or detected by a polynucleotide or polypeptide of the present invention. Examples of such hyperproliferative disorders include, but are not limited to: hypergammaglobulinemia, lymphoproliferative disorders, paraproteinemias, purpura, sarcoidosis, Sezary Syndrome, Waldenström's Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other hyperproliferative disease, besides neoplasia, located in an organ system listed above.

Infectious Disease

A polypeptide or polynucleotide of the present invention can be used to treat or detect infectious agents. For example, by increasing the immune response, particularly increasing the proliferation and differentiation of B and/or T cells, infectious diseases

may be treated. The immune response may be increased by either enhancing an existing immune response, or by initiating a new immune response. Alternatively, the polypeptide or polynucleotide of the present invention may also directly inhibit the infectious agent, without necessarily eliciting an immune response.

- 5 Viruses are one example of an infectious agent that can cause disease or symptoms that can be treated or detected by a polynucleotide or polypeptide of the present invention. Examples of viruses, include, but are not limited to the following DNA and RNA viral families: Arbovirus, Adenoviridae, Arenaviridae, Arterivirus, Bimaviridae, Bunyaviridae, Caliciviridae, Circoviridae, Coronaviridae, Flaviviridae, 10 Hepadnaviridae (Hepatitis), Herpesviridae (such as, Cytomegalovirus, Herpes Simplex, Herpes Zoster), Mononegavirus (e.g., Paramyxoviridae, Morbillivirus, Rhabdoviridae), Orthomyxoviridae (e.g., Influenza), Papovaviridae, Parvoviridae, Picornaviridae, Poxviridae (such as Smallpox or Vaccinia), Reoviridae (e.g., Rotavirus), Retroviridae (HTLV-I, HTLV-II, Lentivirus), and Togaviridae (e.g., 15 Rubivirus). Viruses falling within these families can cause a variety of diseases or symptoms, including, but not limited to: arthritis, bronchiolitis, encephalitis, eye infections (e.g., conjunctivitis, keratitis), chronic fatigue syndrome, hepatitis (A, B, C, E, Chronic Active, Delta), meningitis, opportunistic infections (e.g., AIDS), pneumonia, Burkitt's Lymphoma, chickenpox, hemorrhagic fever, Measles, Mumps, 20 Parainfluenza, Rabies, the common cold, Polio, leukemia, Rubella, sexually transmitted diseases, skin diseases (e.g., Kaposi's, warts), and viremia. A polypeptide or polynucleotide of the present invention can be used to treat or detect any of these symptoms or diseases.

- Similarly, bacterial or fungal agents that can cause disease or symptoms and that 25 can be treated or detected by a polynucleotide or polypeptide of the present invention include, but not limited to, the following Gram-Negative and Gram-positive bacterial families and fungi: Actinomycetales (e.g., Corynebacterium, Mycobacterium, Norcardia), Aspergillosis, Bacillaceae (e.g., Anthrax, Clostridium), Bacteroidaceae, Blastomycosis, Bordetella, Borrelia, Brucellosis, Candidiasis, Campylobacter, 30 Coccidioidomycosis, Cryptococcosis, Dermatocycoses, Enterobacteriaceae (Klebsiella, Salmonella, Serratia, Yersinia), Erysipelothrix, Helicobacter, Legionellosis, Leptospirosis, Listeria, Mycoplasmatales, Neisseriaceae (e.g., Acinetobacter, Gonorrhea, Meningococcal), Pasteurellaceae Infections (e.g., Actinobacillus, Haemophilus, Pasteurella), Pseudomonas, Rickettsiaceae, Chlamydiaceae, Syphilis, 35 and Staphylococcal. These bacterial or fungal families can cause the following diseases or symptoms, including, but not limited to: bacteremia, endocarditis, eye infections (conjunctivitis, tuberculosis, uveitis), gingivitis, opportunistic infections (e.g., AIDS

- related infections), paronychia, prosthesis-related infections, Reiter's Disease, respiratory tract infections, such as Whooping Cough or Empyema, sepsis, Lyme Disease, Cat-Scratch Disease, Dysentery, Paratyphoid Fever, food poisoning, Typhoid, pneumonia, Gonorrhea, meningitis, Chlamydia, Syphilis, Diphtheria,
- 5 Leprosy, Paratuberculosis, Tuberculosis, Lupus, Botulism, gangrene, tetanus, impetigo, Rheumatic Fever, Scarlet Fever, sexually transmitted diseases, skin diseases (e.g., cellulitis, dermatocycoses), toxemia, urinary tract infections, wound infections. A polypeptide or polynucleotide of the present invention can be used to treat or detect any of these symptoms or diseases.
- 10 Moreover, parasitic agents causing disease or symptoms that can be treated or detected by a polynucleotide or polypeptide of the present invention include, but not limited to, the following families: Amebiasis, Babesiosis, Coccidiosis, Cryptosporidiosis, Dientamoebiasis, Dourine, Ectoparasitic, Giardiasis, Helminthiasis, Leishmaniasis, Theileriasis, Toxoplasmosis, Trypanosomiasis, and Trichomonas.
- 15 These parasites can cause a variety of diseases or symptoms, including, but not limited to: Scabies, Trombiculiasis, eye infections, intestinal disease (e.g., dysentery, giardiasis), liver disease, lung disease, opportunistic infections (e.g., AIDS related), Malaria, pregnancy complications, and toxoplasmosis. A polypeptide or polynucleotide of the present invention can be used to treat or detect any of these symptoms or
- 20 diseases.
- Preferably, treatment using a polypeptide or polynucleotide of the present invention could either be by administering an effective amount of a polypeptide to the patient, or by removing cells from the patient, supplying the cells with a polynucleotide of the present invention, and returning the engineered cells to the patient (ex vivo
- 25 therapy). Moreover, the polypeptide or polynucleotide of the present invention can be used as an antigen in a vaccine to raise an immune response against infectious disease.

Regeneration

- A polynucleotide or polypeptide of the present invention can be used to
- 30 differentiate, proliferate, and attract cells, leading to the regeneration of tissues. (See, Science 276:59-87 (1997).) The regeneration of tissues could be used to repair, replace, or protect tissue damaged by congenital defects, trauma (wounds, burns, incisions, or ulcers), age, disease (e.g. osteoporosis, osteoarthritis, periodontal disease, liver failure), surgery, including cosmetic plastic surgery, fibrosis, reperfusion
- 35 injury, or systemic cytokine damage.

Tissues that could be regenerated using the present invention include organs (e.g., pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal

or cardiac), vascular (including vascular endothelium), nervous, hematopoietic, and skeletal (bone, cartilage, tendon, and ligament) tissue. Preferably, regeneration occurs without or decreased scarring. Regeneration also may include angiogenesis.

Moreover, a polynucleotide or polypeptide of the present invention may increase
5 regeneration of tissues difficult to heal. For example, increased tendon/ligament regeneration would quicken recovery time after damage. A polynucleotide or polypeptide of the present invention could also be used prophylactically in an effort to avoid damage. Specific diseases that could be treated include of tendinitis, carpal tunnel syndrome, and other tendon or ligament defects. A further example of tissue
10 regeneration of non-healing wounds includes pressure ulcers, ulcers associated with vascular insufficiency, surgical, and traumatic wounds.

Similarly, nerve and brain tissue could also be regenerated by using a polynucleotide or polypeptide of the present invention to proliferate and differentiate
15 nerve cells. Diseases that could be treated using this method include central and peripheral nervous system diseases, neuropathies, or mechanical and traumatic disorders (e.g., spinal cord disorders, head trauma, cerebrovascular disease, and stroke). Specifically, diseases associated with peripheral nerve injuries, peripheral neuropathy (e.g., resulting from chemotherapy or other medical therapies), localized neuropathies, and central nervous system diseases (e.g., Alzheimer's disease,
20 Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome), could all be treated using the polynucleotide or polypeptide of the present invention.

Chemotaxis

25 A polynucleotide or polypeptide of the present invention may have chemotaxis activity. A chemotactic molecule attracts or mobilizes cells (e.g., monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells) to a particular site in the body, such as inflammation, infection, or site of hyperproliferation. The mobilized cells can then fight off and/or heal the particular
30 trauma or abnormality.

A polynucleotide or polypeptide of the present invention may increase chemotactic activity of particular cells. These chemotactic molecules can then be used to treat inflammation, infection, hyperproliferative disorders, or any immune system disorder by increasing the number of cells targeted to a particular location in the body.
35 For example, chemotactic molecules can be used to treat wounds and other trauma to tissues by attracting immune cells to the injured location. Chemotactic molecules of the present invention can also attract fibroblasts, which can be used to treat wounds.

It is also contemplated that a polynucleotide or polypeptide of the present invention may inhibit chemotactic activity. These molecules could also be used to treat disorders. Thus, a polynucleotide or polypeptide of the present invention could be used as an inhibitor of chemotaxis.

5

Binding Activity

A polypeptide of the present invention may be used to screen for molecules that bind to the polypeptide or for molecules to which the polypeptide binds. The binding of the polypeptide and the molecule may activate (agonist), increase, inhibit
10 (antagonist), or decrease activity of the polypeptide or the molecule bound. Examples of such molecules include antibodies, oligonucleotides, proteins (e.g., receptors), or small molecules.

Preferably, the molecule is closely related to the natural ligand of the polypeptide, e.g., a fragment of the ligand, or a natural substrate, a ligand, a structural
15 or functional mimetic. (See, Coligan et al., Current Protocols in Immunology 1(2):Chapter 5 (1991).) Similarly, the molecule can be closely related to the natural receptor to which the polypeptide binds, or at least, a fragment of the receptor capable of being bound by the polypeptide (e.g., active site). In either case, the molecule can be rationally designed using known techniques.

20 Preferably, the screening for these molecules involves producing appropriate cells which express the polypeptide, either as a secreted protein or on the cell membrane. Preferred cells include cells from mammals, yeast, *Drosophila*, or *E. coli*. Cells expressing the polypeptide (or cell membrane containing the expressed polypeptide) are then preferably contacted with a test compound potentially containing
25 the molecule to observe binding, stimulation, or inhibition of activity of either the polypeptide or the molecule.

The assay may simply test binding of a candidate compound to the polypeptide, wherein binding is detected by a label, or in an assay involving competition with a labeled competitor. Further, the assay may test whether the candidate compound results
30 in a signal generated by binding to the polypeptide.

Alternatively, the assay can be carried out using cell-free preparations, polypeptide/molecule affixed to a solid support, chemical libraries, or natural product mixtures. The assay may also simply comprise the steps of mixing a candidate compound with a solution containing a polypeptide, measuring polypeptide/molecule
35 activity or binding, and comparing the polypeptide/molecule activity or binding to a standard.

Preferably, an ELISA assay can measure polypeptide level or activity in a sample (e.g., biological sample) using a monoclonal or polyclonal antibody. The antibody can measure polypeptide level or activity by either binding, directly or indirectly, to the polypeptide or by competing with the polypeptide for a substrate.

5 All of these above assays can be used as diagnostic or prognostic markers. The molecules discovered using these assays can be used to treat disease or to bring about a particular result in a patient (e.g., blood vessel growth) by activating or inhibiting the polypeptide/molecule. Moreover, the assays can discover agents which may inhibit or enhance the production of the polypeptide from suitably manipulated cells or tissues.

10 Therefore, the invention includes a method of identifying compounds which bind to a polypeptide of the invention comprising the steps of: (a) incubating a candidate binding compound with a polypeptide of the invention; and (b) determining if binding has occurred. Moreover, the invention includes a method of identifying agonists/antagonists comprising the steps of: (a) incubating a candidate compound with
15 a polypeptide of the invention, (b) assaying a biological activity, and (b) determining if a biological activity of the polypeptide has been altered.

Other Activities

20 A polypeptide or polynucleotide of the present invention may also increase or decrease the differentiation or proliferation of embryonic stem cells, besides, as discussed above, hematopoietic lineage.

A polypeptide or polynucleotide of the present invention may also be used to modulate mammalian characteristics, such as body height, weight, hair color, eye color, skin, percentage of adipose tissue, pigmentation, size, and shape (e.g., cosmetic
25 surgery). Similarly, a polypeptide or polynucleotide of the present invention may be used to modulate mammalian metabolism affecting catabolism, anabolism, processing, utilization, and storage of energy.

A polypeptide or polynucleotide of the present invention may be used to change a mammal's mental state or physical state by influencing biorhythms, circadian
30 rhythms, depression (including depressive disorders), tendency for violence, tolerance for pain, reproductive capabilities (preferably by Activin or Inhibin-like activity), hormonal or endocrine levels, appetite, libido, memory, stress, or other cognitive qualities.

A polypeptide or polynucleotide of the present invention may also be used as a
35 food additive or preservative, such as to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional components.

Other Preferred Embodiments

Other preferred embodiments of the claimed invention include an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 50 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1.

Also preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions beginning with the nucleotide at about the position of the 5' Nucleotide of the Clone Sequence and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

Also preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions beginning with the nucleotide at about the position of the 5' Nucleotide of the Start Codon and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

Similarly preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions beginning with the nucleotide at about the position of the 5' Nucleotide of the First Amino Acid of the Signal Peptide and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 150 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X.

Further preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 500 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X.

A further preferred embodiment is a nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the nucleotide sequence of SEQ ID NO:X beginning with the nucleotide at about the position of the 5' Nucleotide of the First Amino Acid of the Signal Peptide and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the complete nucleotide sequence of SEQ ID NO:X.

Also preferred is an isolated nucleic acid molecule which hybridizes under
5 stringent hybridization conditions to a nucleic acid molecule, wherein said nucleic acid molecule which hybridizes does not hybridize under stringent hybridization conditions to a nucleic acid molecule having a nucleotide sequence consisting of only A residues or of only T residues.

Also preferred is a composition of matter comprising a DNA molecule which
10 comprises a human cDNA clone identified by a cDNA Clone Identifier in Table 1, which DNA molecule is contained in the material deposited with the American Type Culture Collection and given the ATCC Deposit Number shown in Table 1 for said cDNA Clone Identifier.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide
15 sequence which is at least 95% identical to a sequence of at least 50 contiguous nucleotides in the nucleotide sequence of a human cDNA clone identified by a cDNA Clone Identifier in Table 1, which DNA molecule is contained in the deposit given the ATCC Deposit Number shown in Table 1.

Also preferred is an isolated nucleic acid molecule, wherein said sequence of at
20 least 50 contiguous nucleotides is included in the nucleotide sequence of the complete open reading frame sequence encoded by said human cDNA clone.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to sequence of at least 150 contiguous nucleotides in the nucleotide sequence encoded by said human cDNA clone.

25 A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to sequence of at least 500 contiguous nucleotides in the nucleotide sequence encoded by said human cDNA clone.

A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the complete nucleotide
30 sequence encoded by said human cDNA clone.

A further preferred embodiment is a method for detecting in a biological sample a nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer
35 as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1; which method

comprises a step of comparing a nucleotide sequence of at least one nucleic acid molecule in said sample with a sequence selected from said group and determining whether the sequence of said nucleic acid molecule in said sample is at least 95% identical to said selected sequence.

5 Also preferred is the above method wherein said step of comparing sequences comprises determining the extent of nucleic acid hybridization between nucleic acid molecules in said sample and a nucleic acid molecule comprising said sequence selected from said group. Similarly, also preferred is the above method wherein said step of
10 comparing sequences is performed by comparing the nucleotide sequence determined from a nucleic acid molecule in said sample with said sequence selected from said group. The nucleic acid molecules can comprise DNA molecules or RNA molecules.

 A further preferred embodiment is a method for identifying the species, tissue or cell type of a biological sample which method comprises a step of detecting nucleic acid molecules in said sample, if any, comprising a nucleotide sequence that is at least 95%
15 identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

20 The method for identifying the species, tissue or cell type of a biological sample can comprise a step of detecting nucleic acid molecules comprising a nucleotide sequence in a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from said group.

25 Also preferred is a method for diagnosing in a subject a pathological condition associated with abnormal structure or expression of a gene encoding a secreted protein identified in Table 1, which method comprises a step of detecting in a biological sample obtained from said subject nucleic acid molecules, if any, comprising a nucleotide sequence that is at least 95% identical to a sequence of at least 50 contiguous
30 nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

35 The method for diagnosing a pathological condition can comprise a step of detecting nucleic acid molecules comprising a nucleotide sequence in a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95%

identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from said group.

Also preferred is a composition of matter comprising isolated nucleic acid molecules wherein the nucleotide sequences of said nucleic acid molecules comprise a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1. The nucleic acid molecules can comprise DNA molecules or RNA molecules.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 90% identical to a sequence of at least about 10 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1.

Also preferred is a polypeptide, wherein said sequence of contiguous amino acids is included in the amino acid sequence of SEQ ID NO:Y in the range of positions beginning with the residue at about the position of the First Amino Acid of the Secreted Portion and ending with the residue at about the Last Amino Acid of the Open Reading Frame as set forth for SEQ ID NO:Y in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 30 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 100 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to the complete amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence at least 90% identical to a sequence of at least about 10 contiguous amino acids in the complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is a polypeptide wherein said sequence of contiguous amino acids is included in the amino acid sequence of a secreted portion of the secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 30 contiguous amino acids in the amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 100 contiguous amino acids in the amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to the amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Further preferred is an isolated antibody which binds specifically to a polypeptide comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Further preferred is a method for detecting in a biological sample a polypeptide comprising an amino acid sequence which is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1; which method comprises a step of comparing an amino acid sequence of at least one polypeptide molecule in said sample with a sequence selected from said group and determining whether the sequence of said polypeptide molecule in said sample is at least 90% identical to said sequence of at least 10 contiguous amino acids.

Also preferred is the above method wherein said step of comparing an amino acid sequence of at least one polypeptide molecule in said sample with a sequence selected from said group comprises determining the extent of specific binding of polypeptides in said sample to an antibody which binds specifically to a polypeptide

comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is the above method wherein said step of comparing sequences is performed by comparing the amino acid sequence determined from a polypeptide molecule in said sample with said sequence selected from said group.

Also preferred is a method for identifying the species, tissue or cell type of a biological sample which method comprises a step of detecting polypeptide molecules in said sample, if any, comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is the above method for identifying the species, tissue or cell type of a biological sample, which method comprises a step of detecting polypeptide molecules comprising an amino acid sequence in a panel of at least two amino acid sequences, wherein at least one sequence in said panel is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the above group.

Also preferred is a method for diagnosing in a subject a pathological condition associated with abnormal structure or expression of a gene encoding a secreted protein identified in Table 1, which method comprises a step of detecting in a biological sample obtained from said subject polypeptide molecules comprising an amino acid sequence in a panel of at least two amino acid sequences, wherein at least one sequence in said panel is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

In any of these methods, the step of detecting said polypeptide molecules includes using an antibody.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a nucleotide sequence encoding a polypeptide wherein said polypeptide comprises an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated nucleic acid molecule, wherein said nucleotide sequence encoding a polypeptide has been optimized for expression of said polypeptide in a prokaryotic host.

Also preferred is an isolated nucleic acid molecule, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Further preferred is a method of making a recombinant vector comprising inserting any of the above isolated nucleic acid molecule into a vector. Also preferred is the recombinant vector produced by this method. Also preferred is a method of making a recombinant host cell comprising introducing the vector into a host cell, as well as the recombinant host cell produced by this method.

Also preferred is a method of making an isolated polypeptide comprising culturing this recombinant host cell under conditions such that said polypeptide is expressed and recovering said polypeptide. Also preferred is this method of making an isolated polypeptide, wherein said recombinant host cell is a eukaryotic cell and said polypeptide is a secreted portion of a human secreted protein comprising an amino acid sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y beginning with the residue at the position of the First Amino Acid of the Secreted Portion of SEQ ID NO:Y wherein Y is an integer set forth in Table 1 and said position of the First Amino Acid of the Secreted Portion of SEQ ID NO:Y is defined in Table 1; and an amino acid sequence of a secreted portion of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1. The isolated polypeptide produced by this method is also preferred.

Also preferred is a method of treatment of an individual in need of an increased level of a secreted protein activity, which method comprises administering to such an individual a pharmaceutical composition comprising an amount of an isolated polypeptide, polynucleotide, or antibody of the claimed invention effective to increase the level of said protein activity in said individual.

Having generally described the invention, the same will be more readily understood by reference to the following examples, which are provided by way of illustration and are not intended as limiting.

Examples

Example 1: Isolation of a Selected cDNA Clone From the Deposited Sample

Each cDNA clone in a cited ATCC deposit is contained in a plasmid vector. Table 1 identifies the vectors used to construct the cDNA library from which each clone was isolated. In many cases, the vector used to construct the library is a phage vector from which a plasmid has been excised. The table immediately below correlates the related plasmid for each phage vector used in constructing the cDNA library. For example, where a particular clone is identified in Table 1 as being isolated in the vector "Lambda Zap," the corresponding deposited clone is in "pBluescript."

<u>Vector Used to Construct Library</u>	<u>Corresponding Deposited Plasmid</u>
Lambda Zap	pBluescript (pBS)
Uni-Zap XR	pBluescript (pBS)
Zap Express	pBK
lafmid BA	plafmid BA
pSport1	pSport1
pCMVSPORT 2.0	pCMVSPORT 2.0
pCMVSPORT 3.0	pCMVSPORT 3.0
pCR®2.1	pCR®2.1

Vectors Lambda Zap (U.S. Patent Nos. 5,128,256 and 5,286,636), Uni-Zap XR (U.S. Patent Nos. 5,128, 256 and 5,286,636), Zap Express (U.S. Patent Nos. 5,128,256 and 5,286,636), pBluescript (pBS) (Short, J. M. et al., Nucleic Acids Res. 16:7583-7600 (1988); Alting-Mees, M. A. and Short, J. M., Nucleic Acids Res. 17:9494 (1989)) and pBK (Alting-Mees, M. A. et al., Strategies 5:58-61 (1992)) are commercially available from Stratagene Cloning Systems, Inc., 11011 N. Torrey Pines Road, La Jolla, CA, 92037. pBS contains an ampicillin resistance gene and pBK contains a neomycin resistance gene. Both can be transformed into E. coli strain XL-1

Blue, also available from Stratagene. pBS comes in 4 forms SK+, SK-, KS+ and KS-. The S and K refers to the orientation of the polylinker to the T7 and T3 primer sequences which flank the polylinker region ("S" is for SacI and "K" is for KpnI which are the first sites on each respective end of the linker). "+" or "-" refer to the orientation of the f1 origin of replication ("ori"), such that in one orientation, single stranded rescue initiated from the f1 ori generates sense strand DNA and in the other, antisense.

Vectors pSport1, pCMVSport 2.0 and pCMVSport 3.0, were obtained from Life Technologies, Inc., P. O. Box 6009, Gaithersburg, MD 20897. All Sport vectors contain an ampicillin resistance gene and may be transformed into E. coli strain DH10B, also available from Life Technologies. (See, for instance, Gruber, C. E., et al., Focus 15:59 (1993).) Vector lafmid BA (Bento Soares, Columbia University, NY) contains an ampicillin resistance gene and can be transformed into E. coli strain XL-1 Blue. Vector pCR[®]2.1, which is available from Invitrogen, 1600 Faraday Avenue, Carlsbad, CA 92008, contains an ampicillin resistance gene and may be transformed into E. coli strain DH10B, available from Life Technologies. (See, for instance, Clark, J. M., Nuc. Acids Res. 16:9677-9686 (1988) and Mead, D. et al., Bio/Technology 9: (1991).) Preferably, a polynucleotide of the present invention does not comprise the phage vector sequences identified for the particular clone in Table 1, as well as the corresponding plasmid vector sequences designated above.

The deposited material in the sample assigned the ATCC Deposit Number cited in Table 1 for any given cDNA clone also may contain one or more additional plasmids, each comprising a cDNA clone different from that given clone. Thus, deposits sharing the same ATCC Deposit Number contain at least a plasmid for each cDNA clone identified in Table 1. Typically, each ATCC deposit sample cited in Table 1 comprises a mixture of approximately equal amounts (by weight) of about 50 plasmid DNAs, each containing a different cDNA clone; but such a deposit sample may include plasmids for more or less than 50 cDNA clones, up to about 500 cDNA clones.

Two approaches can be used to isolate a particular clone from the deposited sample of plasmid DNAs cited for that clone in Table 1. First, a plasmid is directly isolated by screening the clones using a polynucleotide probe corresponding to SEQ ID NO:X.

Particularly, a specific polynucleotide with 30-40 nucleotides is synthesized using an Applied Biosystems DNA synthesizer according to the sequence reported. The oligonucleotide is labeled, for instance, with ³²P-γ-ATP using T4 polynucleotide kinase and purified according to routine methods. (E.g., Maniatis et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press, Cold Spring, NY (1982).)

The plasmid mixture is transformed into a suitable host, as indicated above (such as XL-1 Blue (Stratagene)) using techniques known to those of skill in the art, such as those provided by the vector supplier or in related publications or patents cited above. The transformants are plated on 1.5% agar plates (containing the appropriate selection agent, e.g., ampicillin) to a density of about 150 transformants (colonies) per plate. These plates are screened using Nylon membranes according to routine methods for bacterial colony screening (e.g., Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2nd Edit., (1989), Cold Spring Harbor Laboratory Press, pages 1.93 to 1.104), or other techniques known to those of skill in the art.

Alternatively, two primers of 17-20 nucleotides derived from both ends of the SEQ ID NO:X (i.e., within the region of SEQ ID NO:X bounded by the 5' NT and the 3' NT of the clone defined in Table 1) are synthesized and used to amplify the desired cDNA using the deposited cDNA plasmid as a template. The polymerase chain reaction is carried out under routine conditions, for instance, in 25 μ l of reaction mixture with 0.5 μ g of the above cDNA template. A convenient reaction mixture is 1.5-5 mM $MgCl_2$, 0.01% (w/v) gelatin, 20 μ M each of dATP, dCTP, dGTP, dTTP, 25 pmol of each primer and 0.25 Unit of Taq polymerase. Thirty five cycles of PCR (denaturation at 94°C for 1 min; annealing at 55°C for 1 min; elongation at 72°C for 1 min) are performed with a Perkin-Elmer Cetus automated thermal cycler. The amplified product is analyzed by agarose gel electrophoresis and the DNA band with expected molecular weight is excised and purified. The PCR product is verified to be the selected sequence by subcloning and sequencing the DNA product.

Several methods are available for the identification of the 5' or 3' non-coding portions of a gene which may not be present in the deposited clone. These methods include but are not limited to, filter probing, clone enrichment using specific probes, and protocols similar or identical to 5' and 3' "RACE" protocols which are well known in the art. For instance, a method similar to 5' RACE is available for generating the missing 5' end of a desired full-length transcript. (Fromont-Racine et al., *Nucleic Acids Res.* 21(7):1683-1684 (1993).)

Briefly, a specific RNA oligonucleotide is ligated to the 5' ends of a population of RNA presumably containing full-length gene RNA transcripts. A primer set containing a primer specific to the ligated RNA oligonucleotide and a primer specific to a known sequence of the gene of interest is used to PCR amplify the 5' portion of the desired full-length gene. This amplified product may then be sequenced and used to generate the full length gene.

This above method starts with total RNA isolated from the desired source, although poly-A+ RNA can be used. The RNA preparation can then be treated with phosphatase if necessary to eliminate 5' phosphate groups on degraded or damaged RNA which may interfere with the later RNA ligase step. The phosphatase should then
5 be inactivated and the RNA treated with tobacco acid pyrophosphatase in order to remove the cap structure present at the 5' ends of messenger RNAs. This reaction leaves a 5' phosphate group at the 5' end of the cap cleaved RNA which can then be ligated to an RNA oligonucleotide using T4 RNA ligase.

This modified RNA preparation is used as a template for first strand cDNA
10 synthesis using a gene specific oligonucleotide. The first strand synthesis reaction is used as a template for PCR amplification of the desired 5' end using a primer specific to the ligated RNA oligonucleotide and a primer specific to the known sequence of the gene of interest. The resultant product is then sequenced and analyzed to confirm that the 5' end sequence belongs to the desired gene.

15
Example 2: Isolation of Genomic Clones Corresponding to a Polynucleotide

A human genomic P1 library (Genomic Systems, Inc.) is screened by PCR using primers selected for the cDNA sequence corresponding to SEQ ID NO:X.,
20 according to the method described in Example 1. (See also, Sambrook.)

Example 3: Tissue Distribution of Polypeptide

Tissue distribution of mRNA expression of polynucleotides of the present invention is determined using protocols for Northern blot analysis, described by,
25 among others, Sambrook et al. For example, a cDNA probe produced by the method described in Example 1 is labeled with P³² using the rediprime™ DNA labeling system (Amersham Life Science), according to manufacturer's instructions. After labeling, the probe is purified using CHROMA SPIN-100™ column (Clontech Laboratories, Inc.), according to manufacturer's protocol number PT1200-1. The purified labeled probe is
30 then used to examine various human tissues for mRNA expression.

Multiple Tissue Northern (MTN) blots containing various human tissues (H) or human immune system tissues (IM) (Clontech) are examined with the labeled probe using ExpressHyb™ hybridization solution (Clontech) according to manufacturer's protocol number PT1190-1. Following hybridization and washing, the blots are
35 mounted and exposed to film at -70°C overnight, and the films developed according to standard procedures.

Example 4: Chromosomal Mapping of the Polynucleotides

An oligonucleotide primer set is designed according to the sequence at the 5' end of SEQ ID NO:X. This primer preferably spans about 100 nucleotides. This
5 primer set is then used in a polymerase chain reaction under the following set of conditions : 30 seconds, 95°C; 1 minute, 56°C; 1 minute, 70°C. This cycle is repeated 32 times followed by one 5 minute cycle at 70°C. Human, mouse, and hamster DNA is used as template in addition to a somatic cell hybrid panel containing individual chromosomes or chromosome fragments (Bios, Inc). The reactions is analyzed on
10 either 8% polyacrylamide gels or 3.5 % agarose gels. Chromosome mapping is determined by the presence of an approximately 100 bp PCR fragment in the particular somatic cell hybrid.

Example 5: Bacterial Expression of a Polypeptide

15 A polynucleotide encoding a polypeptide of the present invention is amplified using PCR oligonucleotide primers corresponding to the 5' and 3' ends of the DNA sequence, as outlined in Example 1, to synthesize insertion fragments. The primers used to amplify the cDNA insert should preferably contain restriction sites, such as BamHI and XbaI, at the 5' end of the primers in order to clone the amplified product
20 into the expression vector. For example, BamHI and XbaI correspond to the restriction enzyme sites on the bacterial expression vector pQE-9. (Qiagen, Inc., Chatsworth, CA). This plasmid vector encodes antibiotic resistance (Amp^r), a bacterial origin of replication (ori), an IPTG-regulatable promoter/operator (P/O), a ribosome binding site (RBS), a 6-histidine tag (6-His), and restriction enzyme cloning sites.

25 The pQE-9 vector is digested with BamHI and XbaI and the amplified fragment is ligated into the pQE-9 vector maintaining the reading frame initiated at the bacterial RBS. The ligation mixture is then used to transform the E. coli strain M15/rep4 (Qiagen, Inc.) which contains multiple copies of the plasmid pREP4, which expresses the lacI repressor and also confers kanamycin resistance (Kan^r). Transformants are
30 identified by their ability to grow on LB plates and ampicillin/kanamycin resistant colonies are selected. Plasmid DNA is isolated and confirmed by restriction analysis.

Clones containing the desired constructs are grown overnight (O/N) in liquid culture in LB media supplemented with both Amp (100 ug/ml) and Kan (25 ug/ml). The O/N culture is used to inoculate a large culture at a ratio of 1:100 to 1:250. The
35 cells are grown to an optical density 600 (O.D.⁶⁰⁰) of between 0.4 and 0.6. IPTG

(Isopropyl-B-D-thiogalacto pyranoside) is then added to a final concentration of 1 mM. IPTG induces by inactivating the lacI repressor, clearing the P/O leading to increased gene expression.

5 Cells are grown for an extra 3 to 4 hours. Cells are then harvested by centrifugation (20 mins at 6000Xg). The cell pellet is solubilized in the chaotropic agent 6 Molar Guanidine HCl by stirring for 3-4 hours at 4°C. The cell debris is removed by centrifugation, and the supernatant containing the polypeptide is loaded onto a nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin column (available from QIAGEN, Inc., *supra*). Proteins with a 6 x His tag bind to the Ni-NTA resin with high
10 affinity and can be purified in a simple one-step procedure (for details see: The QIAexpressionist (1995) QIAGEN, Inc., *supra*).

Briefly, the supernatant is loaded onto the column in 6 M guanidine-HCl, pH 8, the column is first washed with 10 volumes of 6 M guanidine-HCl, pH 8, then washed with 10 volumes of 6 M guanidine-HCl pH 6, and finally the polypeptide is eluted with
15 6 M guanidine-HCl, pH 5.

The purified protein is then renatured by dialyzing it against phosphate-buffered saline (PBS) or 50 mM Na-acetate, pH 6 buffer plus 200 mM NaCl. Alternatively, the protein can be successfully refolded while immobilized on the Ni-NTA column. The recommended conditions are as follows: renature using a linear 6M-1M urea gradient in
20 500 mM NaCl, 20% glycerol, 20 mM Tris/HCl pH 7.4, containing protease inhibitors. The renaturation should be performed over a period of 1.5 hours or more. After renaturation the proteins are eluted by the addition of 250 mM imidazole. Imidazole is removed by a final dialyzing step against PBS or 50 mM sodium acetate pH 6 buffer plus 200 mM NaCl. The purified protein is stored at 4°C or frozen at -80°C.

25 In addition to the above expression vector, the present invention further includes an expression vector comprising phage operator and promoter elements operatively linked to a polynucleotide of the present invention, called pHE4a. (ATCC Accession Number 209645, deposited on February 25, 1998.) This vector contains: 1) a neomycinphosphotransferase gene as a selection marker, 2) an E. coli origin of replication, 3) a T5 phage promoter sequence, 4) two lac operator sequences, 5) a
30 Shine-Delgarno sequence, and 6) the lactose operon repressor gene (lacIq). The origin of replication (oriC) is derived from pUC19 (LTI, Gaithersburg, MD). The promoter sequence and operator sequences are made synthetically.

DNA can be inserted into the pHEa by restricting the vector with NdeI and
35 XbaI, BamHI, XhoI, or Asp718, running the restricted product on a gel, and isolating the larger fragment (the stuffer fragment should be about 310 base pairs). The DNA

insert is generated according to the PCR protocol described in Example 1, using PCR primers having restriction sites for NdeI (5' primer) and XbaI, BamHI, XhoI, or Asp718 (3' primer). The PCR insert is gel purified and restricted with compatible enzymes. The insert and vector are ligated according to standard protocols.

- 5 The engineered vector could easily be substituted in the above protocol to express protein in a bacterial system.

Example 6: Purification of a Polypeptide from an Inclusion Body

- 10 The following alternative method can be used to purify a polypeptide expressed in *E. coli* when it is present in the form of inclusion bodies. Unless otherwise specified, all of the following steps are conducted at 4-10°C.

- 15 Upon completion of the production phase of the *E. coli* fermentation, the cell culture is cooled to 4-10°C and the cells harvested by continuous centrifugation at 15,000 rpm (Heraeus Sepatech). On the basis of the expected yield of protein per unit weight of cell paste and the amount of purified protein required, an appropriate amount of cell paste, by weight, is suspended in a buffer solution containing 100 mM Tris, 50 mM EDTA, pH 7.4. The cells are dispersed to a homogeneous suspension using a high shear mixer.

- 20 The cells are then lysed by passing the solution through a microfluidizer (Microfluidics, Corp. or APV Gaulin, Inc.) twice at 4000-6000 psi. The homogenate is then mixed with NaCl solution to a final concentration of 0.5 M NaCl, followed by centrifugation at 7000 xg for 15 min. The resultant pellet is washed again using 0.5M NaCl, 100 mM Tris, 50 mM EDTA, pH 7.4.

- 25 The resulting washed inclusion bodies are solubilized with 1.5 M guanidine hydrochloride (GuHCl) for 2-4 hours. After 7000 xg centrifugation for 15 min., the pellet is discarded and the polypeptide containing supernatant is incubated at 4°C overnight to allow further GuHCl extraction.

- 30 Following high speed centrifugation (30,000 xg) to remove insoluble particles, the GuHCl solubilized protein is refolded by quickly mixing the GuHCl extract with 20 volumes of buffer containing 50 mM sodium, pH 4.5, 150 mM NaCl, 2 mM EDTA by vigorous stirring. The refolded diluted protein solution is kept at 4°C without mixing for 12 hours prior to further purification steps.

To clarify the refolded polypeptide solution, a previously prepared tangential filtration unit equipped with 0.16 µm membrane filter with appropriate surface area

(e.g., Filtron), equilibrated with 40 mM sodium acetate, pH 6.0 is employed. The filtered sample is loaded onto a cation exchange resin (e.g., Poros HS-50, Perseptive Biosystems). The column is washed with 40 mM sodium acetate, pH 6.0 and eluted with 250 mM, 500 mM, 1000 mM, and 1500 mM NaCl in the same buffer, in a
5 stepwise manner. The absorbance at 280 nm of the effluent is continuously monitored. Fractions are collected and further analyzed by SDS-PAGE.

Fractions containing the polypeptide are then pooled and mixed with 4 volumes of water. The diluted sample is then loaded onto a previously prepared set of tandem columns of strong anion (Poros HQ-50, Perseptive Biosystems) and weak anion
10 (Poros CM-20, Perseptive Biosystems) exchange resins. The columns are equilibrated with 40 mM sodium acetate, pH 6.0. Both columns are washed with 40 mM sodium acetate, pH 6.0, 200 mM NaCl. The CM-20 column is then eluted using a 10 column volume linear gradient ranging from 0.2 M NaCl, 50 mM sodium acetate, pH 6.0 to 1.0 M NaCl, 50 mM sodium acetate, pH 6.5. Fractions are collected under constant A_{280}
15 monitoring of the effluent. Fractions containing the polypeptide (determined, for instance, by 16% SDS-PAGE) are then pooled.

The resultant polypeptide should exhibit greater than 95% purity after the above refolding and purification steps. No major contaminant bands should be observed from
Commassie blue stained 16% SDS-PAGE gel when 5 μ g of purified protein is loaded.
20 The purified protein can also be tested for endotoxin/LPS contamination, and typically the LPS content is less than 0.1 ng/ml according to LAL assays.

Example 7: Cloning and Expression of a Polypeptide in a Baculovirus

Expression System

25 In this example, the plasmid shuttle vector pA2 is used to insert a polynucleotide into a baculovirus to express a polypeptide. This expression vector contains the strong polyhedrin promoter of the *Autographa californica* nuclear polyhedrosis virus (AcMNPV) followed by convenient restriction sites such as BamHI, Xba I and Asp718. The polyadenylation site of the simian virus 40 ("SV40") is used for efficient
30 polyadenylation. For easy selection of recombinant virus, the plasmid contains the beta-galactosidase gene from *E. coli* under control of a weak *Drosophila* promoter in the same orientation, followed by the polyadenylation signal of the polyhedrin gene. The inserted genes are flanked on both sides by viral sequences for cell-mediated
homologous recombination with wild-type viral DNA to generate a viable virus that
35 express the cloned polynucleotide.

Many other baculovirus vectors can be used in place of the vector above, such as pAc373, pVL941, and pAcIM1, as one skilled in the art would readily appreciate, as long as the construct provides appropriately located signals for transcription, translation, secretion and the like, including a signal peptide and an in-frame AUG as required. Such vectors are described, for instance, in Luckow et al., *Virology* 170:31-39 (1989).

Specifically, the cDNA sequence contained in the deposited clone, including the AUG initiation codon and the naturally associated leader sequence identified in Table 1, is amplified using the PCR protocol described in Example 1. If the naturally occurring signal sequence is used to produce the secreted protein, the pA2 vector does not need a second signal peptide. Alternatively, the vector can be modified (pA2 GP) to include a baculovirus leader sequence, using the standard methods described in Summers et al., "A Manual of Methods for Baculovirus Vectors and Insect Cell Culture Procedures," Texas Agricultural Experimental Station Bulletin No. 1555 (1987).

The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("GeneClean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested with appropriate restriction enzymes and again purified on a 1% agarose gel.

The plasmid is digested with the corresponding restriction enzymes and optionally, can be dephosphorylated using calf intestinal phosphatase, using routine procedures known in the art. The DNA is then isolated from a 1% agarose gel using a commercially available kit ("GeneClean" BIO 101 Inc., La Jolla, Ca.).

The fragment and the dephosphorylated plasmid are ligated together with T4 DNA ligase. *E. coli* HB101 or other suitable *E. coli* hosts such as XL-1 Blue (Stratagene Cloning Systems, La Jolla, CA) cells are transformed with the ligation mixture and spread on culture plates. Bacteria containing the plasmid are identified by digesting DNA from individual colonies and analyzing the digestion product by gel electrophoresis. The sequence of the cloned fragment is confirmed by DNA sequencing.

Five μ g of a plasmid containing the polynucleotide is co-transfected with 1.0 μ g of a commercially available linearized baculovirus DNA ("BaculoGold™ baculovirus DNA", Pharmingen, San Diego, CA), using the lipofection method described by Felgner et al., *Proc. Natl. Acad. Sci. USA* 84:7413-7417 (1987). One μ g of BaculoGold™ virus DNA and 5 μ g of the plasmid are mixed in a sterile well of a microtiter plate containing 50 μ l of serum-free Grace's medium (Life Technologies Inc., Gaithersburg, MD). Afterwards, 10 μ l Lipofectin plus 90 μ l Grace's medium are added, mixed and incubated for 15 minutes at room temperature. Then the transfection mixture is added drop-wise to Sf9 insect cells (ATCC CRL 1711) seeded in a 35 mm

tissue culture plate with 1 ml Grace's medium without serum. The plate is then incubated for 5 hours at 27° C. The transfection solution is then removed from the plate and 1 ml of Grace's insect medium supplemented with 10% fetal calf serum is added. Cultivation is then continued at 27° C for four days.

- 5 After four days the supernatant is collected and a plaque assay is performed, as described by Summers and Smith, *supra*. An agarose gel with "Blue Gal" (Life Technologies Inc., Gaithersburg) is used to allow easy identification and isolation of gal-expressing clones, which produce blue-stained plaques. (A detailed description of a "plaque assay" of this type can also be found in the user's guide for insect cell culture and baculovirology distributed by Life Technologies Inc., Gaithersburg, page 9-10.)
- 10 After appropriate incubation, blue stained plaques are picked with the tip of a micropipettor (e.g., Eppendorf). The agar containing the recombinant viruses is then resuspended in a microcentrifuge tube containing 200 µl of Grace's medium and the suspension containing the recombinant baculovirus is used to infect Sf9 cells seeded in
- 15 35 mm dishes. Four days later the supernatants of these culture dishes are harvested and then they are stored at 4° C.

- To verify the expression of the polypeptide, Sf9 cells are grown in Grace's medium supplemented with 10% heat-inactivated FBS. The cells are infected with the recombinant baculovirus containing the polynucleotide at a multiplicity of infection
- 20 ("MOI") of about 2. If radiolabeled proteins are desired, 6 hours later the medium is removed and is replaced with SF900 II medium minus methionine and cysteine (available from Life Technologies Inc., Rockville, MD). After 42 hours, 5 µCi of ³⁵S-methionine and 5 µCi ³⁵S-cysteine (available from Amersham) are added. The cells are further incubated for 16 hours and then are harvested by centrifugation. The proteins
- 25 in the supernatant as well as the intracellular proteins are analyzed by SDS-PAGE followed by autoradiography (if radiolabeled).

Microsequencing of the amino acid sequence of the amino terminus of purified protein may be used to determine the amino terminal sequence of the produced protein.

30 **Example 8: Expression of a Polypeptide in Mammalian Cells**

The polypeptide of the present invention can be expressed in a mammalian cell. A typical mammalian expression vector contains a promoter element, which mediates

the initiation of transcription of mRNA, a protein coding sequence, and signals required for the termination of transcription and polyadenylation of the transcript. Additional elements include enhancers, Kozak sequences and intervening sequences flanked by donor and acceptor sites for RNA splicing. Highly efficient transcription is achieved with the early and late promoters from SV40, the long terminal repeats (LTRs) from Retroviruses, e.g., RSV, HTLV1, HIV1 and the early promoter of the cytomegalovirus (CMV). However, cellular elements can also be used (e.g., the human actin promoter).

Suitable expression vectors for use in practicing the present invention include, for example, vectors such as pSVL and pMSG (Pharmacia, Uppsala, Sweden), pRSVcat (ATCC 37152), pSV2dhfr (ATCC 37146), pBC12MI (ATCC 67109), pCMVSPORT 2.0, and pCMVSPORT 3.0. Mammalian host cells that could be used include, human Hela, 293, H9 and Jurkat cells, mouse NIH3T3 and C127 cells, Cos 1, Cos 7 and CV1, quail QC1-3 cells, mouse L cells and Chinese hamster ovary (CHO) cells.

Alternatively, the polypeptide can be expressed in stable cell lines containing the polynucleotide integrated into a chromosome. The co-transfection with a selectable marker such as dhfr, gpt, neomycin, hygromycin allows the identification and isolation of the transfected cells.

The transfected gene can also be amplified to express large amounts of the encoded protein. The DHFR (dihydrofolate reductase) marker is useful in developing cell lines that carry several hundred or even several thousand copies of the gene of interest. (See, e.g., Alt, F. W., et al., *J. Biol. Chem.* 253:1357-1370 (1978); Hamlin, J. L. and Ma, C., *Biochem. et Biophys. Acta*, 1097:107-143 (1990); Page, M. J. and Sydenham, M. A., *Biotechnology* 9:64-68 (1991).) Another useful selection marker is the enzyme glutamine synthase (GS) (Murphy et al., *Biochem J.* 227:277-279 (1991); Bebbington et al., *Bio/Technology* 10:169-175 (1992). Using these markers, the mammalian cells are grown in selective medium and the cells with the highest resistance are selected. These cell lines contain the amplified gene(s) integrated into a chromosome. Chinese hamster ovary (CHO) and NSO cells are often used for the production of proteins.

Derivatives of the plasmid pSV2-dhfr (ATCC Accession No. 37146), the expression vectors pC4 (ATCC Accession No. 209646) and pC6 (ATCC Accession No. 209647) contain the strong promoter (LTR) of the Rous Sarcoma Virus (Cullen et al., *Molecular and Cellular Biology*, 438-447 (March, 1985)) plus a fragment of the CMV-enhancer (Boshart et al., *Cell* 41:521-530 (1985).) Multiple cloning sites, e.g., with the restriction enzyme cleavage sites BamHI, XbaI and Asp718, facilitate the cloning of the gene of interest. The vectors also contain the 3' intron, the

polyadenylation and termination signal of the rat preproinsulin gene, and the mouse DHFR gene under control of the SV40 early promoter.

Specifically, the plasmid pC6, for example, is digested with appropriate restriction enzymes and then dephosphorylated using calf intestinal phosphates by procedures known in the art. The vector is then isolated from a 1% agarose gel.

A polynucleotide of the present invention is amplified according to the protocol outlined in Example 1. If the naturally occurring signal sequence is used to produce the secreted protein, the vector does not need a second signal peptide. Alternatively, if the naturally occurring signal sequence is not used, the vector can be modified to include a heterologous signal sequence. (See, e.g., WO 96/34891.)

The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("GeneClean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested with appropriate restriction enzymes and again purified on a 1% agarose gel.

The amplified fragment is then digested with the same restriction enzyme and purified on a 1% agarose gel. The isolated fragment and the dephosphorylated vector are then ligated with T4 DNA ligase. *E. coli* HB101 or XL-1 Blue cells are then transformed and bacteria are identified that contain the fragment inserted into plasmid pC6 using, for instance, restriction enzyme analysis.

Chinese hamster ovary cells lacking an active DHFR gene is used for transfection. Five μ g of the expression plasmid pC6 is cotransfected with 0.5 μ g of the plasmid pSVneo using lipofectin (Felgner et al., *supra*). The plasmid pSV2-neo contains a dominant selectable marker, the *neo* gene from Tn5 encoding an enzyme that confers resistance to a group of antibiotics including G418. The cells are seeded in alpha minus MEM supplemented with 1 mg/ml G418. After 2 days, the cells are trypsinized and seeded in hybridoma cloning plates (Greiner, Germany) in alpha minus MEM supplemented with 10, 25, or 50 ng/ml of methotrexate plus 1 mg/ml G418. After about 10-14 days single clones are trypsinized and then seeded in 6-well petri dishes or 10 ml flasks using different concentrations of methotrexate (50 nM, 100 nM, 200 nM, 400 nM, 800 nM). Clones growing at the highest concentrations of methotrexate are then transferred to new 6-well plates containing even higher concentrations of methotrexate (1 μ M, 2 μ M, 5 μ M, 10 mM, 20 mM). The same procedure is repeated until clones are obtained which grow at a concentration of 100 - 200 μ M. Expression of the desired gene product is analyzed, for instance, by SDS-PAGE and Western blot or by reversed phase HPLC analysis.

Example 9: Protein Fusions

The polypeptides of the present invention are preferably fused to other proteins. These fusion proteins can be used for a variety of applications. For example, fusion of the present polypeptides to His-tag, HA-tag, protein A, IgG domains, and maltose binding protein facilitates purification. (See Example 5; see also EP A 394,827; Traunecker, et al., Nature 331:84-86 (1988).) Similarly, fusion to IgG-1, IgG-3, and albumin increases the half-life time in vivo. Nuclear localization signals fused to the polypeptides of the present invention can target the protein to a specific subcellular localization, while covalent heterodimer or homodimers can increase or decrease the activity of a fusion protein. Fusion proteins can also create chimeric molecules having more than one function. Finally, fusion proteins can increase solubility and/or stability of the fused protein compared to the non-fused protein. All of the types of fusion proteins described above can be made by modifying the following protocol, which outlines the fusion of a polypeptide to an IgG molecule, or the protocol described in Example 5.

Briefly, the human Fc portion of the IgG molecule can be PCR amplified, using primers that span the 5' and 3' ends of the sequence described below. These primers also should have convenient restriction enzyme sites that will facilitate cloning into an expression vector, preferably a mammalian expression vector.

For example, if pC4 (Accession No. 209646) is used, the human Fc portion can be ligated into the BamHI cloning site. Note that the 3' BamHI site should be destroyed. Next, the vector containing the human Fc portion is re-restricted with BamHI, linearizing the vector, and a polynucleotide of the present invention, isolated by the PCR protocol described in Example 1, is ligated into this BamHI site. Note that the polynucleotide is cloned without a stop codon, otherwise a fusion protein will not be produced.

If the naturally occurring signal sequence is used to produce the secreted protein, pC4 does not need a second signal peptide. Alternatively, if the naturally occurring signal sequence is not used, the vector can be modified to include a heterologous signal sequence. (See, e.g., WO 96/34891.)

Human IgG Fc region:

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GGGATCCGGAGCCCAAATCTTCTGACAAACTCACACATGCCCACCGTGCC
CAGCACCTGAATTCGAGGGTGCACCGTCAGTCTTCCTCTTCCCCCAAACC
CAAGGACACCCTCATGATCTCCCGGACTCCTGAGGTCACATGCGTGGTGGT
GGACGTAAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACG
GCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAAC

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AGCACGTACCGTGTGGTCAGCGTCCTACCGTCCTGCACCAGGACTGGCTG
 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAACCCCC
 ATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGAACCACAGGT
 GTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCT
 5 GACCTGCCTGGTCAAAGGCTTCTATCCAAGCGACATCGCCGTGGAGTGGGA
 GAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTGCTGG
 ACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCA
 GGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGC
 ACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGAGTGC
 10 GACGGCCGCGACTCTAGAGGAT (SEQ ID NO:1)

Example 10: Production of an Antibody from a Polypeptide

The antibodies of the present invention can be prepared by a variety of methods. (See, Current Protocols, Chapter 2.) For example, cells expressing a polypeptide of
 15 the present invention is administered to an animal to induce the production of sera containing polyclonal antibodies. In a preferred method, a preparation of the secreted protein is prepared and purified to render it substantially free of natural contaminants. Such a preparation is then introduced into an animal in order to produce polyclonal antisera of greater specific activity.

20 In the most preferred method, the antibodies of the present invention are monoclonal antibodies (or protein binding fragments thereof). Such monoclonal antibodies can be prepared using hybridoma technology. (Köhler et al., Nature 256:495 (1975); Köhler et al., Eur. J. Immunol. 6:511 (1976); Köhler et al., Eur. J. Immunol. 6:292 (1976); Hammerling et al., in: Monoclonal Antibodies and T-Cell
 25 Hybridomas, Elsevier, N.Y., pp. 563-681 (1981).) In general, such procedures involve immunizing an animal (preferably a mouse) with polypeptide or, more preferably, with a secreted polypeptide-expressing cell. Such cells may be cultured in any suitable tissue culture medium; however, it is preferable to culture cells in Earle's modified Eagle's medium supplemented with 10% fetal bovine serum (inactivated at
 30 about 56°C), and supplemented with about 10 g/l of nonessential amino acids, about 1,000 U/ml of penicillin, and about 100 µg/ml of streptomycin.

The splenocytes of such mice are extracted and fused with a suitable myeloma cell line. Any suitable myeloma cell line may be employed in accordance with the present invention; however, it is preferable to employ the parent myeloma cell line
 35 (SP2O), available from the ATCC. After fusion, the resulting hybridoma cells are selectively maintained in HAT medium, and then cloned by limiting dilution as

described by Wands et al. (Gastroenterology 80:225-232 (1981).) The hybridoma cells obtained through such a selection are then assayed to identify clones which secrete antibodies capable of binding the polypeptide.

Alternatively, additional antibodies capable of binding to the polypeptide can be produced in a two-step procedure using anti-idiotypic antibodies. Such a method makes use of the fact that antibodies are themselves antigens, and therefore, it is possible to obtain an antibody which binds to a second antibody. In accordance with this method, protein specific antibodies are used to immunize an animal, preferably a mouse. The splenocytes of such an animal are then used to produce hybridoma cells, and the hybridoma cells are screened to identify clones which produce an antibody whose ability to bind to the protein-specific antibody can be blocked by the polypeptide. Such antibodies comprise anti-idiotypic antibodies to the protein-specific antibody and can be used to immunize an animal to induce formation of further protein-specific antibodies.

It will be appreciated that Fab and F(ab')₂ and other fragments of the antibodies of the present invention may be used according to the methods disclosed herein. Such fragments are typically produced by proteolytic cleavage, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce F(ab')₂ fragments). Alternatively, secreted protein-binding fragments can be produced through the application of recombinant DNA technology or through synthetic chemistry.

For in vivo use of antibodies in humans, it may be preferable to use "humanized" chimeric monoclonal antibodies. Such antibodies can be produced using genetic constructs derived from hybridoma cells producing the monoclonal antibodies described above. Methods for producing chimeric antibodies are known in the art. (See, for review, Morrison, Science 229:1202 (1985); Oi et al., BioTechniques 4:214 (1986); Cabilly et al., U.S. Patent No. 4,816,567; Taniguchi et al., EP 171496; Morrison et al., EP 173494; Neuberger et al., WO 8601533; Robinson et al., WO 8702671; Boulianne et al., Nature 312:643 (1984); Neuberger et al., Nature 314:268 (1985).)

Example 11: Production Of Secreted Protein For High-Throughput Screening Assays

The following protocol produces a supernatant containing a polypeptide to be tested. This supernatant can then be used in the Screening Assays described in Examples 13-20.

First, dilute Poly-D-Lysine (644 587 Boehringer-Mannheim) stock solution (1mg/ml in PBS) 1:20 in PBS (w/o calcium or magnesium 17-516F Biowhittaker) for a

- working solution of 50ug/ml. Add 200 ul of this solution to each well (24 well plates) and incubate at RT for 20 minutes. Be sure to distribute the solution over each well (note: a 12-channel pipetter may be used with tips on every other channel). Aspirate off the Poly-D-Lysine solution and rinse with 1 ml PBS (Phosphate Buffered Saline). The
- 5 PBS should remain in the well until just prior to plating the cells and plates may be poly-lysine coated in advance for up to two weeks.

- Plate 293T cells (do not carry cells past P+20) at 2×10^5 cells/well in .5ml DMEM(Dulbecco's Modified Eagle Medium)(with 4.5 G/L glucose and L-glutamine (12-604F Biowhittaker))/10% heat inactivated FBS(14-503F Biowhittaker)/1x
- 10 Penstrep(17-602E Biowhittaker). Let the cells grow overnight.

- The next day, mix together in a sterile solution basin: 300 ul Lipofectamine (18324-012 Gibco/BRL) and 5ml Optimem I (31985070 Gibco/BRL)/96-well plate. With a small volume multi-channel pipetter, aliquot approximately 2ug of an expression vector containing a polynucleotide insert, produced by the methods described in
- 15 Examples 8 or 9, into an appropriately labeled 96-well round bottom plate. With a multi-channel pipetter, add 50ul of the Lipofectamine/Optimem I mixture to each well. Pipette up and down gently to mix. Incubate at RT 15-45 minutes. After about 20 minutes, use a multi-channel pipetter to add 150ul Optimem I to each well. As a control, one plate of vector DNA lacking an insert should be transfected with each set of
- 20 transfections.

- Preferably, the transfection should be performed by tag-teaming the following tasks. By tag-teaming, hands on time is cut in half, and the cells do not spend too much time on PBS. First, person A aspirates off the media from four 24-well plates of cells, and then person B rinses each well with .5-1ml PBS. Person A then aspirates off
- 25 PBS rinse, and person B, using a 12-channel pipetter with tips on every other channel, adds the 200ul of DNA/Lipofectamine/Optimem I complex to the odd wells first, then to the even wells, to each row on the 24-well plates. Incubate at 37°C for 6 hours.

- While cells are incubating, prepare appropriate media, either 1%BSA in DMEM with 1x penstrep, or CHO-5 media (116.6 mg/L of CaCl₂ (anhyd); 0.00130 mg/L
- 30 CuSO₄·5H₂O; 0.050 mg/L of Fe(NO₃)₃·9H₂O; 0.417 mg/L of FeSO₄·7H₂O; 311.80 mg/L of KCl; 28.64 mg/L of MgCl₂; 48.84 mg/L of MgSO₄; 6995.50 mg/L of NaCl; 2400.0 mg/L of NaHCO₃; 62.50 mg/L of NaH₂PO₄·H₂O; 71.02 mg/L of Na₂HPO₄; .4320 mg/L of ZnSO₄·7H₂O; .002 mg/L of Arachidonic Acid ; 1.022 mg/L of Cholesterol; .070 mg/L of DL-alpha-Tocopherol-Acetate; 0.0520 mg/L of Linoleic
- 35 Acid; 0.010 mg/L of Linolenic Acid; 0.010 mg/L of Myristic Acid; 0.010 mg/L of Oleic Acid; 0.010 mg/L of Palmitic Acid; 0.010 mg/L of Palmitic Acid; 100 mg/L of

Pluronic F-68; 0.010 mg/L of Stearic Acid; 2.20 mg/L of Tween 80; 4551 mg/L of D-Glucose; 130.85 mg/ml of L- Alanine; 147.50 mg/ml of L-Arginine-HCL; 7.50 mg/ml of L-Asparagine-H₂O; 6.65 mg/ml of L-Aspartic Acid; 29.56 mg/ml of L-Cystine-2HCL-H₂O; 31.29 mg/ml of L-Cystine-2HCL; 7.35 mg/ml of L-Glutamic Acid; 365.0 mg/ml of L-Glutamine; 18.75 mg/ml of Glycine; 52.48 mg/ml of L-Histidine-HCL-H₂O; 106.97 mg/ml of L-Isoleucine; 111.45 mg/ml of L-Leucine; 163.75 mg/ml of L-Lysine HCL; 32.34 mg/ml of L-Methionine; 68.48 mg/ml of L-Phenylalanine; 40.0 mg/ml of L-Proline; 26.25 mg/ml of L-Serine; 101.05 mg/ml of L-Threonine; 19.22 mg/ml of L-Tryptophan; 91.79 mg/ml of L-Tyrosine-2Na-2H₂O; 99.65 mg/ml of L-Valine; 0.0035 mg/L of Biotin; 3.24 mg/L of D-Ca Pantothenate; 11.78 mg/L of Choline Chloride; 4.65 mg/L of Folic Acid; 15.60 mg/L of i-Inositol; 3.02 mg/L of Niacinamide; 3.00 mg/L of Pyridoxal HCL; 0.031 mg/L of Pyridoxine HCL; 0.319 mg/L of Riboflavin; 3.17 mg/L of Thiamine HCL; 0.365 mg/L of Thymidine; and 0.680 mg/L of Vitamin B₁₂; 25 mM of HEPES Buffer; 2.39 mg/L of Na Hypoxanthine; 0.105 mg/L of Lipoic Acid; 0.081 mg/L of Sodium Putrescine-2HCL; 55.0 mg/L of Sodium Pyruvate; 0.0067 mg/L of Sodium Selenite; 20uM of Ethanolamine; 0.122 mg/L of Ferric Citrate; 41.70 mg/L of Methyl-B-Cyclodextrin complexed with Linoleic Acid; 33.33 mg/L of Methyl-B-Cyclodextrin complexed with Oleic Acid; and 10 mg/L of Methyl-B-Cyclodextrin complexed with Retinal) with 2mm glutamine and 1x penstrep. (BSA (81-068-3 Bayer) 100gm dissolved in 1L DMEM for a 10% BSA stock solution). Filter the media and collect 50 ul for endotoxin assay in 15ml polystyrene conical.

The transfection reaction is terminated, preferably by tag-teaming, at the end of the incubation period. Person A aspirates off the transfection media, while person B adds 1.5ml appropriate media to each well. Incubate at 37°C for 45 or 72 hours depending on the media used: 1%BSA for 45 hours or CHO-5 for 72 hours.

On day four, using a 300ul multichannel pipetter, aliquot 600ul in one 1ml deep well plate and the remaining supernatant into a 2ml deep well. The supernatants from each well can then be used in the assays described in Examples 13-20.

It is specifically understood that when activity is obtained in any of the assays described below using a supernatant, the activity originates from either the polypeptide directly (e.g., as a secreted protein) or by the polypeptide inducing expression of other proteins, which are then secreted into the supernatant. Thus, the invention further provides a method of identifying the protein in the supernatant characterized by an activity in a particular assay.

Example 12: Construction of GAS Reporter Construct

One signal transduction pathway involved in the differentiation and proliferation of cells is called the Jaks-STATs pathway. Activated proteins in the Jaks-STATs pathway bind to gamma activation site "GAS" elements or interferon-sensitive responsive element ("ISRE"), located in the promoter of many genes. The binding of a protein to these elements alter the expression of the associated gene.

GAS and ISRE elements are recognized by a class of transcription factors called Signal Transducers and Activators of Transcription, or "STATs." There are six members of the STATs family. Stat1 and Stat3 are present in many cell types, as is Stat2 (as response to IFN-alpha is widespread). Stat4 is more restricted and is not in many cell types though it has been found in T helper class I, cells after treatment with IL-12. Stat5 was originally called mammary growth factor, but has been found at higher concentrations in other cells including myeloid cells. It can be activated in tissue culture cells by many cytokines.

The STATs are activated to translocate from the cytoplasm to the nucleus upon tyrosine phosphorylation by a set of kinases known as the Janus Kinase ("Jaks") family. Jaks represent a distinct family of soluble tyrosine kinases and include Tyk2, Jak1, Jak2, and Jak3. These kinases display significant sequence similarity and are generally catalytically inactive in resting cells.

The Jaks are activated by a wide range of receptors summarized in the Table below. (Adapted from review by Schidler and Darnell, Ann. Rev. Biochem. 64:621-51 (1995).) A cytokine receptor family, capable of activating Jaks, is divided into two groups: (a) Class 1 includes receptors for IL-2, IL-3, IL-4, IL-6, IL-7, IL-9, IL-11, IL-12, IL-15, Epo, PRL, GH, G-CSF, GM-CSF, LIF, CNTF, and thrombopoietin; and (b) Class 2 includes IFN-a, IFN-g, and IL-10. The Class 1 receptors share a conserved cysteine motif (a set of four conserved cysteines and one tryptophan) and a WSXWS motif (a membrane proximal region encoding Trp-Ser-Xxx-Trp-Ser (SEQ ID NO:2)).

Thus, on binding of a ligand to a receptor, Jaks are activated, which in turn activate STATs, which then translocate and bind to GAS elements. This entire process is encompassed in the Jaks-STATs signal transduction pathway.

Therefore, activation of the Jaks-STATs pathway, reflected by the binding of the GAS or the ISRE element, can be used to indicate proteins involved in the proliferation and differentiation of cells. For example, growth factors and cytokines are known to activate the Jaks-STATs pathway. (See Table below.) Thus, by using GAS elements linked to reporter molecules, activators of the Jaks-STATs pathway can be identified.

	<u>Ligand</u>	<u>tyk2</u>	<u>JAKs</u> <u>Jak1</u>	<u>Jak2</u>	<u>Jak3</u>	<u>STATS</u>	<u>GAS(elements) or ISRE</u>
	<u>IFN family</u>						
5	IFN-a/B	+	+	-	-	1,2,3	ISRE
	IFN-g		+	+	-	1	GAS (IRF1>Lys6>IFP)
	Il-10	+	?	?	-	1,3	
	<u>gp130 family</u>						
10	IL-6 (Pleiotrohic)	+	+	+	?	1,3	GAS (IRF1>Lys6>IFP)
	Il-11(Pleiotrohic)	?	+	?	?	1,3	
	OnM(Pleiotrohic)	?	+	+	?	1,3	
	LIF(Pleiotrohic)	?	+	+	?	1,3	
	CNTF(Pleiotrohic)	-/+	+	+	?	1,3	
15	G-CSF(Pleiotrohic)	?	+	?	?	1,3	
	IL-12(Pleiotrohic)	+	-	+	+	1,3	
	<u>g-C family</u>						
20	IL-2 (lymphocytes)	-	+	-	+	1,3,5	GAS
	IL-4 (lymph/myeloid)	-	+	-	+	6	GAS (IRF1 = IFP >>Ly6)(IgH)
	IL-7 (lymphocytes)	-	+	-	+	5	GAS
	IL-9 (lymphocytes)	-	+	-	+	5	GAS
	IL-13 (lymphocyte)	-	+	?	?	6	GAS
	IL-15	?	+	?	+	5	GAS
25	<u>gp140 family</u>						
	IL-3 (myeloid)	-	-	+	-	5	GAS (IRF1>IFP>>Ly6)
	IL-5 (myeloid)	-	-	+	-	5	GAS
	GM-CSF (myeloid)	-	-	+	-	5	GAS
30	<u>Growth hormone family</u>						
	GH	?	-	+	-	5	
	PRL	?	+/-	+	-	1,3,5	
	EPO	?	-	+	-	5	GAS(B-CAS>IRF1=IFP>>Ly6)
35	<u>Receptor Tyrosine Kinases</u>						
	EGF	?	+	+	-	1,3	GAS (IRF1)
	PDGF	?	+	+	-	1,3	
40	CSF-1	?	+	+	-	1,3	GAS (not IRF1)

To construct a synthetic GAS containing promoter element, which is used in the Biological Assays described in Examples 13-14, a PCR based strategy is employed to generate a GAS-SV40 promoter sequence. The 5' primer contains four tandem copies of the GAS binding site found in the IRF1 promoter and previously demonstrated to bind STATs upon induction with a range of cytokines (Rothman et al., Immunity 1:457-468 (1994).), although other GAS or ISRE elements can be used instead. The 5' primer also contains 18bp of sequence complementary to the SV40 early promoter sequence and is flanked with an XhoI site. The sequence of the 5' primer is:

5':GCGCCTCGAGATTTCCCGAAATCTAGATTTCCCGAAATGATTTCCCG
AAATGATTTCCCGAAATATCTGCCATCTCAATTAG:3' (SEQ ID NO:3)

The downstream primer is complementary to the SV40 promoter and is flanked with a Hind III site: 5':GCGGCAAGCTTTTTGCAAAGCCTAGGC:3' (SEQ ID NO:4)

PCR amplification is performed using the SV40 promoter template present in the B-gal:promoter plasmid obtained from Clontech. The resulting PCR fragment is digested with XhoI/Hind III and subcloned into BLSK2-. (Stratagene.) Sequencing with forward and reverse primers confirms that the insert contains the following sequence:

5':CTCGAGATTTCCCGAAATCTAGATTTCCCGAAATGATTTCCCGAAATG
ATTTCCCGAAATATCTGCCATCTCAATTAGTCAGCAACCATAGTCCCGCCC
CTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTTCTCCGC
CCCATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCTCGGC
CTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTT
TGCAAAAAGCTT:3' (SEQ ID NO:5)

With this GAS promoter element linked to the SV40 promoter, a GAS:SEAP2 reporter construct is next engineered. Here, the reporter molecule is a secreted alkaline phosphatase, or "SEAP." Clearly, however, any reporter molecule can be instead of SEAP, in this or in any of the other Examples. Well known reporter molecules that can be used instead of SEAP include chloramphenicol acetyltransferase (CAT), luciferase, alkaline phosphatase, B-galactosidase, green fluorescent protein (GFP), or any protein detectable by an antibody.

The above sequence confirmed synthetic GAS-SV40 promoter element is subcloned into the pSEAP-Promoter vector obtained from Clontech using HindIII and XhoI, effectively replacing the SV40 promoter with the amplified GAS:SV40 promoter element, to create the GAS-SEAP vector. However, this vector does not contain a neomycin resistance gene, and therefore, is not preferred for mammalian expression systems.

Thus, in order to generate mammalian stable cell lines expressing the GAS-SEAP reporter, the GAS-SEAP cassette is removed from the GAS-SEAP vector using Sall and NotI, and inserted into a backbone vector containing the neomycin resistance gene, such as pGFP-1 (Clontech), using these restriction sites in the multiple cloning site, to create the GAS-SEAP/Neo vector. Once this vector is transfected into mammalian cells, this vector can then be used as a reporter molecule for GAS binding as described in Examples 13-14.

Other constructs can be made using the above description and replacing GAS with a different promoter sequence. For example, construction of reporter molecules containing NFK-B and EGR promoter sequences are described in Examples 15 and 16. However, many other promoters can be substituted using the protocols described in these Examples. For instance, SRE, IL-2, NFAT, or Osteocalcin promoters can be substituted, alone or in combination (e.g., GAS/NF-KB/EGR, GAS/NF-KB, IL-2/NFAT, or NF-KB/GAS). Similarly, other cell lines can be used to test reporter construct activity, such as HELA (epithelial), HUVEC (endothelial), Reh (B-cell), Saos-2 (osteoblast), HUVAC (aortic), or Cardiomyocyte.

Example 13: High-Throughput Screening Assay for T-cell Activity.

The following protocol is used to assess T-cell activity by identifying factors, such as growth factors and cytokines, that may proliferate or differentiate T-cells. T-cell activity is assessed using the GAS/SEAP/Neo construct produced in Example 12. Thus, factors that increase SEAP activity indicate the ability to activate the Jaks-STATS signal transduction pathway. The T-cell used in this assay is Jurkat T-cells (ATCC Accession No. TIB-152), although Molt-3 cells (ATCC Accession No. CRL-1552) and Molt-4 cells (ATCC Accession No. CRL-1582) cells can also be used.

Jurkat T-cells are lymphoblastic CD4+ Th1 helper cells. In order to generate stable cell lines, approximately 2 million Jurkat cells are transfected with the GAS-SEAP/neo vector using DMRIE-C (Life Technologies)(transfection procedure described below). The transfected cells are seeded to a density of approximately 20,000 cells per well and transfectants resistant to 1 mg/ml gentamicin selected. Resistant colonies are expanded and then tested for their response to increasing concentrations of interferon gamma. The dose response of a selected clone is demonstrated.

Specifically, the following protocol will yield sufficient cells for 75 wells containing 200 ul of cells. Thus, it is either scaled up, or performed in multiple to generate sufficient cells for multiple 96 well plates. Jurkat cells are maintained in RPMI + 10% serum with 1% Pen-Strep. Combine 2.5 mls of OPTI-MEM (Life Technologies)

with 10 ug of plasmid DNA in a T25 flask. Add 2.5 ml OPTI-MEM containing 50 ul of DMRIE-C and incubate at room temperature for 15-45 mins.

- During the incubation period, count cell concentration, spin down the required number of cells (10^7 per transfection), and resuspend in OPTI-MEM to a final
5 concentration of 10^7 cells/ml. Then add 1ml of 1×10^7 cells in OPTI-MEM to T25 flask and incubate at 37°C for 6 hrs. After the incubation, add 10 ml of RPMI + 15% serum.

The Jurkat:GAS-SEAP stable reporter lines are maintained in RPMI + 10% serum, 1 mg/ml Gentacin, and 1% Pen-Strep. These cells are treated with supernatants containing a polypeptide as produced by the protocol described in Example 11.

- 10 On the day of treatment with the supernatant, the cells should be washed and resuspended in fresh RPMI + 10% serum to a density of 500,000 cells per ml. The exact number of cells required will depend on the number of supernatants being screened. For one 96 well plate, approximately 10 million cells (for 10 plates, 100 million cells) are required.

- 15 Transfer the cells to a triangular reservoir boat, in order to dispense the cells into a 96 well dish, using a 12 channel pipette. Using a 12 channel pipette, transfer 200 ul of cells into each well (therefore adding 100, 000 cells per well).

- After all the plates have been seeded, 50 ul of the supernatants are transferred directly from the 96 well plate containing the supernatants into each well using a 12
20 channel pipette. In addition, a dose of exogenous interferon gamma (0.1, 1.0, 10 ng) is added to wells H9, H10, and H11 to serve as additional positive controls for the assay.

- The 96 well dishes containing Jurkat cells treated with supernatants are placed in an incubator for 48 hrs (note: this time is variable between 48-72 hrs). 35 ul samples
25 from each well are then transferred to an opaque 96 well plate using a 12 channel pipette. The opaque plates should be covered (using sellophene covers) and stored at -20°C until SEAP assays are performed according to Example 17. The plates containing the remaining treated cells are placed at 4°C and serve as a source of material for repeating the assay on a specific well if desired.

- 30 As a positive control, 100 Unit/ml interferon gamma can be used which is known to activate Jurkat T cells. Over 30 fold induction is typically observed in the positive control wells.

Example 14: High-Throughput Screening Assay Identifying Myeloid Activity

The following protocol is used to assess myeloid activity by identifying factors, such as growth factors and cytokines, that may proliferate or differentiate myeloid cells.

- 5 Myeloid cell activity is assessed using the GAS/SEAP/Neo construct produced in Example 12. Thus, factors that increase SEAP activity indicate the ability to activate the Jaks-STATS signal transduction pathway. The myeloid cell used in this assay is U937, a pre-monocyte cell line, although TF-1, HL60, or KG1 can be used.

- 10 To transiently transfect U937 cells with the GAS/SEAP/Neo construct produced in Example 12, a DEAE-Dextran method (Kharbanda et. al., 1994, Cell Growth & Differentiation, 5:259-265) is used. First, harvest 2×10^7 U937 cells and wash with PBS. The U937 cells are usually grown in RPMI 1640 medium containing 10% heat-inactivated fetal bovine serum (FBS) supplemented with 100 units/ml penicillin and 100 mg/ml streptomycin.

- 15 Next, suspend the cells in 1 ml of 20 mM Tris-HCl (pH 7.4) buffer containing 0.5 mg/ml DEAE-Dextran, 8 ug GAS-SEAP2 plasmid DNA, 140 mM NaCl, 5 mM KCl, 375 uM $\text{Na}_2\text{HPO}_4 \cdot 7\text{H}_2\text{O}$, 1 mM MgCl_2 , and 675 uM CaCl_2 . Incubate at 37°C for 45 min.

- 20 Wash the cells with RPMI 1640 medium containing 10% FBS and then resuspend in 10 ml complete medium and incubate at 37°C for 36 hr.

The GAS-SEAP/U937 stable cells are obtained by growing the cells in 400 ug/ml G418. The G418-free medium is used for routine growth but every one to two months, the cells should be re-grown in 400 ug/ml G418 for couple of passages.

- 25 These cells are tested by harvesting 1×10^8 cells (this is enough for ten 96-well plates assay) and wash with PBS. Suspend the cells in 200 ml above described growth medium, with a final density of 5×10^5 cells/ml. Plate 200 ul cells per well in the 96-well plate (or 1×10^5 cells/well).

- 30 Add 50 ul of the supernatant prepared by the protocol described in Example 11. Incubate at 37°C for 48 to 72 hr. As a positive control, 100 Unit/ml interferon gamma can be used which is known to activate U937 cells. Over 30 fold induction is typically observed in the positive control wells. SEAP assay the supernatant according to the protocol described in Example 17.

Example 15: High-Throughput Screening Assay Identifying Neuronal Activity.

When cells undergo differentiation and proliferation, a group of genes are activated through many different signal transduction pathways. One of these genes,
5 EGR1 (early growth response gene 1), is induced in various tissues and cell types upon activation. The promoter of EGR1 is responsible for such induction. Using the EGR1 promoter linked to reporter molecules, activation of cells can be assessed.

Particularly, the following protocol is used to assess neuronal activity in PC12 cell lines. PC12 cells (rat phenochromocytoma cells) are known to proliferate and/or
10 differentiate by activation with a number of mitogens, such as TPA (tetradecanoyl phorbol acetate), NGF (nerve growth factor), and EGF (epidermal growth factor). The EGR1 gene expression is activated during this treatment. Thus, by stably transfecting PC12 cells with a construct containing an EGR promoter linked to SEAP reporter, activation of PC12 cells can be assessed.

15 The EGR/SEAP reporter construct can be assembled by the following protocol. The EGR-1 promoter sequence (-633 to +1)(Sakamoto K et al., Oncogene 6:867-871 (1991)) can be PCR amplified from human genomic DNA using the following primers:

5' GCGCTCGAGGGATGACAGCGATAGAACCCCGG -3' (SEQ ID NO:6)

5' GCGAAGCTTCGCGACTCCCCGGATCCGCCTC-3' (SEQ ID NO:7)

20 Using the GAS:SEAP/Neo vector produced in Example 12, EGR1 amplified product can then be inserted into this vector. Linearize the GAS:SEAP/Neo vector using restriction enzymes XhoI/HindIII, removing the GAS/SV40 stuffer. Restrict the EGR1 amplified product with these same enzymes. Ligate the vector and the EGR1 promoter.

25 To prepare 96 well-plates for cell culture, two mls of a coating solution (1:30 dilution of collagen type I (Upstate Biotech Inc. Cat#08-115) in 30% ethanol (filter sterilized)) is added per one 10 cm plate or 50 ml per well of the 96-well plate, and allowed to air dry for 2 hr.

PC12 cells are routinely grown in RPMI-1640 medium (Bio Whittaker)
30 containing 10% horse serum (JRH BIOSCIENCES, Cat. # 12449-78P), 5% heat-inactivated fetal bovine serum (FBS) supplemented with 100 units/ml penicillin and 100 ug/ml streptomycin on a precoated 10 cm tissue culture dish. One to four split is done every three to four days. Cells are removed from the plates by scraping and resuspended with pipetting up and down for more than 15 times.

35 Transfect the EGR/SEAP/Neo construct into PC12 using the Lipofectamine protocol described in Example 11. EGR-SEAP/PC12 stable cells are obtained by growing the cells in 300 ug/ml G418. The G418-free medium is used for routine

growth but every one to two months, the cells should be re-grown in 300 ug/ml G418 for couple of passages.

To assay for neuronal activity, a 10 cm plate with cells around 70 to 80% confluent is screened by removing the old medium. Wash the cells once with PBS (Phosphate buffered saline). Then starve the cells in low serum medium (RPMI-1640 containing 1% horse serum and 0.5% FBS with antibiotics) overnight.

The next morning, remove the medium and wash the cells with PBS. Scrape off the cells from the plate, suspend the cells well in 2 ml low serum medium. Count the cell number and add more low serum medium to reach final cell density as 5×10^5 cells/ml.

Add 200 ul of the cell suspension to each well of 96-well plate (equivalent to 1×10^5 cells/well). Add 50 ul supernatant produced by Example 11, 37°C for 48 to 72 hr. As a positive control, a growth factor known to activate PC12 cells through EGR can be used, such as 50 ng/ul of Neuronal Growth Factor (NGF). Over fifty-fold induction of SEAP is typically seen in the positive control wells. SEAP assay the supernatant according to Example 17.

Example 16: High-Throughput Screening Assay for T-cell Activity

NF- κ B (Nuclear Factor κ B) is a transcription factor activated by a wide variety of agents including the inflammatory cytokines IL-1 and TNF, CD30 and CD40, lymphotoxin-alpha and lymphotoxin-beta, by exposure to LPS or thrombin, and by expression of certain viral gene products. As a transcription factor, NF- κ B regulates the expression of genes involved in immune cell activation, control of apoptosis (NF- κ B appears to shield cells from apoptosis), B and T-cell development, anti-viral and antimicrobial responses, and multiple stress responses.

In non-stimulated conditions, NF- κ B is retained in the cytoplasm with I- κ B (Inhibitor κ B). However, upon stimulation, I- κ B is phosphorylated and degraded, causing NF- κ B to shuttle to the nucleus, thereby activating transcription of target genes. Target genes activated by NF- κ B include IL-2, IL-6, GM-CSF, ICAM-1 and class I MHC.

Due to its central role and ability to respond to a range of stimuli, reporter constructs utilizing the NF- κ B promoter element are used to screen the supernatants produced in Example 11. Activators or inhibitors of NF- κ B would be useful in treating

diseases. For example, inhibitors of NF- κ B could be used to treat those diseases related to the acute or chronic activation of NF- κ B, such as rheumatoid arthritis.

To construct a vector containing the NF- κ B promoter element, a PCR based strategy is employed. The upstream primer contains four tandem copies of the NF- κ B binding site (GGGGACTTTCCC) (SEQ ID NO:8), 18 bp of sequence complementary to the 5' end of the SV40 early promoter sequence, and is flanked with an XhoI site:
 5':GCGGCCTCGAGGGGACTTTCCCGGGGACTTTCCGGGGACTTTCCGGGGACTTTCCGGGGACTTTCCATCCTGCCATCTCAATTAG:3' (SEQ ID NO:9)

The downstream primer is complementary to the 3' end of the SV40 promoter and is flanked with a Hind III site:

5':GCGGCAAGCTTTTTGCAAAGCCTAGGC:3' (SEQ ID NO:4)

PCR amplification is performed using the SV40 promoter template present in the pB-gal:promoter plasmid obtained from Clontech. The resulting PCR fragment is digested with XhoI and Hind III and subcloned into BLSK2-. (Stratagene)

Sequencing with the T7 and T3 primers confirms the insert contains the following sequence:

5':CTCGAGGGGACTTTCCCGGGGACTTTCCGGGGACTTTCCGGGGACTTTCC
 ATCTGCCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCCA
 TCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGACT
 AATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTC
 CAGAAGTAGTGAGGAGGCTTTTTTTGGAGGCCTAGGCTTTTGCAAAAAGCTT:
 3' (SEQ ID NO:10)

Next, replace the SV40 minimal promoter element present in the pSEAP2- promoter plasmid (Clontech) with this NF- κ B/SV40 fragment using XhoI and HindIII. However, this vector does not contain a neomycin resistance gene, and therefore, is not preferred for mammalian expression systems.

In order to generate stable mammalian cell lines, the NF- κ B/SV40/SEAP cassette is removed from the above NF- κ B/SEAP vector using restriction enzymes Sall and NotI, and inserted into a vector containing neomycin resistance. Particularly, the NF- κ B/SV40/SEAP cassette was inserted into pGFP-1 (Clontech), replacing the GFP gene, after restricting pGFP-1 with Sall and NotI.

Once NF- κ B/SV40/SEAP/Neo vector is created, stable Jurkat T-cells are created and maintained according to the protocol described in Example 13. Similarly, the method for assaying supernatants with these stable Jurkat T-cells is also described in Example 13. As a positive control, exogenous TNF alpha (0.1, 1, 10 ng) is added to wells H9, H10, and H11, with a 5-10 fold activation typically observed.

Example 17: Assay for SEAP Activity

As a reporter molecule for the assays described in Examples 13-16, SEAP activity is assayed using the Tropix Phospho-light Kit (Cat. BP-400) according to the following general procedure. The Tropix Phospho-light Kit supplies the Dilution, Assay, and Reaction Buffers used below.

Prime a dispenser with the 2.5x Dilution Buffer and dispense 15 μ l of 2.5x dilution buffer into Optiplates containing 35 μ l of a supernatant. Seal the plates with a plastic sealer and incubate at 65°C for 30 min. Separate the Optiplates to avoid uneven heating.

Cool the samples to room temperature for 15 minutes. Empty the dispenser and prime with the Assay Buffer. Add 50 μ l Assay Buffer and incubate at room temperature 5 min. Empty the dispenser and prime with the Reaction Buffer (see the table below). Add 50 μ l Reaction Buffer and incubate at room temperature for 20 minutes. Since the intensity of the chemiluminescent signal is time dependent, and it takes about 10 minutes to read 5 plates on luminometer, one should treat 5 plates at each time and start the second set 10 minutes later.

Read the relative light unit in the luminometer. Set H12 as blank, and print the results. An increase in chemiluminescence indicates reporter activity.

Reaction Buffer Formulation:

# of plates	Rxn buffer diluent (ml)	CSPD (ml)
10	60	3
11	65	3.25
12	70	3.5
13	75	3.75
14	80	4
15	85	4.25
16	90	4.5
17	95	4.75
18	100	5
19	105	5.25
20	110	5.5
21	115	5.75
22	120	6

23	125	6.25
24	130	6.5
25	135	6.75
26	140	7
27	145	7.25
28	150	7.5
29	155	7.75
30	160	8
31	165	8.25
32	170	8.5
33	175	8.75
34	180	9
35	185	9.25
36	190	9.5
37	195	9.75
38	200	10
39	205	10.25
40	210	10.5
41	215	10.75
42	220	11
43	225	11.25
44	230	11.5
45	235	11.75
46	240	12
47	245	12.25
48	250	12.5
49	255	12.75
50	260	13

Example 18: High-Throughput Screening Assay Identifying Changes in Small Molecule Concentration and Membrane Permeability

5 Binding of a ligand to a receptor is known to alter intracellular levels of small molecules, such as calcium, potassium, sodium, and pH, as well as alter membrane potential. These alterations can be measured in an assay to identify supernatants which bind to receptors of a particular cell. Although the following protocol describes an assay for calcium, this protocol can easily be modified to detect changes in potassium, sodium, pH, membrane potential, or any other small molecule which is detectable by a
10 fluorescent probe.

The following assay uses Fluorometric Imaging Plate Reader ("FLIPR") to measure changes in fluorescent molecules (Molecular Probes) that bind small molecules. Clearly, any fluorescent molecule detecting a small molecule can be used instead of the calcium fluorescent molecule, fluo-3, used here.

15 For adherent cells, seed the cells at 10,000 -20,000 cells/well in a Co-star black 96-well plate with clear bottom. The plate is incubated in a CO₂ incubator for 20 hours. The adherent cells are washed two times in Biotek washer with 200 ul of HBSS (Hank's Balanced Salt Solution) leaving 100 ul of buffer after the final wash.

A stock solution of 1 mg/ml fluo-3 is made in 10% pluronic acid DMSO. To load the cells with fluo-3, 50 ul of 12 ug/ml fluo-3 is added to each well. The plate is incubated at 37°C in a CO₂ incubator for 60 min. The plate is washed four times in the Biotek washer with HBSS leaving 100 ul of buffer.

5 For non-adherent cells, the cells are spun down from culture media. Cells are re-suspended to 2.5×10^6 cells/ml with HBSS in a 50-ml conical tube. 4 ul of 1 mg/ml fluo-3 solution in 10% pluronic acid DMSO is added to each ml of cell suspension. The tube is then placed in a 37°C water bath for 30-60 min. The cells are washed twice with HBSS, resuspended to 1×10^6 cells/ml, and dispensed into a microplate, 100
10 ul/well. The plate is centrifuged at 1000 rpm for 5 min. The plate is then washed once in Denley CellWash with 200 ul, followed by an aspiration step to 100 ul final volume.

For a non-cell based assay, each well contains a fluorescent molecule, such as fluo-3. The supernatant is added to the well, and a change in fluorescence is detected.

To measure the fluorescence of intracellular calcium, the FLIPR is set for the
15 following parameters: (1) System gain is 300-800 mW; (2) Exposure time is 0.4 second; (3) Camera F/stop is F/2; (4) Excitation is 488 nm; (5) Emission is 530 nm; and (6) Sample addition is 50 ul. Increased emission at 530-nm indicates an extracellular signaling event which has resulted in an increase in the intracellular Ca⁺⁺ concentration.

20

Example 19: High-Throughput Screening Assay Identifying Tyrosine Kinase Activity

The Protein Tyrosine Kinases (PTK) represent a diverse group of transmembrane and cytoplasmic kinases. Within the Receptor Protein Tyrosine Kinase
25 RPTK) group are receptors for a range of mitogenic and metabolic growth factors including the PDGF, FGF, EGF, NGF, HGF and Insulin receptor subfamilies. In addition there are a large family of RPTKs for which the corresponding ligand is unknown. Ligands for RPTKs include mainly secreted small proteins, but also membrane-bound and extracellular matrix proteins.

30 Activation of RPTK by ligands involves ligand-mediated receptor dimerization, resulting in transphosphorylation of the receptor subunits and activation of the cytoplasmic tyrosine kinases. The cytoplasmic tyrosine kinases include receptor associated tyrosine kinases of the src-family (e.g., src, yes, lck, lyn, fyn) and non-receptor linked and cytosolic protein tyrosine kinases, such as the Jak family, members
35 of which mediate signal transduction triggered by the cytokine superfamily of receptors (e.g., the Interleukins, Interferons, GM-CSF, and Leptin).

Because of the wide range of known factors capable of stimulating tyrosine kinase activity, the identification of novel human secreted proteins capable of activating tyrosine kinase signal transduction pathways are of interest. Therefore, the following protocol is designed to identify those novel human secreted proteins capable of activating the tyrosine kinase signal transduction pathways.

Seed target cells (e.g., primary keratinocytes) at a density of approximately 25,000 cells per well in a 96 well Loprodyne Silent Screen Plates purchased from Nalge Nunc (Naperville, IL). The plates are sterilized with two 30 minute rinses with 100% ethanol, rinsed with water and dried overnight. Some plates are coated for 2 hr with 100 ml of cell culture grade type I collagen (50 mg/ml), gelatin (2%) or polylysine (50 mg/ml), all of which can be purchased from Sigma Chemicals (St. Louis, MO) or 10% Matrigel purchased from Becton Dickinson (Bedford, MA), or calf serum, rinsed with PBS and stored at 4°C. Cell growth on these plates is assayed by seeding 5,000 cells/well in growth medium and indirect quantitation of cell number through use of alamarBlue as described by the manufacturer Alamar Biosciences, Inc. (Sacramento, CA) after 48 hr. Falcon plate covers #3071 from Becton Dickinson (Bedford, MA) are used to cover the Loprodyne Silent Screen Plates. Falcon Microtest III cell culture plates can also be used in some proliferation experiments.

To prepare extracts, A431 cells are seeded onto the nylon membranes of Loprodyne plates (20,000/200ml/well) and cultured overnight in complete medium. Cells are quiesced by incubation in serum-free basal medium for 24 hr. After 5-20 minutes treatment with EGF (60ng/ml) or 50 ul of the supernatant produced in Example 11, the medium was removed and 100 ml of extraction buffer ((20 mM HEPES pH 7.5, 0.15 M NaCl, 1% Triton X-100, 0.1% SDS, 2 mM Na₃VO₄, 2 mM Na₄P₂O₇ and a cocktail of protease inhibitors (# 1836170) obtained from Boehringer Mannheim (Indianapolis, IN) is added to each well and the plate is shaken on a rotating shaker for 5 minutes at 4°C. The plate is then placed in a vacuum transfer manifold and the extract filtered through the 0.45 mm membrane bottoms of each well using house vacuum. Extracts are collected in a 96-well catch/assay plate in the bottom of the vacuum manifold and immediately placed on ice. To obtain extracts clarified by centrifugation, the content of each well, after detergent solubilization for 5 minutes, is removed and centrifuged for 15 minutes at 4°C at 16,000 x g.

Test the filtered extracts for levels of tyrosine kinase activity. Although many methods of detecting tyrosine kinase activity are known, one method is described here.

Generally, the tyrosine kinase activity of a supernatant is evaluated by determining its ability to phosphorylate a tyrosine residue on a specific substrate (a

biotinylated peptide). Biotinylated peptides that can be used for this purpose include PSK1 (corresponding to amino acids 6-20 of the cell division kinase cdc2-p34) and PSK2 (corresponding to amino acids 1-17 of gastrin). Both peptides are substrates for a range of tyrosine kinases and are available from Boehringer Mannheim.

- 5 The tyrosine kinase reaction is set up by adding the following components in order. First, add 10ul of 5uM Biotinylated Peptide, then 10ul ATP/Mg₂₊ (5mM ATP/50mM MgCl₂), then 10ul of 5x Assay Buffer (40mM imidazole hydrochloride, pH7.3, 40 mM beta-glycerophosphate, 1mM EGTA, 100mM MgCl₂, 5 mM MnCl₂, 0.5 mg/ml BSA), then 5ul of Sodium Vanadate(1mM), and then 5ul of water. Mix the
- 10 components gently and preincubate the reaction mix at 30°C for 2 min. Initiate the reaction by adding 10ul of the control enzyme or the filtered supernatant.

The tyrosine kinase assay reaction is then terminated by adding 10 ul of 120mM EDTA and place the reactions on ice.

- Tyrosine kinase activity is determined by transferring 50 ul aliquot of reaction
- 15 mixture to a microtiter plate (MTP) module and incubating at 37°C for 20 min. This allows the streptavidin coated 96 well plate to associate with the biotinylated peptide. Wash the MTP module with 300ul/well of PBS four times. Next add 75 ul of anti-phosphotyrosine antibody conjugated to horse radish peroxidase(anti-P-Tyr-POD(0.5u/ml)) to each well and incubate at 37°C for one hour. Wash the well as
- 20 above.

- Next add 100ul of peroxidase substrate solution (Boehringer Mannheim) and incubate at room temperature for at least 5 mins (up to 30 min). Measure the absorbance of the sample at 405 nm by using ELISA reader. The level of bound peroxidase activity is quantitated using an ELISA reader and reflects the level of
- 25 tyrosine kinase activity.

Example 20: High-Throughput Screening Assay Identifying Phosphorylation Activity

- As a potential alternative and/or complement to the assay of protein tyrosine
- 30 kinase activity described in Example 19, an assay which detects activation (phosphorylation) of major intracellular signal transduction intermediates can also be used. For example, as described below one particular assay can detect tyrosine phosphorylation of the Erk-1 and Erk-2 kinases. However, phosphorylation of other molecules, such as Raf, JNK, p38 MAP, Map kinase kinase (MEK), MEK kinase,
- 35 Src, Muscle specific kinase (MuSK), IRAK, Tec, and Janus, as well as any other

phosphoserine, phosphotyrosine, or phosphothreonine molecule, can be detected by substituting these molecules for Erk-1 or Erk-2 in the following assay.

Specifically, assay plates are made by coating the wells of a 96-well ELISA plate with 0.1ml of protein G (1ug/ml) for 2 hr at room temp, (RT). The plates are then
5 rinsed with PBS and blocked with 3% BSA/PBS for 1 hr at RT. The protein G plates are then treated with 2 commercial monoclonal antibodies (100ng/well) against Erk-1 and Erk-2 (1 hr at RT) (Santa Cruz Biotechnology). (To detect other molecules, this step can easily be modified by substituting a monoclonal antibody detecting any of the above described molecules.) After 3-5 rinses with PBS, the plates are stored at 4°C
10 until use.

A431 cells are seeded at 20,000/well in a 96-well Loprodyne filterplate and cultured overnight in growth medium. The cells are then starved for 48 hr in basal medium (DMEM) and then treated with EGF (6ng/well) or 50 ul of the supernatants obtained in Example 11 for 5-20 minutes. The cells are then solubilized and extracts
15 filtered directly into the assay plate.

After incubation with the extract for 1 hr at RT, the wells are again rinsed. As a positive control, a commercial preparation of MAP kinase (10ng/well) is used in place of A431 extract. Plates are then treated with a commercial polyclonal (rabbit) antibody (1ug/ml) which specifically recognizes the phosphorylated epitope of the Erk-1 and
20 Erk-2 kinases (1 hr at RT). This antibody is biotinylated by standard procedures. The bound polyclonal antibody is then quantitated by successive incubations with Europium-streptavidin and Europium fluorescence enhancing reagent in the Wallac DELFIA instrument (time-resolved fluorescence). An increased fluorescent signal over background indicates a phosphorylation.

25

Example 21: Method of Determining Alterations in a Gene Corresponding to a Polynucleotide

RNA isolated from entire families or individual patients presenting with a phenotype of interest (such as a disease) is be isolated. cDNA is then generated from
30 these RNA samples using protocols known in the art. (See, Sambrook.) The cDNA is then used as a template for PCR, employing primers surrounding regions of interest in SEQ ID NO:X. Suggested PCR conditions consist of 35 cycles at 95°C for 30 seconds; 60-120 seconds at 52-58°C; and 60-120 seconds at 70°C, using buffer solutions described in Sidransky, D., et al., Science 252:706 (1991).

35 PCR products are then sequenced using primers labeled at their 5' end with T4 polynucleotide kinase, employing SequiTherm Polymerase. (Epicentre Technologies).

The intron-exon borders of selected exons is also determined and genomic PCR products analyzed to confirm the results. PCR products harboring suspected mutations is then cloned and sequenced to validate the results of the direct sequencing.

5 PCR products is cloned into T-tailed vectors as described in Holton, T.A. and Graham, M.W., Nucleic Acids Research, 19:1156 (1991) and sequenced with T7 polymerase (United States Biochemical). Affected individuals are identified by mutations not present in unaffected individuals.

10 Genomic rearrangements are also observed as a method of determining alterations in a gene corresponding to a polynucleotide. Genomic clones isolated according to Example 2 are nick-translated with digoxigenindeoxy-uridine 5'-triphosphate (Boehringer Mannheim), and FISH performed as described in Johnson, Cg. et al., Methods Cell Biol. 35:73-99 (1991). Hybridization with the labeled probe is carried out using a vast excess of human cot-1 DNA for specific hybridization to the corresponding genomic locus.

15 Chromosomes are counterstained with 4,6-diamino-2-phenylidole and propidium iodide, producing a combination of C- and R-bands. Aligned images for precise mapping are obtained using a triple-band filter set (Chroma Technology, Brattleboro, VT) in combination with a cooled charge-coupled device camera (Photometrics, Tucson, AZ) and variable excitation wavelength filters. (Johnson, Cv. et al., Genet. Anal. Tech. Appl., 8:75 (1991).) Image collection, analysis and chromosomal fractional length measurements are performed using the ISee Graphical Program System. (Inovision Corporation, Durham, NC.) Chromosome alterations of the genomic region hybridized by the probe are identified as insertions, deletions, and translocations. These alterations are used as a diagnostic marker for an associated
25 disease.

Example 22: Method of Detecting Abnormal Levels of a Polypeptide in a Biological Sample

30 A polypeptide of the present invention can be detected in a biological sample, and if an increased or decreased level of the polypeptide is detected, this polypeptide is a marker for a particular phenotype. Methods of detection are numerous, and thus, it is understood that one skilled in the art can modify the following assay to fit their particular needs.

35 For example, antibody-sandwich ELISAs are used to detect polypeptides in a sample, preferably a biological sample. Wells of a microtiter plate are coated with specific antibodies, at a final concentration of 0.2 to 10 ug/ml. The antibodies are either monoclonal or polyclonal and are produced by the method described in Example 10.

The wells are blocked so that non-specific binding of the polypeptide to the well is reduced.

The coated wells are then incubated for > 2 hours at RT with a sample containing the polypeptide. Preferably, serial dilutions of the sample should be used to validate results. The plates are then washed three times with deionized or distilled water to remove unbounded polypeptide.

Next, 50 ul of specific antibody-alkaline phosphatase conjugate, at a concentration of 25-400 ng, is added and incubated for 2 hours at room temperature. The plates are again washed three times with deionized or distilled water to remove unbounded conjugate.

Add 75 ul of 4-methylumbelliferyl phosphate (MUP) or p-nitrophenyl phosphate (NPP) substrate solution to each well and incubate 1 hour at room temperature. Measure the reaction by a microtiter plate reader. Prepare a standard curve, using serial dilutions of a control sample, and plot polypeptide concentration on the X-axis (log scale) and fluorescence or absorbance of the Y-axis (linear scale). Interpolate the concentration of the polypeptide in the sample using the standard curve.

Example 23: Formulating a Polypeptide

The secreted polypeptide composition will be formulated and dosed in a fashion consistent with good medical practice, taking into account the clinical condition of the individual patient (especially the side effects of treatment with the secreted polypeptide alone), the site of delivery, the method of administration, the scheduling of administration, and other factors known to practitioners. The "effective amount" for purposes herein is thus determined by such considerations.

As a general proposition, the total pharmaceutically effective amount of secreted polypeptide administered parenterally per dose will be in the range of about 1 $\mu\text{g/kg/day}$ to 10 mg/kg/day of patient body weight, although, as noted above, this will be subject to therapeutic discretion. More preferably, this dose is at least 0.01 mg/kg/day , and most preferably for humans between about 0.01 and 1 mg/kg/day for the hormone. If given continuously, the secreted polypeptide is typically administered at a dose rate of about 1 $\mu\text{g/kg/hour}$ to about 50 $\mu\text{g/kg/hour}$, either by 1-4 injections per day or by continuous subcutaneous infusions, for example, using a mini-pump. An intravenous bag solution may also be employed. The length of treatment needed to observe changes and the interval following treatment for responses to occur appears to vary depending on the desired effect.

Pharmaceutical compositions containing the secreted protein of the invention are administered orally, rectally, parenterally, intracisternally, intravaginally,

intraperitoneally, topically (as by powders, ointments, gels, drops or transdermal patch), buccally, or as an oral or nasal spray. "Pharmaceutically acceptable carrier" refers to a non-toxic solid, semisolid or liquid filler, diluent, encapsulating material or formulation auxiliary of any type. The term "parenteral" as used herein refers to modes of administration which include intravenous, intramuscular, intraperitoneal, intrasternal, subcutaneous and intraarticular injection and infusion.

The secreted polypeptide is also suitably administered by sustained-release systems. Suitable examples of sustained-release compositions include semi-permeable polymer matrices in the form of shaped articles, e.g., films, or microcapsules.

Sustained-release matrices include polylactides (U.S. Pat. No. 3,773,919, EP 58,481), copolymers of L-glutamic acid and gamma-ethyl-L-glutamate (Sidman, U. et al., *Biopolymers* 22:547-556 (1983)), poly (2- hydroxyethyl methacrylate) (R. Langer et al., *J. Biomed. Mater. Res.* 15:167-277 (1981), and R. Langer, *Chem. Tech.* 12:98-105 (1982)), ethylene vinyl acetate (R. Langer et al.) or poly-D- (-)-3-hydroxybutyric acid (EP 133,988). Sustained-release compositions also include liposomally entrapped polypeptides. Liposomes containing the secreted polypeptide are prepared by methods known per se: DE 3,218,121; Epstein et al., *Proc. Natl. Acad. Sci. USA* 82:3688-3692 (1985); Hwang et al., *Proc. Natl. Acad. Sci. USA* 77:4030-4034 (1980); EP 52,322; EP 36,676; EP 88,046; EP 143,949; EP 142,641; Japanese Pat. Appl. 83-118008; U.S. Pat. Nos. 4,485,045 and 4,544,545; and EP 102,324. Ordinarily, the liposomes are of the small (about 200-800 Angstroms) unilamellar type in which the lipid content is greater than about 30 mol. percent cholesterol, the selected proportion being adjusted for the optimal secreted polypeptide therapy.

For parenteral administration, in one embodiment, the secreted polypeptide is formulated generally by mixing it at the desired degree of purity, in a unit dosage injectable form (solution, suspension, or emulsion), with a pharmaceutically acceptable carrier, i.e., one that is non-toxic to recipients at the dosages and concentrations employed and is compatible with other ingredients of the formulation. For example, the formulation preferably does not include oxidizing agents and other compounds that are known to be deleterious to polypeptides.

Generally, the formulations are prepared by contacting the polypeptide uniformly and intimately with liquid carriers or finely divided solid carriers or both. Then, if necessary, the product is shaped into the desired formulation. Preferably the carrier is a parenteral carrier, more preferably a solution that is isotonic with the blood of the recipient. Examples of such carrier vehicles include water, saline, Ringer's solution, and dextrose solution. Non-aqueous vehicles such as fixed oils and ethyl oleate are also useful herein, as well as liposomes.

The carrier suitably contains minor amounts of additives such as substances that enhance isotonicity and chemical stability. Such materials are non-toxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, succinate, acetic acid, and other organic acids or their salts; antioxidants such as ascorbic acid; low molecular weight (less than about ten residues) polypeptides, e.g., polyarginine or tripeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids, such as glycine, glutamic acid, aspartic acid, or arginine; monosaccharides, disaccharides, and other carbohydrates including cellulose or its derivatives, glucose, manose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; counterions such as sodium; and/or nonionic surfactants such as polysorbates, poloxamers, or PEG.

The secreted polypeptide is typically formulated in such vehicles at a concentration of about 0.1 mg/ml to 100 mg/ml, preferably 1-10 mg/ml, at a pH of about 3 to 8. It will be understood that the use of certain of the foregoing excipients, carriers, or stabilizers will result in the formation of polypeptide salts.

Any polypeptide to be used for therapeutic administration can be sterile. Sterility is readily accomplished by filtration through sterile filtration membranes (e.g., 0.2 micron membranes). Therapeutic polypeptide compositions generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

Polypeptides ordinarily will be stored in unit or multi-dose containers, for example, sealed ampoules or vials, as an aqueous solution or as a lyophilized formulation for reconstitution. As an example of a lyophilized formulation, 10-ml vials are filled with 5 ml of sterile-filtered 1% (w/v) aqueous polypeptide solution, and the resulting mixture is lyophilized. The infusion solution is prepared by reconstituting the lyophilized polypeptide using bacteriostatic Water-for-Injection.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration. In addition, the polypeptides of the present invention may be employed in conjunction with other therapeutic compounds.

Example 24: Method of Treating Decreased Levels of the Polypeptide

It will be appreciated that conditions caused by a decrease in the standard or normal expression level of a secreted protein in an individual can be treated by administering the polypeptide of the present invention, preferably in the secreted form.

- 5 Thus, the invention also provides a method of treatment of an individual in need of an increased level of the polypeptide comprising administering to such an individual a pharmaceutical composition comprising an amount of the polypeptide to increase the activity level of the polypeptide in such an individual.

- 10 For example, a patient with decreased levels of a polypeptide receives a daily dose 0.1-100 ug/kg of the polypeptide for six consecutive days. Preferably, the polypeptide is in the secreted form. The exact details of the dosing scheme, based on administration and formulation, are provided in Example 23.

Example 25: Method of Treating Increased Levels of the Polypeptide

- 15 Antisense technology is used to inhibit production of a polypeptide of the present invention. This technology is one example of a method of decreasing levels of a polypeptide, preferably a secreted form, due to a variety of etiologies, such as cancer.

- For example, a patient diagnosed with abnormally increased levels of a polypeptide is administered intravenously antisense polynucleotides at 0.5, 1.0, 1.5, 20 2.0 and 3.0 mg/kg day for 21 days. This treatment is repeated after a 7-day rest period if the treatment was well tolerated. The formulation of the antisense polynucleotide is provided in Example 23.

Example 26: Method of Treatment Using Gene Therapy

- 25 One method of gene therapy transplants fibroblasts, which are capable of expressing a polypeptide, onto a patient. Generally, fibroblasts are obtained from a subject by skin biopsy. The resulting tissue is placed in tissue-culture medium and separated into small pieces. Small chunks of the tissue are placed on a wet surface of a tissue culture flask, approximately ten pieces are placed in each flask. The flask is 30 turned upside down, closed tight and left at room temperature over night. After 24 hours at room temperature, the flask is inverted and the chunks of tissue remain fixed to the bottom of the flask and fresh media (e.g., Ham's F12 media, with 10% FBS, penicillin and streptomycin) is added. The flasks are then incubated at 37°C for approximately one week.

At this time, fresh media is added and subsequently changed every several days. After an additional two weeks in culture, a monolayer of fibroblasts emerge. The monolayer is trypsinized and scaled into larger flasks.

5 pMV-7 (Kirschmeier, P.T. et al., DNA, 7:219-25 (1988)), flanked by the long terminal repeats of the Moloney murine sarcoma virus, is digested with EcoRI and HindIII and subsequently treated with calf intestinal phosphatase. The linear vector is fractionated on agarose gel and purified, using glass beads.

10 The cDNA encoding a polypeptide of the present invention can be amplified using PCR primers which correspond to the 5' and 3' end sequences respectively as set forth in Example 1. Preferably, the 5' primer contains an EcoRI site and the 3' primer includes a HindIII site. Equal quantities of the Moloney murine sarcoma virus linear backbone and the amplified EcoRI and HindIII fragment are added together, in the presence of T4 DNA ligase. The resulting mixture is maintained under conditions appropriate for ligation of the two fragments. The ligation mixture is then used to
15 transform bacteria HB101, which are then plated onto agar containing kanamycin for the purpose of confirming that the vector has the gene of interest properly inserted.

The amphotropic pA317 or GP+am12 packaging cells are grown in tissue culture to confluent density in Dulbecco's Modified Eagles Medium (DMEM) with 10% calf serum (CS), penicillin and streptomycin. The MSV vector containing the gene is
20 then added to the media and the packaging cells transduced with the vector. The packaging cells now produce infectious viral particles containing the gene (the packaging cells are now referred to as producer cells).

Fresh media is added to the transduced producer cells, and subsequently, the media is harvested from a 10 cm plate of confluent producer cells. The spent media,
25 containing the infectious viral particles, is filtered through a millipore filter to remove detached producer cells and this media is then used to infect fibroblast cells. Media is removed from a sub-confluent plate of fibroblasts and quickly replaced with the media from the producer cells. This media is removed and replaced with fresh media. If the titer of virus is high, then virtually all fibroblasts will be infected and no selection is
30 required. If the titer is very low, then it is necessary to use a retroviral vector that has a selectable marker, such as neo or his. Once the fibroblasts have been efficiently infected, the fibroblasts are analyzed to determine whether protein is produced.

The engineered fibroblasts are then transplanted onto the host, either alone or after having been grown to confluence on cytodex 3 microcarrier beads.

Example 27: Method of Treatment Using Gene Therapy - In Vivo

Another aspect of the present invention is using *in vivo* gene therapy methods to treat disorders, diseases and conditions. The gene therapy method relates to the introduction of naked nucleic acid (DNA, RNA, and antisense
5 DNA or RNA) sequences into an animal to increase or decrease the expression of the polypeptide of the present invention. A polynucleotide of the present invention may be operatively linked to a promoter or any other genetic elements necessary for the expression of the encoded polypeptide by the target tissue. Such gene therapy and delivery techniques and methods are known in the art,
10 see, for example, WO90/11092, WO98/11779; U.S. Patent NO. 5693622, 5705151, 5580859; Tabata H. et al. (1997) Cardiovasc. Res. 35(3):470-479, Chao J et al. (1997) Pharmacol. Res. 35(6):517-522, Wolff J.A. (1997) Neuromuscul. Disord. 7(5):314-318, Schwartz B. et al. (1996) Gene Ther. 3(5):405-411, Tsurumi Y. et al. (1996) Circulation 94(12):3281-3290
15 (incorporated herein by reference).

The polynucleotide constructs of the present invention may be delivered by any method that delivers injectable materials to the cells of an animal, such as, injection into the interstitial space of tissues (heart, muscle, skin, lung, liver, intestine and the like). These polynucleotide constructs can be delivered in a
20 pharmaceutically acceptable liquid or aqueous carrier.

The term "naked" polynucleotide, DNA or RNA, refers to sequences that are free from any delivery vehicle that acts to assist, promote, or facilitate entry into the cell, including viral sequences, viral particles, liposome formulations, lipofectin or precipitating agents and the like. However, the
25 polynucleotides may also be delivered in liposome formulations (such as those taught in Felgner P.L. et al. (1995) Ann. NY Acad. Sci. 772:126-139 and Abdallah B. et al. (1995) Biol. Cell 85(1):1-7) which can be prepared by methods well known to those skilled in the art.

The polynucleotide vector constructs of the present invention used in
30 the gene therapy method are preferably constructs that will not integrate into the host genome nor will they contain sequences that allow for replication. Any strong promoter known to those skilled in the art can be used for driving the expression of DNA. Unlike other gene therapies techniques, one major advantage of introducing naked nucleic acid sequences into target cells is the
35 transitory nature of the polynucleotide synthesis in the cells. Studies have shown that non-replicating DNA sequences can be introduced into cells to provide production of the desired polypeptide for periods of up to six months.

The polynucleotide construct of the present invention can be delivered to the interstitial space of tissues within the an animal, including of muscle, skin, brain, lung, liver, spleen, bone marrow, thymus, heart, lymph, blood, bone, cartilage, pancreas, kidney, gall bladder, stomach, intestine, testis, ovary, uterus, rectum, nervous system, eye, gland, and connective tissue. Interstitial space of the tissues comprises the intercellular fluid, mucopolysaccharide matrix among the reticular fibers of organ tissues, elastic fibers in the walls of vessels or chambers, collagen fibers of fibrous tissues, or that same matrix within connective tissue ensheathing muscle cells or in the lacunae of bone. It is similarly the space occupied by the plasma of the circulation and the lymph fluid of the lymphatic channels. Delivery to the interstitial space of muscle tissue is preferred for the reasons discussed below. They may be conveniently delivered by injection into the tissues comprising these cells. They are preferably delivered to and expressed in persistent, non-dividing cells which are differentiated, although delivery and expression may be achieved in non-differentiated or less completely differentiated cells, such as, for example, stem cells of blood or skin fibroblasts. *In vivo* muscle cells are particularly competent in their ability to take up and express polynucleotides.

For the naked polynucleotide injection, an effective dosage amount of DNA or RNA will be in the range of from about 0.05 g/kg body weight to about 50 mg/kg body weight. Preferably the dosage will be from about 0.005 mg/kg to about 20 mg/kg and more preferably from about 0.05 mg/kg to about 5 mg/kg. Of course, as the artisan of ordinary skill will appreciate, this dosage will vary according to the tissue site of injection. The appropriate and effective dosage of nucleic acid sequence can readily be determined by those of ordinary skill in the art and may depend on the condition being treated and the route of administration. The preferred route of administration is by the parenteral route of injection into the interstitial space of tissues. However, other parenteral routes may also be used, such as, inhalation of an aerosol formulation particularly for delivery to lungs or bronchial tissues, throat or mucous membranes of the nose. In addition, naked polynucleotide constructs can be delivered to arteries during angioplasty by the catheter used in the procedure.

The dose response effects of injected polynucleotide in muscle *in vivo* is determined as follows. Suitable template DNA for production of mRNA coding for the polypeptide of the present invention is prepared in accordance with a standard recombinant DNA methodology. The template DNA, which may be either circular or linear, is either used as naked DNA or complexed with

liposomes. The quadriceps muscles of mice are then injected with various amounts of the template DNA.

Five to six week old female and male Balb/C mice are anesthetized by intraperitoneal injection with 0.3 ml of 2.5% Avertin. A 1.5 cm incision is made on the anterior thigh, and the quadriceps muscle is directly visualized. The template DNA is injected in 0.1 ml of carrier in a 1 cc syringe through a 27 gauge needle over one minute, approximately 0.5 cm from the distal insertion site of the muscle into the knee and about 0.2 cm deep. A suture is placed over the injection site for future localization, and the skin is closed with stainless steel clips.

After an appropriate incubation time (e.g., 7 days) muscle extracts are prepared by excising the entire quadriceps. Every fifth 15 um cross-section of the individual quadriceps muscles is histochemically stained for protein expression. A time course for protein expression may be done in a similar fashion except that quadriceps from different mice are harvested at different times. Persistence of DNA in muscle following injection may be determined by Southern blot analysis after preparing total cellular DNA and HIRT supernatants from injected and control mice. The results of the above experimentation in mice can be use to extrapolate proper dosages and other treatment parameters in humans and other animals using naked DNA of the present invention.

It will be clear that the invention may be practiced otherwise than as particularly described in the foregoing description and examples. Numerous modifications and variations of the present invention are possible in light of the above teachings and, therefore, are within the scope of the appended claims.

The entire disclosure of each document cited (including patents, patent applications, journal articles, abstracts, laboratory manuals, books, or other disclosures) in the Background of the Invention, Detailed Description, and Examples is hereby incorporated herein by reference.

Sequence Listing

(1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Human Genome Sciences, Inc., et al.
- (ii) TITLE OF INVENTION: 207 Human Secreted Proteins
- 10 (iii) NUMBER OF SEQUENCES: 800
- (iv) CORRESPONDENCE ADDRESS:
- 15 (A) ADDRESSEE: Human Genome Sciences, Inc.
- (B) STREET: 9410 Key West Avenue
- 20 (C) CITY: Rockville
- (D) STATE: Maryland
- (E) COUNTRY: USA
- 25 (F) ZIP: 20850
- (v) COMPUTER READABLE FORM:
- 30 (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
- (B) COMPUTER: HP Vectra 486/33
- 35 (C) OPERATING SYSTEM: MSDOS version 6.2
- (D) SOFTWARE: ASCII Text
- 40 (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER:
- 45 (B) FILING DATE:
- (C) CLASSIFICATION:
- 50 (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER:
- 55 (B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Kenley K. Hoover

(B) REGISTRATION NUMBER: 40,302

(C) REFERENCE/DOCKET NUMBER: PZ007PCT

(vi) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (301) 309-8504

(B) TELEFAX: (301) 309-8439

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 733 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGGATCCGGA GCCCAAATCT TCTGACAAAA CTCACACATG CCCACCGTGC CCAGCACCTG	60
AATTCGAGGG TGCACCGTCA GTCTTCCTCT TCCCCCAAA ACCCAAGGAC ACCCTCATGA	120
TCTCCCGGAC TCCTGAGGTC ACATGCGTGG TGGTGGACGT AAGCCACGAA GACCCTGAGG	180
TCAAGTTCAA CTGGTACGTG GACGGCGTGG AGGTGCATAA TGCCAAGACA AAGCCGCGGG	240
AGGAGCAGTA CAACAGCACG TACCGTGTGG TCAGCGTCCT CACCGTCCTG CACCAGGACT	300
GGCTGAATGG CAAGGAGTAC AAGTGCAAGG TCTCCAACAA AGCCCTCCCA ACCCCCATCG	360
AGAAAACCAT CTCCAAAGCC AAAGGGCAGC CCCGAGAACC ACAGGTGTAC ACCCTGCCCC	420
CATCCCGGGA TGAGCTGACC AAGAACCAGG TCAGCCTGAC CTGCCTGGTC AAAGGCTTCT	480
ATCCAAGCGA CATCGCCGTG GAGTGGGAGA GCAATGGGCA GCCGGAGAAC AACTACAAGA	540
CCACGCCTCC CGTGCTGGAC TCCGACGGCT CCTTCTTCCT CTACAGCAAG CTCACCGTGG	600
ACAAGAGCAG GTGGCAGCAG GGAACGTCT TCTCATGCTC CGTGATGCAT GAGGCTCTGC	660
ACAACCACTA CACGCAGAAG AGCCTCTCCC TGTCTCCGGG TAAATGAGTG CGACGGCCGC	720
GA CTCTAGAG GAT	733

(2) INFORMATION FOR SEQ ID NO: 2:

267

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
Trp Ser Xaa Trp Ser
1 5

- 15 (2) INFORMATION FOR SEQ ID NO: 3:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 86 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
25 GCGCCTCGAG ATTTCCCCGA AATCTAGATT TCCCCGAAAT GATTCCCCG AAATGATTTC 60
CCCGAAATAT CTGCCATCTC AATTAG 86

30

- (2) INFORMATION FOR SEQ ID NO: 4:

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
GCGGCAAGCT TTTTGCAAAG CCTAGGC 27

45

- (2) INFORMATION FOR SEQ ID NO: 5:

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 271 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
CTCGAGATTT CCCCAGAAATC TAGATTTCCT CGAAATGATT TCCCCGAAAT GATTCCCCG 60
AAATATCTGC CATCTCAATT AGTCAGCAAC CATAGTCCCG CCCCTAACTC CGCCCATCCC 120

60

268

GCCCCTAACT CCGCCCAGTT CCGCCCATTC TCGCCCCAT GGCTGACTAA TTTTTTAT 180
TTATGCAGAG GCCGAGGCCG CCTCGGCCTC TGAGCTATTC CAGAAGTAGT GAGGAGGCTT 240
5 TTTTGGAGGC CTAGGCTTTT GCAAAAAGCT T 271

10 (2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

20 GCGCTCGAGG GATGACAGCG ATAGAACCCC GG 32

25 (2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

35 GCGAAGCTTC GCGACTCCCC GGATCCGCCT C 31

40

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
45 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

50 GGGGACTTTC CC 12

55

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
60 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

5 GCGGCCTCGA GGGGACTTTC CCGGGGACTT TCCGGGGACT TTCCGGGACT TTCCATCCTG 60
CCATCTCAAT TAG 73

10

(2) INFORMATION FOR SEQ ID NO: 10:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 256 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CTCGAGGGGA CTTTCCCGG GACTTTCGG GGACTTTCG GGACTTTCCA TCTGCCATCT 60
25 CAATTAGTCA GCAACCATAG TCCCGCCCCT AACTCCGCCC ATCCCGCCCC TAACTCCGCC 120
CAGTTCGCC CATTCTCCGC CCCATGGCTG ACTAATTTT TTTATTTATG CAGAGGCCGA 180
GGCCGCCTCG GCCTCTGAGC TATTCAGAA GTAGTGAGGA GGCTTTTTTG GAGGCCTAGG 240
30 CTTTTCGAAA AAGCTT 256

35

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2526 base pairs
40 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

45 GACAGGCTAT CCGAGAATCT GAGAGCTGGG CCCGGCAATT CCTCCAGYTA CCCTGTGAC 60
CTAAGTCCAG TCACACATTT CCCAAAGTTT CTCTTGTCA TAACCCTGGT CTGGCTGGTT 120
50 TTGRGGRCTT GAGAATGGT CAGGGACTCC AGGCCAAGTC CAACAGAGAC CCCAAACCCA 180
CCACACACCA GCAGCCACAA CCTCACCACC AACAAAGAGG ACTTTTGTGG GGCCACAAGT 240
AAGAGGTCAT TTCTGGAATG GACTCAGACC TTAAACAGG AGAGTTGAGC ACTTCCAGKS 300
55 AGTTTAAAG CAAGGCATGG GGAACAGGA ATAGAACCTT TCAAAGAGGT TGCCCAGAGA 360
AAAGCTGGGC CTCTTGCAAT CGGCTTCCTT GGAGCAGCCT CTCTGGCAG AAAGCCATCA 420
60 GGTGCTCAAT CATCTTCTCC TGGCCAAGGC TCTGACCATG CTTAGTACTG GAATAGAGGT 480

	GGCCAGGCCC CCAGCGACTC TTCTTGGCCT GATGTTTGTC CTCACAGGCA TGCCACGTGG	540
	CCTGAGATGA TTCAGAACAA ATCATGCTAA CTTTGAATCC ATCCAGCCAC TTGCAAATGA	600
5	TAATCAGAAG TCAGCTTGTT CACTGTTAGA AAGAACTAA CAAAAGAGAA CCCAGAGCAA	660
	TCTAGAATCT TTGAGTGCTT GGCTTTCCAA GGATACTGCG GAGACTCTGG CCAAGCTGAT	720
10	GAMCTTCTGA ARTGTCACTG GCACCATATG CAACAAGAAC CACCATTAC TGAGTAGCTA	780
	ATGGGTTTGG GGCCTGGGAC ATTCCATCTG AGGTCCTTCC TGAACATGTC ACTCCACAGC	840
	AGAGGACCGG TTGCAGCTTA CCCAGAACCA CTCCTCCAGG AGAGCTGGAT GTTTTGCGTG	900
15	CAACACCTTG AGCACTGACT GCTATTGTTT AAAAAAGCC TTTGCTGCAT TCGGAGGACT	960
	GCCCCGTGCC CTGAGGTGAC TTCTAACTA TGTGGTTTCA TTAGCGAATT TATTTTGT	1020
20	GCTGGGTGGA CATTTGTATT TTGTTAGGTT GCTGTTTAA CTCAAGTTG CTGTGCTCTC	1080
	TGCAGCTACA AAACATCTTG GCATATTTAA GAKTGGCTTT TATAAATAGC TTTATCTGA	1140
	TATTAATCAG ATTCCCAACT TTAGTGAGAA TTAAGGACTG GGTACTTTA AAGAAATGCA	1200
25	AATAGCAATT GAAGAACCAC TGCTGCAGGT GGTAGCCCTG GCTAGACTGA ATTACACTAG	1260
	AAATCAGCCA GAAGGAAGCG TCCTTGGGAT CCCAGATCAC TCTTTTTTTT TTTTTTTT	1320
30	AAAGGGCAG CCCCTTGATG GCTCATCTCT CTGAATAACA GTTACGTCTT CATATCGATA	1380
	CCAGATGCCT TCTTCATCAT GCCACTGAAG CCACTCACCA CCTTCAAGAA CATGCCAACC	1440
	TCTGTCAGAT TCACTTACCC ACAACAAGG AGGCACGTTT GGCACAAAGT GTTGTCCTCC	1500
35	AGGTCCAAGT GGACTCTACA GAGTGCTTGA CCTCAACACA CTGGATTCCA GGTGGACTGG	1560
	ACCAAGAGCA GGCAAGACA CGGGAAGTGA AAACTCCAC AGGGTTTGA GAATAGAAAT	1620
40	GAAAAGCCAC GTCATATAAC TCAAGAATAA ATGGTGTTTT GGAAATTTT AAATTATCAT	1680
	CGAAGGTGGT GAACTATTT CAGGCCCAA TGAAAGGAAA TCGCCAGTTG GGGATGAAAT	1740
	CACAGAGCCT GTGTTTTATG ATATGGTTGG ATGTCCACTG ATGAAATTTT AAAGGAGTTT	1800
45	CATTTTTAAA AGTGCGCATG ATTCTACATA TGAGAATTCT TTAGCCAAG AACTGTCTCT	1860
	TGGCTCAGAG GTGTTGGGAA TTAAAGCAGA GAGAAGCCAT TCGTGATGCT TAGAACCAAG	1920
50	GATGGTCATG TACACAAAGA CCATCGAGAC GGCCATTCTT GTTTACAAA CACTTACCA	1980
	GAAAGCACTT TGTAGGGGAA CTTTAGTAAG TTCTTCTCAT TTCATTATGT TTCTTCCAAG	2040
	GAAACAGGAG AGACTGAATT AATAATTCTC TCTTCTCTT TAAGCACTTT TAAATAATA	2100
55	AAGTACATCT TGAAATTTGG GGGGCATCT CTGATTTAAA AAAAGAAAAA GGCTGCTTGA	2160
	TGTATGTTAT GCAGAGACAC TCTGCCTCTG GTGGCTGCAG AGCAATACCC AAGCCTCATT	2220
60	TGGAAGGCTC AACATTGGA ATTGCACTTT AATTGATTAA TCCTCAATTC ATGTGGCCTT	2280

ACGGGATGGT GGGTCTGGGA CCCCAATTCA TTCTTATCTG CCAAAGAATT ATCTAGAAGC 2340
ACATCAAATA CCAGCACCCC ACCTGCACAA TGGGGGTGGA AAACCTTTGT ATCCCTAAGC 2400
5 ATATTATTTT ATAGTGCTG CCATGCCATG TGGAAATACT TTATTTTAA CCTCAGGATT 2460
TAAATAAAGT AAACACTATG ACATTTAAAA AAAAAAAAAA AAAACTCGAG GGGGGCCCGG 2520
10 TACCCA 2526

15 (2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1131 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

25 CACTGCACCA GCTTTGTTAT CTGTAAATG ATGATAATAC CAACACCTTC TTCTTGGGGT 60
ACTGAAGATG AGAGAACATG ATATGTGTAA AGTGCCCTCC ACAATACCCA GAACATAGCA 120
AACATGTAAT GAATGTAGTA ATAGTAATTA TTTTATTTTC TTTTGATTCA GTTGGGACTA 180
30 TGTTCAGCTG TAACAGAATA CCCAAAATAA CTGTTTTTAA CAAATTAAAG TTTWGTGTG 240
AAGTTTGTGTT ACGAATTCAG ACAATCCAGG GCTTTTATAG ATGCACCAGG ATCAGCAGGT 300
35 ACAAAGGCAT CTTTCCTGAT TTCTGCCAGT CTCAATGCAT GGGTTGCAAT CCAGARTCCA 360
RGATGGCAGT TCCAGCCCTG GTTACGCCCA TATTAGCACA CAGAAAGAAA GAGAAAGGGA 420
TGTGCCTCTT CACTTTAATC ATAGCTCCCA CTAGATGCAC CCACTACTTC TGCTGATACT 480
40 CCATTAGCTA ATGCTTGCTT ACATGGTCAC ACTTAGTTTC CAGAGAGACA TGTCTGGACA 540
GTCATGTGCT CAATTAATAT CCAAGTGTC AATTACTGAG AAAAAAGAA ACTAGCACCT 600
45 TTGCTTGGTT GCATTCCTCT TAGCATAAGC CACATTCTTT TTATGAAGTT GTCCTCAGTT 660
ACTTGGATGC CTCAGTTGTC CTTTCAWTTA GAAAWGCYCC TKGGACAYCC TGAAWCTGAC 720
TTCTTTTGTC ATCAGCACCA TCACTACCAC TGCCYTCTTC AAAGCCACCA CGTTCTGTCC 780
50 CCAGGATGGT TGCAACAACC ACCATAGGGA CTTTTTGCCT TCTACTTCCA CACAATAGNC 840
CAGAGTAAGC TTTTGAAAAT GTAGGTCAGA TCATGTCTCT CTCTTCCTCT TCAAAACCCT 900
55 CCCGATGGCT TTTCATATTA CTCAAAAGAA AACCTAAAC TTGCTGTGA GATCTATGTG 960
ACCCGGCTTA TTCTTCCTCT TACTTTATCT CTGTATTGCT CTTCTCACT CTACTCCAGC 1020
CATCCACCT CTTGCTGCT TGTCTATAC TCCTAAAAGA AGTTCAGTCT TCCCTTATGA 1080
60

TATTTGCACT TAAATAGAA AAAAAAAAAA AAAAAAACT CGAGGGGGGC C

1131

5

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 941 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

15

GGCAGGAGTA GCATTTTCATT TAATCTGCAG GTATATTCTC CCAACAGTTT ATTGTCATGT 60

GATGTCCTCA GCCAAGATTG TRAGGCAGAG AGGAGCTGTC CCAACCTACT ATACCACCGA 120

20

GGCTGGAGAG ATCATATTTT TGGTATTAAA CTGGAGTCTC TCCATCCTTC ACATTGTTGA 180

TGTCTCTGT AGCAAACCGG AAAAGTCAGT GACAGAAGAT GCCGCTAGCG GTTTGAGCCA 240

25

GAGAATGACA GCTCTGGTTT GGAGAAAAGG GCCGGATGGT GGCTCTAGAA AGCCCATCCT 300

TCTGCTCTTC TTTTITCTCC CCCTTATATT GTGCTTTCAT TCATTCATTC ATTCATCAAA 360

CATTTGTTGA GCACCTATTA TGTGTCAAGC TCTGTGCTAG CCTCTGGAAA ACCTGCCCTC 420

30

ATGTAGCTCA CTGTGGAGTA GGAGAAACAA TGACTACACT ATGATAAGCA CGGGTTGTCA 480

GGGTCTCACA GAGCAGTGGC CCCTCATCCA GACCGATGAG GTCAAAGAAG GCATCCAGGC 540

35

GAGGATGGTG TCAGAGCTAA CTGAAGAATG AGAGGGAGCT GCACCASCAG GGGTTGGAAC 600

TGAAGGTGGC AGTGCCTGGA GTCTTGATTC CAGCAGAGGG AGAGCAGTCT GTGAAAAGGC 660

ACCAAGGGTG GGAGAGGGCA GAGCACATGG AGGAACTTCA GGTAGTTCTG GATGGCSCTG 720

40

GGGCAAAGCT AGAGAGGTAA GAAGAATCTA CAAATGTTCC TCGAGTTACA TGAACCTCCA 780

TCCCAATAAA CCCATTGGAA ACGAAAAATT TAAGTCAGAA GTGCATTTAA GGCTGGTCCG 840

45

AGTAGAATGA TTTTACAAAC GAATTGATCA CAACCAAGTTA CAGATGTCTT TGTTCTTCT 900

CCACTCCCAC TGCTTCACCT GACTAGCCTT TAAAAA A 941

50

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 843 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

60

CNAGGGATAA CCCCAAAGNT GGGAAATAAA CCCTCAATTA AAGGGGGAAC CAAAAAGCTG 60
 GGAAGTTCCC CCCCGCGGTG GCGGCCNGNT CTAGGAACTA GTGGAATCCC CCGGGGCTGC 120
 5 AGGGAATTCG GCACGGAGTG GGAATGTTGT TTGTATGATA CTATTTCAC AAWATGCATT 180
 GAGACTTGGT KTGTGGCCTA GGACATGGTC AATTCTTTYT AAATATTCCG TGAATTCTT 240
 TAGTGCATAT TCTCCGATGG GGGCTGTGGG GACAGAGTTC TAAATATGCC CATTAGATTA 300
 10 AATCTCTTCA TTCTGTTGCT CACATCTTCT ATATCCTTAT TAATCTGTCA ATCTCTTCAA 360
 GAGAGGTGTT ATTAAATCT CTCACTGTAT GTGTCACTTT GCCCTTAAAA TTCTGATGAT 420
 15 TTGCTTTATA AATGGTTATA ACCATTTTCC AGGAAGAACA TTAAAGAACT TTCCATTGGC 480
 ATTATCCAGT TTCCTTCAA ATACTGGTTT TTTTATTTT GGCTNCTAAG CAGCTATGAA 540
 TCCAGTTTCT CAGAAGCCCT TGTCTCAAGG CATTTGTTTC CAGATTACCT TGTTAGCATC 600
 20 CACACTATGG GCTATTTTAG AAAACA AAAAAGTATCAA AATCATATAG CTATGATTTT 660
 CCTGTGCTTG AAGGAGCCTT AAAGCTCATC TAGTCCAGCC AGTATTTGTT CATCCAAATT 720
 25 CTGCCAAGAA ATCTCTATG TCAAGATATT CTTTACCATC TTTGGGACAT TCTCATTATT 780
 AGAAACAAAT CCTAAGAAGA AATTCTGCCA TAKACAACCC ATCCGTTCTT TAAAAA AAA 840
 30 AAA 843

35 (2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1018 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CTGTAATTTT TAATTTTCAT ATACCGTGCT TTGATTCTAA TTTTATTTT TGAGTTCTCT 60
 45 GAAGGTACA TATACAGAGT GCTTCAGGAA TGATCATTTT GTTATTATTC ATGCTTCTTA 120
 ACAATGTTGT TTTAGTCCAA GAAGATAATT GCCAGAGAAA GAATACAGTG CAGGAAAGAA 180
 50 GARGCTGGAG CCAGTGGTGA AGARGGATG AGARGACAGA CATGTGGGA ATGAAATCAT 240
 GAATAATCGT GTTTTGAAT TGTCCAAAA CTCTACAAA CCATGAAATG TTGGAGTTTA 300
 AATCTAATTG TTGAAAAATT CCCACATTC CTGTATCCC TTAGGTTGAG CATAATTCCA 360
 55 CATCCGTGGA CTGATGCACT TCCCAAGAGG GGGCCTCATT AACTCTCCG AGGCAGCAGC 420
 AGCAAGGGCA CCCCCTCCTT TCCCCCACA CCCCAATTCT CATGGCTCTT CTTCTCTCA 480
 60 TCTCATGCTT AGGITAGAAA AGGGCACAAG GTAAGGAAGC CCTTGGGAAT AGGCTGAATC 540

5 TGGCTATCTA ATTTGGTGCC AAATACTTAA TGTGCTTGAA TTAAAAACA GCAAACATGT 600
AGAAAGGTAA TTATAATTAT GAGGCCAGTT CTMTAAGCTA GCTTTTTTTC CCCTCTCAAA 660
CAGCATATTG GCTTGGATGT CAGCAGGAGA AAGTGTMTT TGCAATACAC ATAATGCATA 720
TATGGTCCTG TTAGCAATCT ATAGAAAATA GATATTGCTC ATTAAGGTAA ATATMTTGT 780
10 TGATGAATGA TCTGGAATGG TCTGACTTG TTGTGTGAAC AGGAAATTGC TCTGTAGGCT 840
TTGACTTGTG AGGTAAAGAG TGAGGCTGGT AAGATTAATT AAAGTAAATA CTGTGACAAT 900
AGGATGTCAA AACCAAAAAC GTGTTTCTGA AACTCAAGGA ATTAATGACA CATAGGGAAG 960
15 TMTTGGCCAT ATTAAGCATA GAGTAGGAGA GGCAAGTCAA GAATAAAAAA AAAAAAAA 1018

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(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:
25 (A) LENGTH: 661 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

TTTAAGAAAT TAGTGAATCC CCGNTGCAG GGAATTCGGC ACGAGGAGGA GGCCGTCAGC 60
TGGCAGGAGC GCAGGATGGC AGCTGYTCCC CCGGTTGCA CCCCCCAGY TCTGCTGGAC 120
35 ATAAGYTGGT TAACAGAGAG CCTGGGAGCT GGGCAGCCTG TACCTGTGGA GTGCCGGCAC 180
CGCCTGGAGG TGGCTGGGCC AAGGAAGGGG CCTCTGAGCC CAGCATGGAT GCCTGCCTAT 240
GCCTGCCAGC GCCCTACGCC CCTCACACAC CACAACACTG GCCTMTCCGA GCTGCTGGAG 300
40 CATGGAGTGT GTGAGGAGGT GGAGAGAGTT CGGCGCTCAG AGAGGTACCA GACCATGAAG 360
GTGCGCAGGG CAGGGCTCGG ACCTACCCCA GGAATGTCCT GCCCTGGGAA TGACAACACA 420
GTCCACACCA TGCACGGGGA GGCAAACAGG GGCAGCTGAC CCAGCCCAGG GGTGAGANGA 480
GGTCTTGCCG AGGAAGTGGC AGCTAAGCTG ATACCTGATA TGCACWAGKC AGCCARGYGG 540
AGACAGGCAA GGAAGAAGCT TGTMTTGAGG ACAGAATMTT CTAGATCACT CAGCACCATC 600
50 TGGCTMTTGG GGCTMTTGT TTTATMTTGT TTTGAGACG GGTCTCGCT CTGTGCCCCA 660
N 661

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(2) INFORMATION FOR SEQ ID NO: 17:

60

(i) SEQUENCE CHARACTERISTICS:

275

- (A) LENGTH: 553 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

GGCACAGGGC TATTTGCCCC TCTCTCCACA TGACAGAACT GCTCTAAGTT TCTTTGCTGC 60
TCTTCTCAGC TGTGACACGG CTGCTGCTT GTTTTCCACA CCACCATGTC TATTCCTTGC 120
TGTCTTWC TCTGCTGTT TTTTCTCTT TGTATTTCTT CTGGCTCTTG TCCCTTTTCC 180
CACGTGTCWC AGCTTTCCTT TATTGCCACT TTCAGTCAGA GCAGTCCTGT GCTTCTGGTG 240
COGGCATAACA ATACTTACTT GAGTTTCTTG GCTTTTCTTG ACTGTGCATC TCTTACTTCA 300
ACATAGGAAT AGCCTGTCAT AGAATTCTC CAGTCCAGG GCTCAAGAGG GAGAGTGCCA 360
GAAAATGAG ACTGTTTTCC CTGCTCTGGA TTGAATTCAT AAAGCAAAC CAGTGTGTGT 420
GTGAGGGTTT GCTGTGTCAT GCCTATAGGT TGTTTGGGTG CAAACCTATA GAATCCAGCC 480
TGCGAAAAGA AAGRAACCAG AGAATANCAG CATCAGAACA ATGCTTGACA TCATTCTCA 540
ATCAAGCAGT CCA 553

30

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 869 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

40

GGCACAGGCT GCCAACACTG AGGTCTTCGT GGCTTCTCAC ATCTAGATGT ATCCCTCTCA 60
AATCTATCCT CTATCCAGGC ACCAGATTGA GGTATCTAAA ATGTCAACTT TCCAGTTACT 120
CCTTCTTATA CTAGCCCAAT CAACTTACAA GATAAAGTCC AAGCCCTTC ATATGACAAA 180
CCACACCCTG CTAACTCTC CAGGTTTGAA TCCTTCATCT CCTACTTTAA ACTTTAAAAC 240
CCAGCAGCAC GAAAGTGTCT CCTATGCATG TTGCCATATG CGTTCTCTCC ATCATGCATT 300
TGCTTGAGCA AGATGTCTTG AGTTAACATC TTATTCCTTA AGACTCATTG TGGTGGTAGA 360
CAGCCTTTAA TAACGGATCC TTGGCCAGGC ACAGTGACTC ACACCTGTAA TCCCAGAACT 420
TTGAAAGGCC AAAGAAGGAA GAAAGCTTGA GGCCAGTAGT TTGAGACCAG CCTGGGAAAC 480
AGAGAGATAT CCCATCTGTA CCAAAAATTT AAAAAATAT TAGCAGGGAG TAGTGGCATG 540
CACAAGTGGT CCCAGCTCCA TGGGAGASTG AGGTAGGAAC ATCACTTGAG CCCAGGAAGT 600

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276

CAAGGCTGCA GTGAACCATG ATCAGAACAT TGCANTCCAG CTTGGGTAAC AGAGTGAGAC 660
CTTAGGTCAG AAAAATGAAT AAATAAGCAT AAAATTTTAA AACTTTAGCC AGGCATGGTG 720
5 GCACACATCT GTGGTCCCTG CTACTTAGGA GGCTGAGGTG AGAGGATCCT TGAGCCCAGG 780
AGGTCAACAC TACAGTGAGC TATGATTGTG CCACTAAACT CCAACCTGGG TGAAAAAGCA 840
AAACCCCTGCC AAAAAAAAAA AAAAAAACT 869

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(2) INFORMATION FOR SEQ ID NO: 19:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 959 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GGCGAGCCGA GATCGTGCCA TTGCACTCCA GCCTGGGCAA CAAGAGTGAA ACTCTGTCTC 60
25 AAAAAAAAAA AATTATAATA CTATATGCCA TAAATGACA TTTCATATTT AAAGAGTTTT 120
TTAAACTCT TGTATTCACA TGCCATAATT TGAAACCCTA TTCTACTGAA TGAGAATGGT 180
30 ATCTGTGTGTC CTCATTTTTT CATTTTTATC CTTAACAATT TCCACCACAG CCAGTGCATA 240
TAATGGCAAT GACACCCAGG GATGGAATGA TAAGTTCAT CRMGCTCAG TCAAGACGCA 300
GACTTGATGT GGCCCAACA ACAGTCAATA ATGGAGTCTC CAAATAAAG CTCTATAGGA 360
35 AAGGTAAATA CCCGTGCAC AAGAAACCAC AGCATCTAGG TTCTAACCCC ATCTCTATGA 420
AGAGCTTGCT GGGAGAGTTT TGACATWAA CAATCTGTCT GATKGCCAAT TTTYTTCTTC 480
40 TATAAATGA TAATGTTKGA YTCAAAGATC CAAAGTCAAT TCATGGTCTA AACTTAATG 540
ATTTTTTTAG GTTTTGKGAC ATTTCACTGT AACTGTAGT AATTTATATC TTATTTTCCC 600
ACTAATTTAG AAAAATATYT AAATGATCCT TAATTGGCAA TGGGTCCTAA GAATTTTGTT 660
45 TTAAATCCCT GTTACCCAAA AGAGCCCTTT TTTGTATCTC GCAGTAGMTA CAAGGATCTT 720
TCTAAATCTT AAAAAAAAAA AAAAAAGAAA GAAAGAAAAG AAAAGAAAAA AAGTCAGCCG 780
50 GCGGTGGTGG CTCATGCCTG TAATCCCAGC ACTTTGGGAC CAAGGTGGAC AGATCAGGAG 840
GTCAGGAGAT GGAGACCATC CCGGCCAACA TGGAGAAACC CTGTCTCTAC TAAAAAAAAA 900
AAAAACTCGA GGGGGGCCCG GTACCCAATN CGCCGGCTAG TGGTCGTAAA ACAATCAA 959

55

(2) INFORMATION FOR SEQ ID NO: 20:

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1446 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

CGGGGCAGGG CTGTGTGGCA CCGCCAGGGA GCGGGCCAC CTGAGTCACT TTATTGGGTT 60
10 CAGTCAACAC TTTCTTGCTC CCTGTTTTCT CTTCTGTGGG ATGATCTCAG ATGCAGGGGC 120
TGGTTTTGGG GTTTTCCTGC TTGTGCCAAG GGCTGGACAC TGCTGGGGGG CTGAAAGCC 180
15 CCTCCCTTCC TGCTCTCTG TGGCTCCAT CCCCTCATGG GTGCTGCCAT CCTTCCTGGA 240
GAGAGGGAGG TGAAAGCTGG TGTGAGCCCA GTGGGTTCCT GCCCACTCAC CCAGGAGCTG 300
GCTGGGCCAG GACCGGGAGA GGGAGCACTG CTGCCCTCCT GGCCCTGCTC CTTCCGCACT 360
20 TAGGGGTGGA CCGAGCCTCG CTTTCCCCAC TGTCTGGAG GGAAGGGGAA GGAGGGGGTC 420
TTCAGGCTGG AGCCAGGCTG GGGGTGCTGG GTGGAGAGAT GAGATTAGG GGTGCCTCA 480
25 TGGGGTGGG AGGCCTGGG TGAAATRAGA AAGCCCAGA ACGTGCAGGT CTGCGGAGG 540
GAAGTGTCTT GAGTGAAGGA GGGGACCCCC ATCCTGGGGG ATGCTGGGAG TGAGTGAGTG 600
AGATGGCTGA GTGAGGGTTA TGGGAGCCT GAGGTTTTAT GGGCCTGTGT ATCCCCTTCT 660
30 CCGGGCCCCA GCCTGCCTCC CTCCTGCCCC CTTGGCCAC AGGTCTCCCT CTGGTCCCTG 720
TCCCTCTGGT GGTGGGGAT GGAGCGGCAG CAAGGGGTGT AATGGGGCTG GGTCTGTCT 780
35 TCTACAGGCC ACCCCGAGGT CTCAGTGGT TGCCTGGGA GCCGACGGG GCTCCTGAGG 840
GGTACAGGTT GGGTGGGCC TCCCTGAGG TCTGGGTCA GGTCTTGGCT CTGCTGCCTC 900
TCAGTCACCA AGTCACCTCC CTCTGAAAAT CCAGTCCCTT CTTGGATGT CCTTGTGAGT 960
40 CACTCTGGG CTGGCTGTG TCCCTCTCA GCTTCTGTG CTTGGGACAA GGTCAAGCC 1020
AGGATGGGCC CAGGCCTGG ATCCCCACC CCAGGACCCC CAGGCCCCCT CCCCTGCTGC 1080
45 TTTGCGGGG GCAGGCAGA AATGGAATCC TTTTGGGTCC CCGAGGTGG GTCCCTCCC 1140
AGCCCTGCAT CCTCCGTGCC STAGACCTGC TCCCCAGAG AGGGGCCTTG ACCACAGGA 1200
CGTGTGGTGG CGCCTGGCAC TCAGGGACCC CCAGCTGCC CAGCCCTGGT CTCTGGCGCA 1260
50 TCTCTCCCT CTTGTCCGA AGATCTGCG CTCTAGTGC TTTGAGGGG TTCCCATCAT 1320
CCCTCCCTGA TATGTATTG AAAATATTAT GCACACTGTT CATGCTTCTA CTAATCAATA 1380
55 AACGCTTTAT TTAAAGCCAA AAAAAAAAAA AAAAACTCG AGGGGGGGCC CGTACCCAAT 1440
TCGCCA 1446

60

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1471 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

10 CAAAAAATAA TAATGATAAT TTAAAATAAA TAAGTAACTA ATAAAAAGAT TTTATATCCC 60
 AGTCTTATGA TGTGGTTGG CAAGGCTAGA TAAAAAGATG TTAGAATGAA AGAACATATT 120
 15 TTTAGTGATA TGTAAATGAA GGATTCTACA ATAGTCATAT ATTTTATAT GAATGAATGT 180
 TGGGTTGGGC TGGAGAGGTA TGTGTGTGTA AATATAAAGG TCTCACATTC AGAGTATAGC 240
 20 TCTGAAATAA TGGAACTCAT GTCTACAATT CAACATGCAT CTGTATAGTT ACATCTCATG 300
 TAAATATACA CAGACATATT TTGCAGCCAG TAATTGACAG TTAATGTCCA AAACAGGTGA 360
 TTGATAGGTA ACAGAAATTA GATAACCACC AATTTTGCCC AAGAGAAAGA CTAGAAGGAC 420
 25 TAAAAGCAGT TGAATGTATG GTACTGACAT TGTCATAAGC AGTCTGATAA CCAGTTTATT 480
 GAAACGTGTG CATTAAACAGA GAATTTAATT TTAAACCCAT AATTTCTCCT ATCCATTAAA 540
 30 ATATTATAAT TGTTAGTAGT ATGAAACCAA CAGGAAATGT TTTTAAATCA TTTAGTGAGG 600
 TGATTCATTT GTTTCATGGG CAAACACTAT CCAGGAAAAG CCTTGCTTGC CTGTTTCCCA 660
 AAGAGCTCTA AGAAATAGAA TCAAGTGTA AATGGTTCAG ACCATTTCAGG ATTTCTTGTC 720
 35 ACTCTTCTCA ACCCCGATCT TCCTGTTATT ACTGATGTTT GAAACCCTGT CATTAGCCCC 780
 GGCCTGGTTA AAGCCCCTCA GAGTCACCTC TCATTCATAG CAATAGAAIT CAACCCCAAG 840
 40 TGGTTGATGG TGTCCCAGC ACAGCCGAGA GACCTGATCT CTGGATTTCAG TGCTTTTAGC 900
 TCTTCGAGTT TACCCTAAGA TACCTTCGGG CAATATTTTT AACCAACCCA AAAGCTCTTC 960
 AGGTCATTTC TGAAGAGGAC AAGGTGAATC TTGGCTTGA ACACCATTTT TGGGCTCTTG 1020
 45 CTAAGAATG AATCAGAAAG GAATTTTTTC TGAAGAGCAT TAGAAAGTAA AGGAGATGTT 1080
 AAAATAAGTT CTTGAAGTAT GTTTTATATT TATCTAAAAC ACTGATTTTA AAAGTTTACA 1140
 50 TTCAAATGTG TATTCAAAG AAGTACTGAT TTGTAATTAT TATAGTTTGT GTGTATCATC 1200
 CCCTTTTAAC CGTGCCTAAC AACTGTACTT AAATTTTGTT TTCCTAGTGT AACAAATGTT 1260
 TCCCATAAGA TTTTCTAGAG CCAAATAATG GGAGTGAAAA ATTCCCTAAG TGTATATATA 1320
 55 GAAAATATAT TAGAAAATCA GCTTTGGATT ATACGATTTC TAAAATATAC TAATACAGAA 1380
 TCCTCAGTAA TATGTTTTGA ATTGGATTTT TTCTCAGAAC TGTTACATAA TAAATAATAC 1440
 60 ATCAACCAGA AAAAAAAAAA AAAAAAATTN C 1471

5 (2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1402 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

15 AGGGACGTCT TGCCTGAGGA GATGCCCATT TCTGTCCTGG RTTACCCTCA CTGCGTGGTG 60
CATGAGCTGC CAGAGCTGAC GCGGAGAGT TTGGAAGCAG GTGACAGTAA CCAATTTTGC 120
TGGAGGAACC TCTTTTCTTG TATCAATCTG CTTGGGATCT TGAACAAGCT GACAAAGTGG 180
20 AAGCATTCAA GGACAATGAT GCTGGTGGTG TTCAAGTCAG CCCCATCTT GAAGCGGGCC 240
CTAAAGGTGA AACAAGCCAT GATGCAGCTC TATGTGCTGA AGCTGCTCAA GGTACAGACC 300
25 AAATACTTGG GCGGCGAGTG GCGAAAGAGC AACATGAAGA CCATGTCTGC CATCTACCAG 360
AAGGTGCGGC ATCGGCTGAA CGACGACTGG GCATACGGCA ATGATCTTGA TGCCCGGCCT 420
TGGGACTTCC AGGCAGAGGA GTGTGCCCTT CGTGCCAACA TTGAACGCTT CAACGCCCCG 480
30 CGCTATGACC GGGCCACAG CAACCCTGAC TTCCTGCCAG TGGACAACTG CCTGCAGAGT 540
GTCTTGGGCC AACGGGTGGA CCTCCCTGAG GACTTTCAGA TGAACATGA CCTCTGGTTA 600
35 GAAAGGGAGG TCTTCTCCAA GCCCATTTC TGGGAAGAGC TGCTGCAGTG AGGCTGTGTTG 660
TTAGGGGACT GAAATGGAGA GAAAAGATGA TCTGAAGGTA CCTGTGGGAC TGTCTAGTT 720
CATTGCTGCA GTGCTCCCAT CCCCCACCAG GTGGCAGCAC AGCCCCACTG TGTCTTCCGC 780
40 AGTCTGTCTT GGGCTTGGGT GAGCCCAGCT TGACCTCCCC TTGGTTCCCA GGGTCTGCT 840
CCGAAGCAGT CATCTCTGCC TGAGATCCAT TCTTCTTTA MITCCCCCAM CCTCCTCTCT 900
45 TGGATATGGT TGGTTTGGC TCATTTTACA ATCAGCCCAA GGYTGGGAAA GCTGGAATGG 960
GATGGGAACC CCTCCGCCGT GCATCTRAAT TTCAGGGGTC ATGCTGATGC CTCTCGAGAC 1020
ATACAAATCC TTGCCTTTGT CAGCTTGCAA AGGAGGAGAG TTTAGGATTA GGGCCAGGGC 1080
50 CAGAAAGTCG GTATCTTGGT TGTGCTCTGG GGTGGGGGTG GGGTGTCTT GATGTTATTC 1140
CAGCCTCCTG CTACATTATA TCCAGAAGTA ATTGCGGAGG CTCCTTCAGC TGCCTCAGCA 1200
55 CTTTGATTTT GGACAGGGAC AAGGTAGGAA GAGAAGCTTC CCTTAACCAG AGGGGCCATT 1260
TTTCCTTTTG GCTTTCGAGG GCCTGTAAAT ATCTATATAT AATTCTGTGT GTATTCTGTG 1320
TCATGTTGGG GTTTTAAATG TGATTGTGTA TTCTGTTTAC ATTAAAAAGA AGCAAAAATA 1380
60

ATAAAAAAAAAA AAAAAAAAAA CT

1402

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(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 1047 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

15

GGCACAGGGG ACTACAGGCA CCCACGACCA TACCCAGCTA ATTTTGTAT TTTTGTAG 60

AGATGGGGTT TCACGATGTC GCCCAGGCTG GTCTTGAACCT CCTGGGCTTG AGCGATCTTC 120

20

CCATCTTTCC ATCTTGGCCT CCTAAAGTGC TGGGACTGCA GGCATGAGCC ACCATGCCCA 180

GCCAAGATTC TTATTGATTA CCATGTTGCT TCAAGAAGCC AAGCCAGTTT CCAATATTCC 240

CCATTTGCTG GAGTCTTGGT ACTTTGGGTA GAAGCAACTG GTAAATTGTT AATTGGAACA 300

25

NTTGGTGGTG TAGATAACCA CGTATGGCCA AACCTAGAGC ATCTAGGCTC ACAATTACTA 360

TCCTGACTTG ATAACAAGTG TTCTGATATT AACCTGAAAA TGGGAATAAT GCCAAATCTG 420

30

TGTAACCTAA CATCTATATA CACAGTGGGG AGAACTGAAG TTATTAAACC TGGAATCTCT 480

GTGATCAAGG CTAACAGTAG TTATCTAAGA AGCAAAGGAC CTACAATTCT TAGACTTGGA 540

35

GTCATATTCT TTAAGGACGT GTTCTGAAAC TATATCAAGC ATCTGGTTTC CACGTATTTT 600

TCCCTCAGAA ATTATGAAGT ACAAGTAAAA ATGAAGGTAC AGGGTAAGAC ACATGCTGCT 660

TTCTTGCTCT TGAGTGGAGA CAGTTTCCA GCCATCTTAA CCCCTTWACA CAAAACAATT 720

40

TGTGTTTTAT AGCAAATAAG TGAATCAACA TAATTCAAT ATGATGTTTA TCCACCAGTA 780

CTTTCCTTTC AGCTTCTAGT CCCATAARTG GTTTGTGAAG TCATCGGTTA CATTAGCCAA 840

GATAGGCCTA GACTTGAAGT CTAGAATGTT TTTCCCACTA TATGCCAAAG TAGAATGTGG 900

45

GTATCTCAGG GTCATTTTTC TTGTTCAATT TCCACCTGT ACAGTTGTTA TGATTCACCT 960

TCCTTATGTG TCTAATAAAT CTTGTTCCAT GAAATGATCA AAAAAAAAAA AAAAAAACT 1020

50

CGAGGGGGGG CCCGGTACCC AAATCGC 1047

55

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 990 base pairs

(B) TYPE: nucleic acid

60

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

5 TTGGAAGGG TCTAGCTCTT TCTCATTCAC CAACTATATT AGAAGCACTT GAGGGAAATT 60
 TACCACTCCA AATCCAAAGC AATGAACAGT CTTTCTGGA TGATTTTATT GCCTGTGTCC 120
 CAGGATCAAG TGGTGAAGG CTTGCAAGGT GGCTTCAGCC AGATTCATAT GCGGATCCTC 180
 10 AGAAAACATC TTTGATCCTG GAATAAGGAT GATATTCGTT GTGGTTGGCC TACCACCATA 240
 ACTGTTCAAA CAAAAGACCA GTATGGGGAT GTGGTACATG TTCCAATAT GAAGGTAATT 300
 15 ATAAGTGGAT TAAATTAGCA GACATCTATA TACTGGCTGC AATGACTGAT AAAATTTTAG 360
 AAATGCCAAG TGCTGAGRGT CCATTTGTTT TACCCTCTTT ATATAAAGGG TGATGCTGAA 420
 AGTTTGTTTA AATGACTTGT TTATATTAAT TAGTCCCAA GTGTCCAAGT TACACCTGTT 480
 20 TTTTGTGTA GTTGTCTCTT TACATTTTGC TACCTGTAC GGGGACTCAA AGGAGGGATA 540
 AGAAAGTATC CATCTAAAGA GTGCTAGACA CACACAGTGA AGCCCTCAA TATGTATTGA 600
 25 TTGAATAAAT GCATGAAAGA ATACATTTTT AAATTTGTG TATAGTTTTG AAAGACTCAA 660
 GTACGTTCTG TGTGTTGTAT TACTGAAACC ACATTTTAAA AATAACACTC ATTAAGTTAG 720
 AAATATATGA GTTTAGATTG TAAAGAATG AGGAATTGAA ATAGTTGTAT ACCATATGTA 780
 30 TGAATATAGA GTTTTAGGA TACCTCTTAC CTGAAATATT AATAATAATG TTTNCAGAGC 840
 ATATTATACA TAATTATTG TGATTTAATC TGTTAATATG AATATCTCAT TAAAACTTT 900
 35 TATTCTGAA AAAATTATAT TGAATAAAT TTTATATAGG CAGTCCCAG CCCTTTCCTC 960
 CTTCAAAGTT GTCTTATAGA GTGATTGGTT 990

40

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1208 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

TAATCGCTAC TATAGGGAAA GCTGGTCGCT GCAGGTACCG GTCCGGAATT CCGGGTCGAC 60
 CCACGCGTCC GAGCGAAATG GCGCTCCGG CCCCCGCCC GGCCTCCGGC GGCTCCGGG 120
 55 AGGTAGACGA GCTGTTGAC GTAAAGAACG CCTTCTACAT CGGCAGCTAC CAGCAGTGCA 180
 TAAACGAGGC GCASGGGTGA AGCTRTCAAG CCCAGAGAGA GACGTGGAGA GGGACGCTT 240
 60 CCTGTATAGA GCGTACCTGG CGCAGAGGAA GTTCGGTGTG GTCCTGGATG AGATCAAGCC 300

CTCTCGGCC CCTGAGCTCC AGGCCGTGCG CATGTTTGCT GACTACCTCG CCCACGAGAG 360
 TCGGAGGGAC AGCATCGTGG CCGAGCTGGA CCGAGAGATG AGCAGGAGCK TGGACGTGAC 420
 5 CAACACCACC TTCCTGCTCA TGGCCGCTC CATCTATCTC CACGACCAGA ACCCGGATGC 480
 CGCCCTGCGT GCGCTGCACC AGGGGGACAG CCTGGAGTGC ACAGCCATGA CAGTGCAGAT 540
 10 CCTGCTGAAG CTGGACCGCC TGGACCTCGC CCGGAAGGAG CTGAAGAGAA TGCAGGACCT 600
 GGACGAGGAT GCCACCCTCA CCCAGCTCGC CACTGCCTGG GTCAGCCTGG CCACGGGTGG 660
 TGAGAAGCTG CAGGATGCCT ACTACATCTT CCAGGAGATG GCTGACAAGT GCTCGCCAC 720
 15 CCTGCTGCTG CTCAATGGGC AGGCGGCTG CCACATGGCC CAGGGCCGCT GGGAGGCCGC 780
 TGAGGGCTG CTGCAGGAGG CGCTAGACAA GGATAGTGGC TACCCRGAGA CGCTGGTCAA 840
 20 CCTCATCGTC CTGTCCCAGC ACCTKGGCAA GCCCCCTGAG GTGACAAACC GATACCTGTC 900
 CCAGCTGAAG GATGCCACA GGTCCATCC CTTTCATCAAG GAGTACCAGG CCAAGGAGAA 960
 CGACTTTGAC AGGCTGGTGC TACAGTACGC TCCCAGCGCT GAGGCTGGCC CAGAGCTGTC 1020
 25 AGGACCATGA AGCCAGGACA GAGGCCAGGA GCCAGCCCTG CAGCCCTCCC CACCCGGCAT 1080
 CCACCTGCAT CCCTCTGGGG CAGGAGCCCA CCCCCAGCAC CCCCATCTGT TAATAAATAT 1140
 30 CTCAACTCCA RGGTGTCCA CCTGAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1200
 AAAAAAAAAA 1208

35

(2) INFORMATION FOR SEQ ID NO: 26:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1922 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

GTGCTGCGCT ACTGAGCAGC GCCATGGAGG ACTCTGAAGC ACTGGGCTTC GAACACATGG 60
 GCCTCGATCC CCGGCTCCTT CAGGCTGTCA CCGATCTGGG CTGGTCGCGA CCTACGCTGA 120
 50 TCCAGGAGAA GGCCATCCCA CTGGCCCTAG AAGGAAGGA CCTCCTGGCT CGGGCCCGCA 180
 CGGGCTCCGG GAAGACGGCC GCTTATGCTA TTCCGATGCT GCAGCTGTG CTCCATAGGA 240
 55 AGGCGACAGG TCCGGTGGTA GAACAGGCAG TGAGAGGCCT TGTTCCTGTT CCTACCAAGG 300
 AGCTGGCAGC GCAAGCACAG TCCATGATTC AGCAGCTGGC TACCTACTGT GCTCGGGATG 360
 TCCGAGTGGC CAATGTCTCA GCTGCTGAAG ACTCAGTCTC TCAGAGAGCT GTGCTGATGG 420
 60

AGAAGCCAGA TGTGGTAGTA GGGACCCCAT CTCGCATATT AAGCCACTTG CAGCAAGACA 480
GCCTGAAACT TCGTGACTCC CTGGAGCTTT TGGTGGTGGA CGAAGCTGAC CTTCTTTTTT 540
5 CCTTTGGCTT TGAAGAAGAG CTCAAGAGTC TCCTCTGTCA CTGCCCCGG ATTTACCAGG 600
CTTTTCTCAT GTCAGCTACT TTTAACGAGG ACGTACAAGC ACTCAAGGAG CTGATATTAC 660
ATAACCCGGT TACCCTTAAG TTACAGGAGT CCCAGCTGCC TGGGCCAGAC CAGTTACAGC 720
10 AGTTTCAGGT GGTCTGTGAG ACTGAGGAAG ACAAATTCCT CCTGCTGTAT GCCCTGCTCA 780
AGCTGTCATT GATTCGGGGC AAGTCTCTGC TCTTTGTCAA CACTCTAGAA CGGAGTTACC 840
15 GGCTACGCCCT GTTCTTGGA CAGTTCAGCA TCCCCACCTG TGTGCTCAAT GGAGAGCTTC 900
CACTGCGCTC CAGGTGCCAC ATCATCTCAC AGTTCAACCA AGGCTTCTAC GACTGTGTCA 960
TAGCAACTGA TGCTGAAGTC CTGGGGGCCC CAGTCAAGGG CAAGCGTCGG GGCCGAGGGC 1020
20 CNAAAGGGGA CAAGGCCTCT GATCCGGAAG CAGGTGTGGC CCGGGGCATA GACTTCCACC 1080
ATGTGTCTGC TGTGCTCAAC TTTGATCTTC CCCCACCCC TGAGGCCTAC ATCCATCGAG 1140
25 CTGGCAGGAC AGCACGCGCT AACAACCCAG GCATAGTCTT AACCTTTGTG CTTCCACGG 1200
AGCAGTTCCA CTTAGGCAAG ATTGAGGAGC TTCTCAGTGG AGAGAACAGG GGCCCCATTC 1260
TGCTCCCTTA CCAGTTCCGG ATGGAGGAGA TCGAGGGCTT CCGCTATCGC TGCAGGGATG 1320
30 CCATGCGCTC AGTGACTAAG CAGGCCATTC GGGAGGCAAG ATTGAAGGAG ATCAAGGAAG 1380
AGCTTCTGCA TTCTGAGAAG CTTAAGACAT ACTTTGAAGA CAACCCTAGG GACCTCCAGC 1440
35 TGCTGCGGCA TGACCTACCT TTGCACCCCG CAGTGGTGAA GCCCCACCTG GGCCATGTTT 1500
CTGACTACCT GGTTCCTCCT GCTCTCCGTG GCCTGGTRCG CCCTCACAAG AAGCGGAAGA 1560
AGCTGTCTTC CTCTGTAGG AAGGCCAAGA GAGCAAAGTC CCAGAACCCA CTGCGCAGCT 1620
40 TCAAGCACAA AGGAAAGAAA TTCAGACCCA CAGCCAAGCC CTCCTGAGGT TGTGCGCCT 1680
CTCTGGAGCT GAGCACATG TGGAGCACAG GCTTACACCC TTCGTGGACA GCGGAGGCTC 1740
45 TGGTGCTTAC TGCACAGCCT GAACAGACAG TTCTGGGGCC GGCAGTGCTG GGCCCTTTAG 1800
CTCCTTGGA CTTCCAAGCT GGCATCTTGC CCCTTGACAA CAGAATAAAA ATTTAGCTG 1860
CCCCAAAAA AAAAAAAAAA AAAAAAATC GAGGGGGGGC CCGTACCCAA TTCGCCCTAT 1920
50 AA 1922

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(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1951 base pairs

(B) TYPE: nucleic acid

60

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

5	TCGTCCCCAG AGCGGGCTGA GCCCCAGGCG SAGGGTGGCG GGGGAGCCTG GGGGAGCCGC	60
	CGCCACCTCC ACGGGCCTCT CTGAGCTCGG ACACCAGCGC CCTGTCCTAT GACTCTGTCA	120
10	AGTACACCT GGTGGTAGAT GAGCATGCAC AGCTGGAGCT GGTGAGCCTG CGCCGTGCTT	180
	CGGAGACTAC AGTGACGAGA GTGACTCTGC CACCGTCTAT GACAACTGTG CCTCCGTCTC	240
	CTCGCCCTAT GAGTCGGCCA TCGGAGAGGA ATATGAGGAG GCCCCGCGGC CCCAGCCCCC	300
15	TGCCTGCCTC TCCGAGGAAC TCCACGCCTG ATGAACCCGA CGTCCATTTC TCCAAGAAAT	360
	TCCTGAACGT YTTCATGAGT GGCCGCTCCC GCTCCTCCAG TGCTGAGTCC TTCGGGCTGT	420
20	TCTCCTGCAT CATCAACGGG GAGGAGCAGG AGCAGACCCA CCGGGCCATA TTCAGGTTTG	480
	TGCCTCGACA CGAAGACGAA CTTGAGCTGG AAGTGGATGA CCCTCTGCTA GTGGAGCTCC	540
	AGGCTGAAGA CTACTGGTAC GAGGCCTACA ACATGCGCAC TGGTGCCCGG GGTGTCTTTC	600
25	CTGCCTATTA CGCCATCGAG GTCACCAAGG AGCCCGAGCA CATGGCAGCC CTGGCCAAAA	660
	ACAGTGACTG GGTGGACCAG TTCCGGGTGA AGTTCCTGGG CTCAGTCCAG GTTCCTTATC	720
30	ACAAGGGCAA TGACGTCTC TGTGCTGCTA TGCAAAAGAT TGCCACCACC CGCCGGCTCA	780
	CCGTGCACTT TAACCCGCCC TCCAGCTGTG TCCTGGAGAT CAGCGTGCGG GGTGTGAAGA	840
	TAGGCGTCAA GGCCGATGAC TCCCAGGAGG CCAAGGGGAA TAAATGTAGC CACTTTTTC	900
35	AGTTAAAAAA CATCTCTTTC TCGGATATC ATCCAAAGAA CAACAAGTAC TTTGGGTTCA	960
	TCACCAAGCA CCCC GCCGAC CACCGGTTTG CCTGCCACGT CTTTGTGTCT GAAGACTCCA	1020
40	CCAAAGCCCT GGCAGAGTCC GTGGGAGAG CATTCCAGCA GTTCTACAAG CAGTTTGTGG	1080
	AGTACACCTG CCCCACAGAA GATATCTACC TGGAGTAGCT GTGCAGCCCC GCCCTCTGCG	1140
45	TCCCCAGCC CTCAGGCCAG TGCCAGGACA GCTGGCTGCT GACAGGATGT GGCAGTCTT	1200
	GAGGAGGGGC ACCTGCCACC GCCAGAGGAC AAGGAAGTGG GCGCTGGCC CAGGGTAGGG	1260
	GAGGGTGGGG CAATGGGGAG AGGCAAATGC AGTTTATTTGT AATATATGGG ATTAGATTCA	1320
50	TCTATGGAGG GCAGAGTGGG CTGCCTGGGG ATTGGGAGGG ACAGGGCTTG GGGAGCAGGT	1380
	CTCTGGCAGA GAAGGATGTC CGTTCAGGA GCACACGGCC CTGCCCCATC CTGGGCCTTA	1440
	CCTCCCCTGC CAGGGCTCGG GCGCTGTGGC TCCTGCCTTG ATGAAGCCCG TGTCTGCCT	1500
55	TGATGAAGCC TGTGCCACCT GCAAGTGCCC GCCCTGCCCC TGCCCCAACC CCCACCGAAG	1560
	AGCCCTGAGC TCAGGCTGAG CCCAGCCACC TCCCAAGGAC TTTCCAGTGA GGAAATGGCA	1620
60	ACACGTGGAG GTGAAGTCCC TGTTCACAGC TCCGTCTCTT GCGGGGCTTC TGGGTGGCTC	1680

CTGCCACTGA CCTCACCGGC ATGCTGGCCT GTGGCAGGCC TAGGACCTCA GCGGGGAGG 1740
AGGAGCTGCC GCAAGGCCCT GTCCCAGCAG AAGAGGGAGG CTTCTGACT GACACAGGCC 1800
5 AGCCCCATCT TGGTCCTGTC ACCCTGGCCC CAACTATTAA AGTGCCATTT CCTGTCAAAA 1860
AAAAAAAAA AAAATCGGGG GGGGCCCGGA ANCCAATTTC CCCCAAAAAG GGGGGTTATA 1920
10 AAAATCCCN GCGNGTGTTC TTAAAAATTC G 1951

15 (2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3989 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

25 GGCACAGGCC GCAGGNACC TATGGGCGCA TATAGGTTGT AATGAACTG TAGTCTCAGT 60
TGGAAGCCTA GACATGAAAT GGGTCAGTGA GCAAGGCTCT ATTCCTAGTC TCCAGCCATG 120
CCTGTGGAAC CTGARCCRC TCTCAGCACA TTGGACCCAG GCAGATGYAA AAAATTCACA 180
30 GAACTATGAT TTGGACTCAA GGGTTTGTAG ATTTCTCCTC TCATTCTAAT TTCAGTGTCT 240
AAAATTCTTG CATCCRTGAA CGAGCTGGGC ATTTGATGAG ACAGGGCYGA ATACTGCAGT 300
35 TTTCCTCCTA GAAATCATCT GGGGCATTTT CTTTGAAC TGGAACAA TTAGGCATAA 360
CTGTTTGAC AACTTGGGA TAARTGATTT TGGGATAACG ATCTACCAGA ATGGGGATAT 420
TTCACCCTTG GTTCTGAGAT GCAAACCAA GAATATCATG ACCAGCTTTC AGGCCTCCTG 480
40 AAGTATATCT CTCACATTGT CTGTTCTCA TGCTGAGGAG CCTGAGATCC CTGTGTGGGG 540
ATTAGACAGT GGAAGTTAT GGGTGTAGT GAATTGGCTT ATTTGTCTG TCCCTGTCTG 600
45 AATGTATTGC AGGAAYTAA AAGACCAAG AAGAGGAAGA AGACCAAGGC CCACCATGCC 660
CCAGGCTCAG CAGGGAGCTG CTGGAGGTAG TAGAGCCTGA AGTCTTGAC GACTCACTGG 720
ATAGATGTTA TTCAACTCCT TCCAGTTGTC TTGAACAGCC TGAATCCTGC CAGCCCTATG 780
50 GAAGTTCTT TTATGCATTG GAGGAAAAAC ATGTTGGCTT TTCTCTTGAC GTGGGAGAAA 840
TTGAAAAGAA GGGGAAGGGG AAGAAAAGAA GGGGAAGAAG ATCAAAGAAG GAAAGAAGAA 900
55 GGGGAAGAAA AGAAGGGGAA GAAGATCAA ACCCACCATG CCCAGGCTC AGCAGGGAGC 960
TGCTGGATGA GAAAGRGCTT GAAGTCTTGC AGGACTCACT GGATAGATGT TATTCAACTC 1020
CTTCAGTTGT GTTGAACGTG GTGACTCATG CCAGCCCTAC AGAAGTGCCT TTTATGTATT 1080
60

	GGAGCAACAG CATGTTGGCT TGGCTGTTGA CATGGATGAA ATTGAAAAGT ACCAAGAAGT	1140
	GGAAGAAGAC CAAGACCCAT CATGCCCCAG GCTCAGCAGG GAGCTGCTGG ATGAGAAAGA	1200
5	GCCTGAAGTC TTGCAGGACT CACTGGATAG ATGTTATTTC ACTCCTTCAG GTTATCTTGA	1260
	ACTGCCTGAC TTAGGCCAGC CCTACAGCAG TGCKGTTTAC TCATTGGAGG AMCAKTACCT	1320
	TGGCTTTKCT CTTGACGTGG ASAAATTGAA AAGAAGGGGA AGGGGAARAA AAGAAGGGGA	1380
10	AGAAGATCAA AGAAGGAAAG AAGAAGGGGA AGAAAAGAAG GGAAGAAGA TCAAAACCCA	1440
	CCATGCCCCA GGCTCAGCAG GGAGCTGCTG GATGAGAAAG GGCCTGAAGT CTTGCAGGAC	1500
15	TCACTGGATA GATGTTATTC AACTCCTTCA GGTGTCTTTG AACTGACTGA CTCATGCCAG	1560
	CCCTACAGAA GTGCCTTTTA YRTATTGGAG CAACAGYGTG TTGGCTTGGC TGTTGACATG	1620
	GATGAAATG AAAAGTACCA AGAAGTGGAA GAAGACCAAG ACCCATCATG CCCCAGGCTC	1680
20	AGCAGGGAGC TGCTGGATGA GAAAGAGCCT GAAGTCTTGC AGGACTCACT GGATAGATGT	1740
	TATTGCATC CTTCAGGTTA TCTTGAAGT CTTGACTTAG GCCAGCCCTA CAGCAGTGCT	1800
25	GTTTACTCAT TGGAGGAACA GTACCTTGGC TTGGCTCTTG ACGTGGACAG AATTAAAAAG	1860
	GACCAAGAAG AGGAAGAAGA CCAAGGCCCA CCATGCCCCA GGCTCAGCAG GGAGCTGCTG	1920
	GAGGTAGTAG AGCCTGAAGT CTTGCAGGAC TCACTGGATA GATGTTATTC AACTCCTTCC	1980
30	AGTTGTCTTG AACAGCCTGA CTCTGCCAG CCCTATGGAA GTTCCTTTTA TGCATTGGAG	2040
	GAAAAACATG TTGGCTTTTC TCTTGACGTG GGAGAAATG AAAAGAAGGG GAAGGGGAAG	2100
35	AAAAGAAGGG GAAGAAGATC AAMGAAGRAA AGAAGAAGGG GAAGAAAAGA AGGGGAAGAA	2160
	GATCAAAACC CACCATGCCC CAGGCTCAAC GGCCTGCTGA TGAAGTGA AGAGCSTGAA	2220
	GTCTTACAGG ACTCACTGGA TAGATGTTAT TCGACTCCGT CAATGTACTT TGAACCTACT	2280
40	GACTCATTC AGCACTACAG AAGTGTGTTT TACTCATTTG AGGAACAGCA CATCAGCTTC	2340
	GCCCTTTACG TGGACAATAG GTTTTTTACT TTGACGGTGA CAAGTCTCCA CCTGGTGTTC	2400
45	CAGATGGGAG TCATATTCCC ACAATAAGCA GCCCTTASTA AKCCGAGAGA TGTCATTCTT	2460
	GCAGGCAGGA CCTATAGGCA MGTGAAGATT TGAATGAAAG TACAGTTCCA TTTGGAAGCC	2520
	CAGACATAGG ATGGGTCAGT GGGCATGGCT CTATTCCTAT TCTCAAACCA TGCCAGTGGC	2580
50	AACCTGTGCT CAGTCTGAAG ACAATGGACC CACGTTAGGT GTGACACGTT CACATAACTG	2640
	TGCAGCACAT GCCGGGAGTG ATCAGTCRGA CATTTTAATT TGAACCACGT ATCTCTGGGT	2700
55	AGCTACAAAA TTCTCAGGG ATTTCATTTT GCAGGCATGT CTCTGAGCTT CTATACCTGC	2760
	TCAAGGTCAK TGTCATCTTT GTGTTAGCT CATCCAAAGG TGTTACCCTG GTTTCAATGA	2820
60	ACCTAACCTC ATTCTTTGTG TCTTCAGTGT TGGCTTGTTC TAGCTGATCC ATCTGTAACA	2880

	CAGGAGGGAT CCTTGGCTGA GGATTGTATT TCAGAACCAC CAACTGCTCT TGACAATTGT	2940
	TAACCCGCTA GRCTCCTTTG GTTAGAGAAG CCACAGTCCT TCAGCCTCCA ATTGGTGTCA	3000
5	GTACTTAGGA AGACCACAGC TAGATGGACA AACAGCATTG GGAGGCCTTA GCCCTGCTCC	3060
	TCTCRATTC ATCCTGTAGA GAACAGGAGT CAGGAGCCGC TGGCAGGAGA CAGCATGTCA	3120
10	CCCAGGACTC TGCCGGTGCA GAATATGAAC AAYGCCATGT TCTTGCAGAA AACGCTTAGC	3180
	CTGAGTTTCA TAGGAGGTAA TCACCAGACA ACTGCAGAAT GTRGARCACT GAGCAGGACA	3240
	GCTGACCTGT CTCCTTCACA TAGTCCATRT CACCACAAAT CACACAACAA AAAGGAGARG	3300
15	AGATATTTTG GGTTCAAAAA AAGTAAAAAG ATAATGTAGC TGCATTTCTT TAGTTATTTT	3360
	GARCCCAAAA TATTTCTCA TCTTTTGTGTT GTTGTCATKG ATGGTGGTGA CATGGACTTG	3420
20	TTTATAGAGG ACAGGTCAGC TGTCTGGCTC AGTGATCTAC ATTCTGAAGT TGTCTGAAAA	3480
	TGTCTTCATG ATTAAATTCA GCCTAAACGT TTTGCCGGA AACTGCAGA GACAATGCTG	3540
	TGAGTTTCCA ACCTYAGCCC ATCTCGGGC AGAGAAGGTC TAGTTTGTC ATCASCATTA	3600
25	TCATGATATC AGGACTGGTT ACTTGGTTAA GGAGGGTCT AGGAGATCTG TCCCTTTTAG	3660
	AGACACCTTA CTTATAATGA AGTATTTGGG AGGGTGGTTT TCAAAATTAG AAATGTCCTG	3720
30	TATTCCRATG ATCATCCTGT AAACATTTTA TCATTTATTA ATCATCCCTG CCTGTGTCTA	3780
	TTATTATATT CATATCTCTA CGCTGGAAAC TTTCTGCCTC AATGTTTACT GTGCCTTTGT	3840
	TTTTGCTAGT GTGTGTTGTT GAAAAA AAAACATTCTCTG CCTGAGTTT AATTTTGTGTC	3900
35	CAAAGTTATT TTAATCTATA CAATTAAAAG CTTTGCCTA TCAAAAAA AAAAAA	3960
	AAAAA AAAAAAGCGGA CGCGTGGC	3989

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(2) INFORMATION FOR SEQ ID NO: 29:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3735 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

- 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

	CTGCTGTTCG CTGGCTGGGC TCCGAGCAG GCTTGGCCAG CSGCTGACGG GTCGGCGGGC	60
	GGGTTTGTGT GAACAGGCAC GCAGCTGCAG ATTTTATTCT GGTAGTCAN CCCTCTCAA	120
55	GGTTGAAGGA ACTGATGTAA CAGGGATTGA AGAAGTAGTA ATTCCAAAA AGAAAACTTG	180
	GGATAAAGTA GCCGTCTTC AGGCACCTGC ATCCACAGTA AACAGGGATA CCACAGCTGT	240
60	GCCTTATGTG TTTCAAGATG ATCCTTACCT TATGCCAGCA TCATCTTTGG AATCTCGTTC	300

	ATTTTACTG GCAAAGAAAT CCGGGGAGAA TGTGGCCAAG TTTATTATTA ATTCATACCC	360
	CAATATTTTT CAGAAGGACA TAGCTGAACC TCATATACCG TGTTTAATGC CTGAGTACTT	420
5	TGAACCTCAG ATCAAAGACA TAAGTGAAGC CGCCCTGAAG GAACGAATTG AGCTCAGAAA	480
	AGTCAAAGCC TCTGTGGACA TGTGTGATCA GCTTTTGCAA GCAGGAACCA CTGTGTCTCT	540
10	TGAAACAACA AATAGTCTCT TGGATTTWTT GTGTTACTAT GGTGACCAGG AGCCCTCAAC	600
	TGATTACCAT TTTCAACAAA CTGGACAGTC AGAAGCATTG GAAGAGGAAA ATGATGAGAC	660
	ATCTAGGAGG AAAGCTGGTC ATCAGTTTGG AGTTACATGG CGAGCAAAAA ACAACGCTGA	720
15	GAGAATCTTT TCTCTAATGC CAGAGAAAAA TGAACATTCC TATTGCACAA TGATCCGAGG	780
	AATGGTGAAG CACCGAGCTT ATGAGCAGGC ATTAACTTG TACACTGAGT TACTAAACAA	840
20	CAGACTCCAT GCTGATGTAT ACACATTTAA TGCATTGATT GAAGCAACAG TATGTGCGAT	900
	AAATGAGAAA TTTGAGGAAA AATGGAGTAA AATACTGGAG CTGCTAAGAC ACATGGTTGC	960
	ACAGAAGGTG AAACCAAATC TTCAGACTTT TAATACCATT CTGAAATGTC TCCGAAGATT	1020
25	TCATGTGTTT GCAAGATCGC CAGCCTTACA GGTTTTACGT GAAATGAAAG CCATTGGAAT	1080
	AGAACCCTCG CTTGCAACAT ATCACCATAT TATTCGCCTG TTTGATCAAC CTGGAGACCC	1140
30	TTTAAAGAGA TCATCCTTCA TCATTTATGA TATAATGAAT GAATTAATGG GAAAGAGATT	1200
	TTCTCCAAAG GACCCCGATG ATGATAAGTT TTTTCAGTCA GCCATGAGCA TATGCTCATC	1260
	TCTCAGAGAT CTAGAACTTG CCTACCAAGT ACATGGCCTT TTAAAAACCG GAGACAACCTG	1320
35	GAAATTCATT GGACCTGATC AACATCGTAA TTTCTATTAT TCCAAGTTCT TCGATTGAT	1380
	TTGTCTAATG GAACAAATTG ATGTTACCTT GAAGTGGTAT GAGGACCTGA TACCTTCAGC	1440
40	CTACTTTCCC CACTCCCAA CAATGATACA TCTTCTCCAA GCATGGATG TGGCCAATCG	1500
	GCTAGAAGTG ATTCCTAAAA TTTGGAAAGA TAGTAAAGAA TATGGTCATA CTTTCCGCAG	1560
	TGACCTGAGA GAAGAGATCC TGATGCTCAT GGCAAGGGAC AAGCACCCAC CAGAGCTTCA	1620
45	GGTGGCATTT GCTGACTGTG CTGCTGATAT CAAATCTGCG TATGAAAGCC AACCCATCAG	1680
	ACAGACTGCT CAGGATTGGC CAGCCACCTC TCTCACTGT ATAGCTATCC TCTTTTAAAG	1740
50	GGCTGGGAGA ACTCAGGAAG CCTGGAAAAT GTTGGGGCTT TTCAGGAAGC ATAATAAGAT	1800
	TCCTAGAAGT GAGTTGCTGA ATGAGCTTAT GGACAGTGCA AAAGTGCTTA ACAGCCCTTC	1860
	CCAGGCCATT GAAGTAGTAG AGCTGGCAAG TGCCTTCAGC TTACCTATTT GTGAGGGCCT	1920
55	CACCCAGAGA GTAATGAGTG ATTTTGCAAT CAACCAGGAA CAAAAGGAAG CCCTAAGTAA	1980
	TCTAACTGCA TTGACCAGTG ACAGTGATAC TGACAGCAGC AGTGACAGCG ACAGTGAÇAC	2040
60	CAGTGAAGGC AAATGAAAGT GGAGATTCAG GAGCAGCAAT GGTCTCACCA TAGCTGCTGG	2100

	AATCACACCT GAGAACTGAG ATATACCAAT ATTTAACATT GTTACAAAGA AGAAAAGATA	2160
	CAGATTTGGT GAATTTGTTA CTGTGAGGTA CAGTCAGTAC ACAGCTGACT TATGTAGATT	2220
5	TAAGCTGCTA ATATGCTACT TAACCATCTA TTAATGCACC ATTAAGGCT TAGCATTTAA	2280
	GTAGCAACAT TCGGTTTTC AGACACATGG TGAGGTCCAT GGCTCTTGTC ATCAGGATAA	2340
10	GCCTGCACAC CTAGAGTGTC GGTGAGCTGA CCTCACGATG CTGTCTCGT GCGATTGCC	2400
	TCTCTGCTG CTGGACTTCT GCCTTTGTTG GCCTGATGTG CTGCTGTGAT GCTGGTCCTT	2460
	CATCTTAGGT GTTCATGCAG TTCTAACACA GTTGGGGTTG GGTCAATAGT TTCCCAATTT	2520
15	CAGGATATTT CGATGTCAGA AATAACGCAT CTTAGGAATG ACTAAACAAG ATAATGGCAG	2580
	TTTAGGCTGC ACAACTGGTA AAATGACTGT AGATAAATGT TGTAAITAGT GTACACGTTT	2640
20	GTATTTTGT TAATATAGCC GCTGCCATAG TTTTCTAACT TGAACAGCCA TGAATGTTTC	2700
	ATGTCTCCCT TTTTTTTTTG TCTATAGCTG TTACCTATTT TAGTGGTTGA AATGAGAGCT	2760
	AGTGATGACA GAAGGATGTG GAATGTCTTC TTGACATCAT TGTGTATTGC TGGTAATCAA	2820
25	GTGCGTAACG ACTACTTCTA GCAGCTCTTA CCACTATGAC TTAAGTGGTC CTGGAAGGCA	2880
	GTAAGTGGAG GTTTCGACGA TTCTGCCTT CATGAGGGCT TCTACCACTG ACCACTTTGC	2940
30	ACGTACCTGG CTCCCAGATT TACTTAGGTA CCCCACGAGT CGTCCACATA AGCAGCTTCA	3000
	TCTTTACCTT GCCAGAGTTG ACAATTATGG GATACTCTAG TCTACTTATA CTTGTGTTCC	3060
	CATCTGTCTG CCATCCTCTG AAGGCCAGGA CCCAGTCATA CATCCTTAGA AACCAAAGTA	3120
35	TGGTTTTGT TTTCTCTGG AATGTCAGGT CTTAAGGCAT TTAATTGAGG GACAAAAAA	3180
	AAAAAAGCC GATATAGTAG CTAGCTACTT AAGCATCCAT GGGTATTGCT CCATATCAAA	3240
40	GCAGATTTGC AGGACAGAAA GAGTAAATTA GCCTTCAGTC TTGGTTTACA GCTTCCAAGG	3300
	AGAGCCTTGG CCACCTGAAA TGTTAACTCG GTCCCTTCCT GTCTCTAGTT CATCAGCACC	3360
	TGCAGATGCC TGA CTCTTGT TAGCCTTACT ATTCAATACA GTCCTTAGAT TCACGGTATG	3420
45	CCTCTTCCTA TCCAGGCACC TATTCTGAAT CACCATGTTG CTCTGCAGCT AGAGTTGATA	3480
	GGAGAAAATC CATTTGGTA GATGGCCTAT GAATTTGTAG TAGACTTTCA AAATGAGTGA	3540
50	TTTGTTAGCT TGGTACTTTT AAGTTGTGG TACAGATCCT CCAAACCCAT ACTCTGAGCA	3600
	ATTAAGTCCC TTGAACATAG AGAAAATTAA GGCCTCACAG GATGAGTCTC CATCTCTGT	3660
	AAATGCTTAT TTTATCATAG TCTTTAGCCN CTACTATGAG TAAAATGTTT TCTTCNGCCG	3720
55	GGTGTGGTGA CTCAC	3735

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1667 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

10 TAGTAATTCA TTAACTCCT CTTACATGAG TAGCGACAAT GAGTCAGATA TCGAAGATGA 60
AGACTTAAAG TTAGAGCTGC GACGACTACG AGATAAACAT CTCAAAGAGA TTCAGGACCT 120
15 GCAGAGTCGC CAGAAGCATG AAATTGAATC TTTGTATACC AAAGTGGGCA AGGTGCCCCC 180
TGCTGTTATT ATTCCCCCAG CTGCTCCCTT TTCAGGGAGA AGACGACGAC CCACTAAAAG 240
CAAAGGCAGC AAATCTAGTC GAAGCAGTTC CTTGGGGAAT AAAAGCCCCC AGCTTTCAGG 300
20 TAACCTGTCT GGTGAGAGTG CAGCTTCAGT CTTGCACCCC CAGCAGACCC TCCACCTCC 360
TGGCAACATC CCAGAGTCCG GGCAGAATCA GCTGTACAG CCCCTTAAGC CATCTCCCTC 420
25 CAGTGACAAC CTCTATTTCAG CCTTCACCAG TGATGGTGCC ATTTTCAGTAC CAAGCCTTTC 480
TGCTCCAGGT CAAGGAACCA GCAGCACAAA CACTGTGGG GCAACAGTGA ACAGCCAAGC 540
CGCCCAAGCT CAGCCTCCTG CCATGACGTC CAGCAGGAAG GGCACATTCA CAGATGACTT 600
30 GCACAAGTIG GTAGACAATT GGGCCCGAGA TGCCATGAAT CTCTCAGGCA GGAGAGGAAG 660
CAAAGGGCAC ATGAATTATG AGGGCCCTGG AATGGCAAGG AAGTCTCTG CACCTGGGCA 720
35 ACTGTGCATC TCCATGACCT CGAACCTGGG TGGCTCTGCC CCCATCTCTG CAGCATCAGC 780
TACCTCTCTA GTTCACTTCA CCAAGTCTAT GTGCCCCCA CAGCAGTATG GCTTTCAGC 840
TACCCCATTT GGCCTCAAT GGAGTGGGAC GGTGGGCCA GCACCACAGC CACTTGGCCA 900
40 GTTCCAACCT GTGGAACTG CCTCCTTGCA GAATTTCAAC ATCAGCAATT TGCAGAAATC 960
CATCAGCAAC CCCCAGGCT CCAACCTGCG GACCACTTAG ACCTAGAGAC ATTAAGTAA 1020
45 TAGATCTGGG GGCAGGAGAT GGAATGCTGA GGGGGTGGT GGGGTGGGA AGTAGCCTAT 1080
ATACTAACTA CTAGTGCTGC ATTAACTGG TTATTCTTG CCAGAGGGA ATGTTTTTAA 1140
TACTGCATTG AGCCCTCAGA ATGGAGAGTC TCCCCGCTC CAGTTATTGG AATGGGAGAG 1200
50 GAAGGAAAGA ACAGCTTTT TGTCAAGGGG CAGCTTCAGA CCATGCTTTC CTGTTTATCT 1260
ATACTCAGTA ATGAGGATGA GGGCTAGGAA AGTCTGTTC ATAAGGAAGC TGGAGAACTC 1320
55 AATGTAAAT CAAACCATC TGAATTTTC AGTGGGTGGA GCTCTTGCTT TTGGTACATG 1380
CCCTGAATCC CTCCTCCCT CAAGAATCCG AACCACAGGA CAAAACAC CTAAGGGCT 1440
CTCTCCTACC CTGCCCTCCT CCTTTTTTT TACCCCTCTC TTTTTATTT TTTCTTGCT 1500
60

	CTTTAGAACC CAGTGAAAAA TACCAGGGTA CTGGGGTGCA ACTCTTCTT ATGATAGGTC	1560
	ATTAGTGCTT TAAGCAAAAG ATATTAGCAG CTTTGACTGC AGCATTAGCA ATTAGGRAAA	1620
5	AAAAAANWA AAAACTCGAG GGGGGGCCG GTTACCCAAT TCGCCCT	1667
10	(2) INFORMATION FOR SEQ ID NO: 31:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 1408 base pairs	
	(B) TYPE: nucleic acid	
15	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:	
20	ATTACACACC TGAGCACTGT GCCTGGCAAG ACCTGTCCTA ATAGATTAGA GAACCACTGA	60
	TAGATGGTCA GCTTCTGTGA GCAGTGAGAA CCCTACATTT CAAATGTGGA TAGCACCTTT	120
	GCGGGGAAAC ATCACTTGGC ACATCTGCAT TCTTTTGTGA CACAGGGTCT CACTCTGTTG	180
25	CCCAGGCTAG AGTGCATGGC ACGATCTTAG CTCACTGCAA CCTCCACCTC CCAAGTTCAA	240
	GCGATTCTTC TGCCTCAGCC TCCTGAGCAG CTGGGATCAC AGACATGCGC TACCATGCCC	300
30	AGCTAATTTT TTGTATTTTT TGTKGTGTTG TTTTGTGTTK TAAGTAGAGA CGGGCTTTCA	360
	CCACGTTGGS CAGGCAGGTC TCGAACTCCT GAMCTCAGGT GATCCACCCA CATCTGCGTT	420
	CCAATATCTT TCTCAACATA ATGATAGCCG TAATTAATAT TTTCCAGTAC ATTTTATGTC	480
35	CTTTACACAC GAGAGTGGTA GACAGACACA AAGCCAGATC TGCTGACTC CAAAGCCCGT	540
	TGTGTCATCAT TCCTTTTACG GTATCCTATA GTGGTATCCT TTACAGAAAG ACAGCTTTTA	600
40	CCCAACAAAG ACTTAACCTC CCAGGATGCC AGAAGGACAA AGCGGATGTC CTTTAAAGRA	660
	GRAAGTTATC AAGAMCTTAT TTTATAAATG AGATTAGATA GGGAAAGGCA ATTTATCTTT	720
	ATTAAAACT GAAAAGGCCA GCATAGGGAA GGAGGTCCTT CGGTGGTCTT TTTCAGGGAA	780
45	ATACTTCAGT TGCTTTTATT AGAAACAGAT AGTACCTAAG GTTTTGAGGT AGGWACAGCT	840
	TAAGGCATGC TAATGKTCAT GGGTCCTTCC ATAGTCATTT TKGATATTTG GTTWACATTT	900
50	GAGCAATAGG CAGCCCTTCA CTGCTGCTGG AYTCAATCCT GCCAYTATTA CAGGTGACAG	960
	AGGAGACAGG AGGTATGTCT TTTCTATTTT TAWACATGCT TTATATTTAA CACAAGCTCT	1020
	TGGGTATCTT AGATAAACAG AAGTTGCCTA GCACTCCTTT TAGTGCAATTG AACCTTTTAA	1080
55	CATTTAAGCA AAATAATAAA CAGTCTTTTG AGGTTCTTA ACAATGAAAC GTGTTGAGT	1140
	GGCAGCAGCG GAATCCATGC YCTTCTCCT GGAGTGTGCA AKAGTCCGTG GTCCTGAGTA	1200
60	TCTCACACAG ATGTGGCATT TTATGTGTGA TGCTCTAATT AAGGCCATTG GTACAGAACC	1260

AGATTGAGAC GTCTCTCAG AATAATGCA TTCTTTTGCA AAGGTGAATA TTTTCTCTT 1320
 AAAAAATATG TATPAGGTGG TATGTTCAAT TATTAGTCTT GCTAAAAAAA AAAAAAAAAA 1380
 5 ACTTGAGGGG GGGGNCGGT ACCCAATT 1408

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(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 2031 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

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AGGATATGCA TGATTCTTAA CCAGGCTATA TGTAAAAAA AAATTGGAAT ATGCAATACA 60
 TTTTATTATA TACAARCTAC AGAATGAGTA TGCAAGTTT ATTTATCAAA ATGTAATGGA 120
 25 TTTTAAAGG CTGAGAAAT TTCTTATAC CTACCTTTC AGTTATTTA ATTATACCAA 180
 ATTATCAACT AGAATAGCTT CATCCATATG AAATATAAAA TGAAGAGACA CCTAGGCTCT 240
 ATCAGGCTTA GGATTCTTTG AACTTATTT CACTTTAATT TCTCAGTGA AGTTAAGAGG 300
 30 GGTGAGAAAA CAAAGAGGG GAAAACTGA CAACTAACAA AACCAGCACC ACATCGCTAG 360
 GTGGTGCTTA CTAAATACCT TCTCAGGATT TTCTCAGAT TGAAAAGCTT ATGAGGATTT 420
 35 CTGCGGACTC TTAATAACCT GCCTGTTAGT ACAGAGCTTT CCTGATGATA TTTACTCTTG 480
 AGCATATGTG GTTGTAACAC CTTAACTTTC TTTCTCCAGG AGGTGGTGA TAGAAACAGA 540
 TGGTAGTATT TATGAACCTG TGTCTCGTG AAATGTTGAG GGTGGGGAGA AAAGACTTTA 600
 40 AGGGAGGAGA GCCATCTATT TTGTTCTTAA AGCCACCTCT CAGCAGAATC GTCATGTTTT 660
 TCTGATGCAC CCCTCTCTTT CATGCCAAG ATGACTTGCG AGGCAATCTC AGGAGCTGTG 720
 45 GACTTAACCR TTGCAAAGCA CACTGTCTTT CTCAGCGTTC TCTGCAAGTC AGTAGGTGTT 780
 AGTATGGTTG CAAAGTTCAC TGTCTCAGCA AAGTTGAACT GGGCTACCTC TCTACAGCTG 840
 TTTCTCTAGA GGGAAAAATC TTGAGACCAG ATGGTGGAGC TCTGGAGTCA GAGGAAATGG 900
 50 GTGTCTTCAG CACAAAGCTG CTGCTTTTAC TTCAGCCACT TCTGACATTT TTACATACCG 960
 AGCCTGAGAT TRGTGATTA TCTCAATCA AATCACTTTG ATGGAGATAA ATAATCAAAA 1020
 55 CTGTTTATA GTCAATTGATT TGGTGAGAAC AGTAATGGAA AATGGTGTG AAGGACTTCT 1080
 CATTTTGGGA GCTTTCTTC CAGAGTCTTG GCTGATTGGT GTTCGCTGTT CATCTGAGCC 1140
 60 CCAAAAAGCA TTATTACTGA TACTTGACA CAGTCAAAAG CGCAGACTGG ATGGATGGTC 1200

TTTTATAAGG CATTTAAGGG TACACTACTG TGTTCACCTG ACCATACATT TTTCTTAGCC 1260
 CCTCAAGTAA TATAGCACAG AGTTATGAAT GACAATTCCC CTAACCATTC CTCTTCATAT 1320
 5 CTGCCTCTTC CCCTTACCAT CGTAATTCTC CAACTGGTC ATAAAGGCAC TCTGTGAAGA 1380
 TATTGGGGAC TGACATCTTA AGCTCTCACC TGGCTGCAGT AGGAAAGGCC AACTGACGA 1440
 CAAAAAAAAA ATTCTTTATA AAGATGATAT GGTAACATGT ATCTTTGCCC TGGGTCTGGG 1500
 10 TGGGTCCAGT CAGTCTCAGA TTTACAAGCA TTTAGGAGCC TAGGTAAAAG CTGCTAGTAT 1560
 TCTTTTAAAA GTTACATTTA TGACTTGCAA TGATAGAAAA CTCCTTCCAA TTAAATGGCA 1620
 15 TTTTATAATA TTATGTGTGT ACTTCACAGT GTTAAAAATA CCCTCATACG TTATTGCATT 1680
 TGATCTTCAC AGAAAGTGCA TTTTAACCAG TACTCTGGGT GCAATAAATA ATATGTAGAA 1740
 ATTTAAGTCC TCCAATTCCA GCATATCCAG TGAGTTTGA CAGTGTGTTT ATGTGGAATG 1800
 20 TTTAAGGATA TACAATTGTA CTTTATATAA ATTGGTCTT GTTCTTCTTA AATGTGACAT 1860
 GAAATAATTG TGCTGCTACA TTATACTGGA AATTAACAGG GGAAAAGGGA AGAGCTCTTG 1920
 25 GCTCCCTTGA GGTCTGCTA GTGGTGTAG GAGTGGTAC AACTGAGCTT TTAGTAACCA 1980
 TTTAACCGTA TGTAAGTGT GTTTCTAATT AAAAAAAAAAT TTCTTTTCC A 2031

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(2) INFORMATION FOR SEQ ID NO: 33:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 971 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

CGCGTCGGAA CTCGGCCGCG GGACATCCAC GGGGCGCGAG TGACACGCGG GAGGGAGAGC 60
 AGTGTCTGCG TGGAGCCGAT GCCAAAAACC ATGCATTTCT TATTCAGATT CATTGTTTTC 120
 45 TTTTATCTGT GGGGCCCTTT TACTGCTCAG AGACAAAAGA AAGAGGAGAG CACCGAAGAA 180
 GTGAAATAG AAGTTTGTGA TCGTCCAGAA AACTGCTCTA AGACAAGCAA GAAGGGAGAC 240
 50 CTACTAAATG CCCATTATGA CGGCTACCTG GCTAAAGACG GCTCGAAATT CTACTGCAGC 300
 CGGACACAAA ATGAAGGCCA CCCCAAATGG TTTGTTCTTG GTGTTGGGCA AGTCATAAAA 360
 GGCCTAGACA TTGCTATGAC AGATATGTGC CCTGGAGAAA AGCGAAAAGT AGTTATACCC 420
 55 CCTTCATTTG CATACGGAAA GGAAGGCTAT GCAGAAGGCA AGATTCCACC GGATGCTACA 480
 TTGATTTTTG AGATTGAACT TTATGCTGTG ACCAAAGGAC CACGGAGCAT TGAGACATTT 540
 60 AAACAAATAG ACATGGACAA TGACAGGCAG CTCTCTAAAG CCGAGATAAA CCTCTACTTG 600

CAAAGGGAAT TTGAAAAAGA TGAGAAGCCA CGTGACAAGT CATATCAGGA TGCAGTTTTA 660
GAAGATATTT TTAAGAAGAA TGACCATGAT GGTGATGGCT TCATTTCTCC CAAGGAATAC 720
5 AATGTATACC AACACGATGA ACTATAGCAT ATTTGTATTT CTACTTTTTT TTTTGTAGCTA 780
TTTACTGTAC TTTATGTATA AAACAAAGTC ACTTTTCTCC AAGTTGTATT TGCTATTTTT 840
10 CCCCTATGAG AAGATATTTT GATCTCCCA ATACATTGAT TTTGGTATAA TAAATGTGAG 900
GCTGTTTTGC AAACCTAAAA AAAAAWWAAA AAAACTSGAG GGGGGCCCGT ACCCAANTCG 960
COGNATATGA T 971
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20 (2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1792 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:
GAACCCCTT TCTCCTGGTA AAGGGTAAGG GGGGGGATAA TGTTTACCAC AGGTACGAAA 60
30 TAGTCACTTT AACATTGAGA CCTCTGCCTC ATTGAATTCA GGTTTTTTAA GTACTTGAAA 120
CTCTTCAGAT TCTCCTTATT TTAGTTTCTT TTTACATTTA TGAAGTAGAA AGCATTGTTT 180
35 TGAAACTGT TTTGAAAATA AATAGCCTAG TCTCTTATCC TCTTTAGCGT GGATTAAAGG 240
TGAAGTTCTG CAAATGGGAG AGTGTTTACA GTAGATAGCT CAGATTGATT GAACACATTT 300
GAGGAAGAGA CTCCTGCATG AGATACCAGC ATTTTACAA ATACTTTTAA TGTACATTCT 360
40 TTATTTTGTG ATTTTGTCAA CCCTCTCCCC AAGCACATCT TCTTTCCTTT TACTATGTCT 420
ATGTAGGGAA AAACAAAACA AAAAATTGCA CTTACGTTAC ACTCCCAAAA TGTGGGTAAT 480
45 CCGTGTCTTT CAAAAACAT TTCTGTTTTT TGTTTTGT TTGGTCAGTCC ATTGCATAAG 540
TGACAAGTTT GGTGCTTGT GGCACGTATG TATGAAGCGG GAGGGGGATG ASAATTGCCT 600
GTCCCTCAGT ARGCTGTAAA AGTAATTAC ATGTAAGTAA AAAGGGAAAA TAGAATAGAT 660
50 GCCAAAGTCA TTTATTCAGT CCTTAGTTTT CTTATGTGGC ATTACTGCAT CTGCTAGTTA 720
GTGAGAAAGC ACCCTCAGCT TTTACTGCTC CCCTCCCTGC CTGCCAACAC ACTTGATGTG 780
55 TGCAACAGC CCTCAAGTAT CTGTGATG ACCTATATAA GGTATTGAAT AAGGTATTCT 840
TGTCAGTTTA GAAATGGACT GGATAAACT TACTTGGTTG TCATTATTTT ATCTCATTTG 900
TCCTGTTACA TGCCCTATGT TAAGATAATT ATATTGCCAC TAATAATCAA GATGCTAAAT 960
60

GAGTATTACA ACTGGCTAAT ATCATTTTTT ATATACAAGG GTATGTGTAT ATTTGGAATT 1020
 GRTATGAGAA ACTCATTTGT ACCCATTTGA GTGATATTGC ACAACAAACA CAGATAYCTA 1080
 5 CAGACTCCGT TTTCATTTTC TCGTGTCTT TATGATAATG ATCTTTGTAG ATTGGTTATT 1140
 TCTGTACTTT ATCTGTAATA AACTTTGTAG ATCCTGTGAA CCATTACTTT GCCTAAATCA 1200
 CTTGAGACTT GAGTCTTTAA TAACAAAGCA TCAATATTCA CTAAAGTCAA TCTCTTTTGA 1260
 10 GTTCTGTGA CTTGGCTAGA AGCTCTTGAC ACTAAGGGAT TAGTGTTAAT TTTCCCTGGG 1320
 GGTGTCCAC TAGGGCATT CTGTATAATG ACTTGATGTT GCCACATAGA CTTCAAGATA 1380
 15 TATAATATTT TGAGGATTTT GTTGATTGGC CTATGTTTTA TTGCATAGTG TGAAACGTGT 1440
 AAAGCTTGGT TAACCTGTAT ATAGATAGCT TATTGTTGAC TAGTTATAGT GTATTTAGGG 1500
 TTGCCTGTAA TATTTAAGCT TCTTTACTGA TGTGTGTGCT GGTAGGAACA TATAATTTTT 1560
 20 GTACATTATA TTTACTGAGA TGTGCTTTT TTTATTTTAC AAATACTTTG GAATTCCAAT 1620
 GTGTTTTTTG CTTCCGTGAG GATTAAATTG GAAAGTTTT TAATGACATT CCACTGATT 1680
 25 CAGATTTTGC TTGAGATTGA CTTCAATAAA TTGTCCTGTA TGTTCAAAA AAAAATTAAA 1740
 AACTCGAGG GGGGCCCGGT ACCCAANNCG CCGGATATGA TCGTAAACAA TC 1792

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(2) INFORMATION FOR SEQ ID NO: 35:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 896 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

AGTTGNANAC AACAGGACCT GAGTCCTTGG GCAGCACCAG TAGGTTGCCC CYTGCYTCYT 60
 GCCAGCYTCA CYTGCCACYT TYTGCCCTY TCGGGATGCC TTGCAGACA GAGYTYTTTCG 120
 45 CTGCCGTGG TGGCCAYTCT TTGCTTTGG TTYTCTTGCC CCTTGGCCTC CCTTTTGTGTC 180
 CCCGGGCAGC CTGTGTGTAC CTGCCCTTTT CCTCCCTTC CTTTCCAGGA CAAGCACGCC 240
 50 GAGGAGGTGC GGAAAAACAA GGAGCTGAAG GAAGAGGCCT CCAGGTAAAG CCTAGAGGCC 300
 AAAGAACTTT CCAGGTCAGC CGACAGCTC CAGCAGCTCC ACGTTCCAGG CAGCCTCGMC 360
 CGCCGGCTGC GCTCCAGCA CTGGGTTTG GGGGAGGGG GGTGGCCAAG GGGCGTTTCC 420
 55 TCTGCTTTTG GTGTTGTAC ATGTTAAGAA TTGACCAGTG AAGCCATCCT ATTGTTTCC 480
 GGGGAACAAT GACGGGTGG GARAGGGAG AGGAGAGAGT TTGGGAAAG GAGATGGAGA 540
 60 AGAACTCAAG GACATTGCAA CCTGCCCGG CGCAGATCTG ATTTTCACAT CTCTACCTGG 600

ACATTGAGCC TCCCAGGCAC CATGTTGAGG AGAGATGAAA ACCAGGGCGG TAGAACTTCA 660
GGGTGAAGGA CAGAGTCCTG GGTGGGGCAG CGGCTGCAGG GCGCACCAGA GAACCCAGCC 720
5 AGAGGGGGTG TGAGTACCAG TGGTGTGCT TCCACCCTGC AGCAGGTGGG ATGAGGTCTG 780
TGTGTGTGTG TGAACCATCA TTTTGTGATC ATCATGACCA ATGAAACATT GAAAAAAAAA 840
10 AAAAAAATG GAGGGGGGCC CGTACCCAAN TCGCCGNATA GTGATCGTAA ACAATC 896

15 (2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 912 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

25 TCGACCCACG CGTCCGGTCA GCCAGTCGCA TCCAGCCATG ACAGCCTTCT GCTCCCTGCT 60
CCTGCAAGCG CAGAGCCTCC TACCCAGGAC CATGGCAGCC CCCCAGGACA GCCTCAGACC 120
AGGGGAGGAA GACGAAGGGA TGCAGCTGCT ACAGACAAAG GACTCCATGG CCAAGGGAGC 180
30 TAGGCCCGGG GCCAKCCGCG GCAGGGCTCG CTGGGGTCTG GCCTACACGC TGCTGCACAA 240
CCCAACCCTG CAGGTCTTCC GCAAGACGGC CCTGTTGGGT GCCAATGGTG CCCAGCCCTG 300
35 ARGGCAGGGA AKGTCAACCC ACCTGCCCAT CTGTGCTGAG GCATGTTCTT GCCTACCATC 360
CTCCTCCCTC CCCGGCTCTC CTCQCAGCAT CACACCAGCC ATGCAGCCAG CAGGTCTCTC 420
GGATCACYGT GGTTKGGTGG AGGTCTGTCT GCACTGGGAG CCTCARGARG GCTCTGCTCC 480
40 ACCCACTTGG CTATGGGAGA GCCAGCAGG GTTCTGGAGA AAAAAACTGG TGGGTTAGGG 540
CCTTGGTCCA GGAGCCAGTT GAGCCAGGGC AGCCACATCC AGGCGTCTCC CTACCCTGGC 600
45 TCTGCCATCA GCCTTGAAGG GCCTCGATGA AGCCTTCTCT GGAACCACTC CAGCCCAGCT 660
CCACCTCAGC CTTGGCCTTC ACGCTGTGGA AGCAGCCAAG GCACTTCCTC ACCCCYTCAG 720
CGCCACGGAC CTYTYTGGGG AGTGGCCGGA AAGCTCCCSG GCCTYTGGCC TGCAGGGCAG 780
50 CCCAAGTCAT GACTCAGACC AGGTCCCACA CTGAGCTGCC CACTCTCGAG AGCCAGATAT 840
TTTTGTAGTT TTTATKCCTT TGGCTATTAT GAAAGAGGTT AGTGTGTTCC CTGCAATAAA 900
55 CTTGTTCTCTG AG 912

60 (2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1382 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

10 AATTCGGCAC GAGCGGAGGC GAGGGAAACT RAGGGCGAAA GTTGTGTGTC GTGTTGGCAG 60
GAGGGCCTAG AAGGGAAAGA CTGTCTAGTG GGACAAATGTC ATATTATAAA TTTGGAATGC 120
TGAATAGAAA ATTATAGATT TTGATATTGA AGGAAATGAA GCGAAGCYTA AATGAAAATT 180
15 CAGCTCGAAG TACAGCAGGC TGTTCGCTG TTCCGTGTGT CAATCAGAAA AAGAGGAACA 240
GACAGCCATT AACTTCTAAT CCACTTAAAG ATGATTCAGG TATCAGTACC CCTTCTGACA 300
20 ATTATGATTT TCCTCCTCTA CCTACAGATT GGGCCTGGGA AGCTGTGAAT CCAGAGTTKG 360
CTCCTGTAAT GAAAACAGTG GACACCGGGC AAATACCACA TTCAGTTTCT CGTCCTCTGA 420
GAAGTCAAGA TTCTGTCTTT AACTCTATTC AATCAAATAC TGGAAGAAGC CAGGGTGGTT 480
25 GGAGCTACAG AGATGGTAAC AAAAATACCA GCTTGAAAAC TTGGRATAAA AATGATTTTA 540
AGCCTCAATG TAAACGAACA AACTTAGTGG CAAATGATGG AAAAAATTCT TGTCCAATGA 600
30 GTTCGGGAGC TCAACAACAA AAACAATTAA GAACACCTGA ACCTCCTAAC TTATCTCGCA 660
ACAAAGAAAC CGAGCTACTC AGACAAACAC ATTCATCAAA AATATCTGGC TGCACAATGA 720
GAGGGCTAGA CAAAACAGT GCACTACAGA CACTTAAGCC CAATTTTCAA CAAATCAAT 780
35 ATAAGANACA AATGTTGGAT GATATTCCAG AAGACAACAC CCTGAAGGAA ACCTCATTGT 840
ATCAGTTACA GTTTAAGGAA AAAGCTAGTT CTTTAAGAAT TATTTCTGCA GTTATTGAAA 900
40 GCATGAAGTA TTGGCGTGAA CATGCACAGA AACTGTACT TCTTTTGTAA GTATTAGCTG 960
TTCTTGATTC AGCTGTTACA CCTGGCCCAT ATTATTGAA GACTTTTCTT ATGAGGGATG 1020
GGAAAAATAC TCTGCCTTGT GTCTTTTATG AAATCGATCG TGAACCTCCG AGACTGATTA 1080
45 GAGGCCGAGT TCATAGATGT GTTGCAACT ATGACCAGAA AAAGAACATT TTCCAATGTG 1140
TTTCTGTCAG ACCGGCGTCT GTTCTGAGC AAAAACTTT CCAGGCATTT GTCAAAATTG 1200
50 CAGATGTTGA GATGCAGTAT TATATTAATG TGATGAATGA AACTTAAGTA GTGATAAAAG 1260
GAAGTTTAGC ATAAATTATA GCAGTTTCTT GTTATTGCTT AATTACCAT CTCCATAGTT 1320
TTATAGCTAC TATTGTATTT CACTTGTTGA ATTAAAGTAT TTGAATCTT TAAAAAATA 1380
55 AA 1382

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 872 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

10 GGGCTACTTC AAAGCCCTGG GCCTTATTTT TTCAGGTAAA AAAATATAAA GTCAGATCTC 60
ATCCCGGCTG GCCATGCTGT TAGACCCTTT CATCCTTCTC TTCTGCCTCT TCTCAACAGC 120
15 TGCCCACTCC TGTTTGAAT TCATATACAT ACAGTTCTAA TACTGATGTA TTTACCCTCA 180
TAAGCCACTC AACCCAGAAT CTTATTTGAA TTATAATCCA GAAACATCAG GTGACGTGTG 240
AGACTACTGT ATGAGAAAGA GACAGTTTAA GGGTCAGTCC AATGGAAAAA AGAGTTCTCA 300
20 GAGCTTTCTT TAGCTTATTC TCATCAAAGA GCTTTCTCTG CAGAAGGAAC CTACTGGTTC 360
CTCCTTTCCA GTCCTAGAAA TCCTGACCTA GAGTGGCTTA ATCCTGCTAG CACCTCTCTC 420
25 TCGCACTCTG GTGCCAAATG ACTCCAGGAA CTGGGCCATG ATGTGGTGGG AATGACCTTA 480
CCCTGAGCAT GTCATCATG CATTGAACAA CAGCTAAGAG CAGAGCTTAG AGCTTAGAGC 540
TGGGCCCTGT AAGGTGAGAG GAATCACATC CTCGAGAAGT CTGTCCTGAG AAGCAGGTAC 600
30 TCCTGTCA CA GCAGAGACAC AGTGATACC TGAGTAACAA TAATACAAGA CAGGACGTGG 660
GMACAGCAA AGATTTGGGT GTCAGAAGAR GCCGAGAACA CTTYCAGGCA GGAACATTCA 720
35 RARITGTTCT TGGAGGAART AGGCMCSAAG GCTGGGCAGG ATTCMCGGG GCAGAGATGG 780
AGCAAGCAAT TGAAATGAAA GCCATGGCAT GGGAAAAGGA GCACTGGCCA CAGGGAGTGC 840
AACGTGTGA TGCAAGGCCA CTGTGGAGCC AT 872
40

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 812 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

55 GGCAGAGGCT CACCCAGCA GAGATTGAGG GGAACCGTG ATGAAATTTT TAAGTATTCT 60
GCTTGATGAT AATAATTTT CTCTATGTT AATGTTGGCT CCGTTGGGT GTTTAGCTTT 120
TGAAAGGAGT ATGAAATGC GGAATGGGC TTTGGGCTT GAGGAGGTGT GATCTCTAGT 180
60 GTTTAAAAA TTTAATTGCA CAAATAGAAA TAATCACCC ACATTATTGA ACCCCACTAA 240

AGCATATCCT TTTTGTCCAT ATTCTTTTCC TGCTGCCCTC GTGTGTACCA TTATTACTCA 300
 GTTGTGATTT GAGCTCGTTC CACTTAAAGT CATTCATAGA TACTTTTGCG TCGTGTTKGA 360
 5 ATATTATTG AATTCTTATT CTGTGTTTTA CTTAATTACT TTATTATGGA ACCTTTACAC 420
 AGGTCTGGTG TACTTGTCTT TTGAAAAGTC TTATGTTGAC CACCATCACT GAGCATATAG 480
 10 CTTTTTCCTT ATTTCTTGG GATAATTACC CGAAGTGGAA ATACCGAATC AAACCTCTGT 540
 TTTCTTTCTT TGGCACTATT ATATAAATTG TTTTCCAAAC AAGGCATGTT TACAATAGAC 600
 ATTTTTCAAA ATCTGGGTAT TTGTCCTATT TTGCTCTCTG TATGCAGAAT TCAGCGGGGT 660
 15 GCCAAGTCGT TTTCTGTGTG GGTGAGAGA CAGGCTGTGC AGCCCACTGT TGCATAGGAC 720
 TAACTACTAC AAATCATGCT GAGACCGAGC TATTTTGTCT GCTTAGARGC TTTGCAGCCT 780
 20 TGAGTAAGTT TCGNCATCTG GAAACNTTGN AA 812

25 (2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1515 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

35 AATTCGGCAC GAGGGAAATT CAAGCACTTT TCCTAAAAGA AGGGGGAATG GATGCTGAAA 60
 CAACACGTNT CCCACAAAGG GAGCAGACAC TGGGCTGTG AAGCTGCCCC ATACCTTCCC 120
 CACAGAACTG GGGTCCGGCC TCCCTGACAT GCAGATTTC ACCCAGAAGA CAGAGAAGGA 180
 40 GCCAGTGGTC ATGGAATGGG CTGGGGTCAA AGACTGGGTG CCTGGGAGCT GAGGCAGCCA 240
 CCGTTTCAGC CTGGCCAGCC CTCTGGACCC CGAGGTTGGA CCCTACTGTG ACACACCTAC 300
 45 CATGCGGACA CTCTCAACC TCCTCTGGCT TGCCCTGGCC TGCAGCCCTG TTCACACTAC 360
 CCTGTCAAAG TCAGATGCCA AAAAAGCCGC CTCAAAGACG CTGCTGGAGA AGAGTCAGTT 420
 TTCAGATAAG CCGGTGCAAG ACCGGGGTTT GGTGGTGACG GACCTCAAAG CTGAGAGTGT 480
 50 GGTCTCTGAG CATCGCAGCT ACTGCTCGGC AAAGGCCCGG GACAGACACT TTGCTGGGGA 540
 TGTACTGGGC TATGTCACTC CATGGAACAG CCATGGCTAC GATGTCACCA AGGTCTTTGG 600
 55 GAGCAAGTTC ACACAGATCT CACCCGTCTG GCTGCAGCTG AAGAGACGTG GCCGTGAGAT 660
 GTTTGAGGTC ACGGGCCTCC ACGACGTGGA CCAAGGGTGG ATGCGAGCTG TCAGGAAGCA 720
 TGCCAAGGGC CTGCACATAG TGCCTCGGCT CCTGTTTGTG GACTGGACTT ACGATGATTT 780
 60

300

CCGGAACGTC TTAGACAGTG AGGATGAGAT AGAGGAGCTG AGCAAGACCG TGGTCCAGGT 840
 GGCAAAGAAC CAGCATTTTCG ATGGCTTCGT GGTGGAGGTC TGGAACCAGC TGCTAAGCCA 900
 5 GAAGCGCGTG ACCGACCAGC TGGGCATGTT CACGCACAAG GAGTTTGAGC AGCTGGCCCC 960
 CGTGCTGGAT GGTTCAGCC TCATGACCTA CGACTACTCT ACAGCGCATC AGCCTGGCCC 1020
 TAATGCACCC CTGTCCTGGG TTCGAGCCTG CGTCCAGGTC CTGGACCCGA AGTCCAAGTG 1080
 10 GCGAAGCAAA ATCCTCCTGG GGCTCAACTT CTATGGTATG GACTACGCGA CCTCCAAGGA 1140
 TGCCCGTGAG CCTGTTGTG GGGCCAGGTA CATCCAGACA CTGAAGGACC ACAGGCCCCG 1200
 15 GATGGTGTGG GACAGCCAGG YCTCAGAGCA CTTCTTCGAG TACAAGAAGA GCCGCAGTGG 1260
 GAGGCACGTC GTCCTCTACC CAACCCTGAA GTCCCTGCAG GTGCGGCTGG AGCTGGCCCCG 1320
 GGAGCTGGGC GTTGGGGTCT CTATCTGGGA GCTGGGCCAG GGCCTGGACT ACTTCTACGA 1380
 20 CCGTCTCTAG GTGGGCATG CGGCCTCCGC GGTGGACGTG TTCTTTTCTA AGCCATGGAG 1440
 TGAGTGAGCA GGTGTGAAAT ACAGGCCTTC ACTCCGTTAA AAAAAAAAAA AAAAAAAAAA 1500
 25 AAAAAAAAAA AAAAA 1515

30 (2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 704 base pairs

(B) TYPE: nucleic acid

35 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

40 AAGATGGTGG CGCCAGAGC TTCGCTCTAT GCTGCTCCCC TGAGAGAGGC GTTTCATCA 60
 ACCAGTTTTC CAAGGAGTTC AATGAGAGGA CAAAGGACAT CAAGGAAGGC ATTCCTCTGC 120
 CTACCAAGAT TTTAGTGAAG CCTGACAGGA CATTTGAAAT TAAGATTGGA CAGCCCACTG 180
 45 TTTCTACTT CCTGAAGGCA GCAGCTGGGA TTGAAAAGGG GGGCCGGCAA ACAGGGAAAG 240
 AGGTGGCAGG CCTGGTGACC TTGAAGCATG TGTATGAGAT TGCCCGCATC AAAGCTCAGG 300
 50 ATGAGGCATT TGCCCTGCAG GATGTACCCC TGTGCTCTGT TGTCCGCTCC ATCATCGGGT 360
 CTGCCCGTTC TCTGGGCATT CGCGTGGTGA AGGACCTCAG TTCAGAAGAG CTTGCAGCTT 420
 TCCAGAAGGA ACGAGCCATC TTCCTGGCTG CTCAGAAGGA GGCAGATTTC GCTGCCCAAG 480
 55 AAGAAGCTGC CAAGAAGTGA CCCTTGCCCC ACCAACTCCC AGATTTCAAA GGAGGTAGTT 540
 GCAAAGCTG TGCCCAAGGG GAGGAAGGAG GTCACACCAA TATGATGATG GTTTTCATGA 600
 60 CTTTGAATGA TATATTTTTC TACATCTAGC TGTATCGAGG CATCAGGCCT GAATAACAT 660

CCTTTCTTAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAA

704

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(2) INFORMATION FOR SEQ ID NO: 42:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1094 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

GGCAGCTTTC TTACAAACCC ATCCTTCTGA AATGTTGCTT CAAATTCATC CTCTGCTCCC	60
CAGTCCCACCT ATTCCACACA TACTGTTACT GTTCTTTTAT CCTACTTTCT CAATTTTGGG	120
ACATAGTTGC AGTTACTGCA TTGAATACCT GTGGGTTTGC CTGTTGTTCT GTCTGTCTCT	180
GTGGTTCTTG TAATANITGA TCCAGAGAT AAAATGGACA GTGTGNATGC ACAGTTAATT	240
CAGAACTAG ACCTTACTTG CTGTGTGAAA TACCAACTAA ATTCTCAGTG AACTCAGCTG	300
ANCTTTATCT CCTTTTGTTC CCCCAATTTA TAATTTTCAGT TCAGGCCAG AAAGATGGAA	360
TCCAGCTAA GAAATACAAG TTACACCTG TACTAGCAGC CCATGTGTGC ATGTTCTTTA	420
AGTGCTCTTG CAGCTATGTC ATTTATATTG ATTTCCCTGT ATTATTATAA GCAAAGCAAA	480
TTTGAGGAAA AAAACCCATA ATACCACACC TCATTTTTTT CAAGTAATAG GGTGATAAGT	540
CTCATYCTYC ATATAATATG TTGAGTATGC AGTATATTAT GTGTTAGGCT CTGGANAGGC	600
AGAGGTTAGA TCATGTWACA GATCATATCK GATTAGGCAG ATAAACAGTA TTTTAACCTT	660
TTCTTTATTA TATGTAACCT GCTTTCAGGT TTTTAAATGT TACTATTATG TCTTTAATAT	720
ATTATCTTTA TTTGTACTTT TGTATACAGA GTGATTTTCC TTTTAAAAA AAAATGTGT	780
CTTTAGGATG GATTCCAAAG ATGTGGAATC AGTAGGTTTA AGGAATATGG ATATTTTGGC	840
TGGCAAGGTG GCTCACACCT GTAATCCCAG CACTTTGGGA GGCTGAGGTG GGTGGATCAC	900
CTGAAGTCAG GAGTTCGAGA CCAGCCTGAC CAACATGGCG AAACCTGTT TTTACTAAAG	960
ACACACWAA AATTGCCCAG TGGTGGTGGC ATGTGCTTGT AGTCCCACCT AGCTACTCGA	1020
GAGGCTGAGG CAGGAGAATC GCTTGAACCC GGGAGGCAGA GGTGTCAGTG AGGCAAGATG	1080
GCACCTCTAC ACTC	1094

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(2) INFORMATION FOR SEQ ID NO: 43:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1321 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

	TGGCTTAGGC CATCACCCCTT CCCTTGGCTG GAACTACTGG ACAGACCCCTT TTGAGATGTG	60
10	CCTGTGGTGC TGTGAGATG TGTGTAGTGG TCTTAGCTCT TTGTTGAGCT TGTGTGTGTG	120
	TTGTGTAGTC TTACTGTAT GCTGAAATTG GCGGTGTGTT GGAGGGCTTC TTAGCTCTTT	180
15	GGTGAGATTG TATTTCTATG TGTGTATATC ASCTGAATGT TGCTGGAAAT AAAACCTTGG	240
	TTTGTAAGG CTCATTTTTC TGGGAAGTAA GTAGGGGAAA AGGTCTTTGA GGGTTCCTAG	300
	GCTCCTTTGT ACAACAGGAA AATGCCTCAA AGCCTTGCTT CCCAGCAACC TGGGGCTGGT	360
20	TCCCACTGCC TGGTCTGCC CCTTCCTGGT TCTTATCTCA AGGCAGAGCT TCTGAATTTT	420
	AGGCCTTCAT TCCAGAGCCC TCTGTGTGCC AGGCCTTCCT TTGCTGGAGG AAGGTACACA	480
25	GGTGAAGCT CATGTGTAC TTGGGGGATC TCCTTGGCCT GTTCCACCAA GTGAGAGAAG	540
	GTACTTACTC TGTACCTCC TGTTCAGCCA GGTGCATTAA CAGACCTCCC TACAGCTGTA	600
	GGACTACTG TCCAGAGCT GAGGCAAGGG GATTTCTCAG GTCATTTGGA GAACAAGTGC	660
30	TTTASTACTA GTTAAAGTA GTAAGTCTA CTGTATTTAG TGGGGTGGAA TTCAGAAGAA	720
	ATTGAAGAC CAGTCATGG GTGTCTGCA TGTGAATGAA CAGGAATGAG CCGACAGCC	780
35	TGGCTGTCT TCTTTCTTC CTCCCCATT GGACCCCTCT CTGCCCTTAC ATTTTGTITT	840
	CTCCATCTAC CACCATCCAC CAGTCTATTT ATTAACCTAG CAAGAGGACA AGTAAAGGGC	900
	CCTCTTGGCT TGATTTTCT TCTTTCTTTC TGTGGAGGAT ATACTAAGTG CGACTTTGCC	960
40	CTATCCTATT TGGAAATCCC TAACAGAAAT GAGTTTCTA TTAAGGATCC AAAAAGAAAA	1020
	ACAAAATGCT AATGAAGCCA TCAGTCAAGG GTCACATGCC AATAAACAAT AAATTTTCCA	1080
45	GAAGAAATGA AATCCAATA GACAAATAA GTAGAGCTTA TGAAATGGTT CAGTAAGGAT	1140
	GAGTTTGTG TTTTGTGTT TGTTTTGMT TGTTTTTTA AAGACGGAGT CTCGCTCTGT	1200
	CACTCAGGCT GGAGTGAGT GGTATGATCT TGGCTCACTG TAACCTCCGC CTCCCGGTT	1260
50	CAAGCCATTC TCCTGCCTCA GTCTCCTGAG TAGCTGGGAT TACAGGTGCG TGCCACCATG	1320
	CCTGGCTAAT TTTGTGTTT TTAGTAGAGA CAGGGTTTCA CCATGTTGGT CGGGCTGGTC	1380
55	TCAAACTCT GACCTCTGA TCCGCCTGCC TTGGCCTCCC AAAGTGATGG GATTACAGAT	1440
	GTGAGCCACC CGTCCCTAG CCAAGGATGA GATTTTAAA GTATGTTTCA GTTCTGTGTC	1500
	ATGGTTGGA GACAGAGTAG GAAGGATATG GAAAAGGTCA TGGGAAGCA GAGGTGATTC	1560
60	ATGGCTCTGT GAATTTGAGG TGAATGTTT CTATTGTCT AGGCCACTTG TGAAGAATAT	1620

5 GAGTCAGTTA TTGCCAGCCT TGAATTTAC TTCTCTAGCT TACAATGGAC CTTTGAAC 1680
GGAAAACACC TTGTCTGCAT TCACTTTAAA ATGTCAAAAC TAATTTTAT AATAAATGTT 1740
TATTTTCACA TTGAAAAAA AAAAAAATT AAAAACYCGG GGGGGGCCCS G/ACCCCAT 1800
NGCCCCTAAG GGGGGGGTT T 1821

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(2) INFORMATION FOR SEQ ID NO: 44:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1024 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

GGGCGACAGT TGAAGAAGCG ACCGAGGGAC TGGGAGTCGT TAGTGAGGAT GACGCGGCAT 60
25 GGCAAGAACT GCACCGCAGG GCCGTCTACA CCTACCACGA GAAGAAGAAG GACACAGCGG 120
CCTCGGGCTA TGGGACCCAG AACATTGAC TGAGCCGGA TGCCGTGAAG GACTTCGACT 180
GCTGTTGTCT CTCCCTGCAG CCTTGCCACG ATCCTGTTGT CACCCAGAT GGCTACCTGT 240
30 ATGAGCGTGA GGCCATCCTG GAGTACATTC TGCACCAGAA GAAGGAGATT GCGCGCAGA 300
TGAAGGCCTA CGAGAAGCAG CGGGGCACCC GCGCGAGGA GCAGAAGGAG CTTGAGCGGG 360
35 CGGCCTCGCA GGACCATGTG CGGGCTTCC TGGAGAAGGA GTCGGCTATC GTGAGCCGGC 420
CCCTCAACCC TTTCACAGCC AAGGCCCTCT CGGGCACCAG CCCAGATGAT GTCCAACCTG 480
GGCCAGTGT GGTCTCTCCA AGTAAGGACA AGGACAAAGT GCTGCCCAGC TTCTGGATCC 540
40 CGTCGCTGAC GCGCAAGCC AAGGCCACCA AGCTGGAGAA GCCGTCCCGC ACGGTGACCT 600
GCCCCATGTC AGGGAAGCCC CTGCGCATGT CGGACCTGAC GCCGTGCAC TTCACACCGC 660
45 TAGACAGCTC CGTGGACCGC GTGGGGCTCA TCACCCGAG CGAGCGCTAC GTGTGTGCCG 720
TGACCCGCGA CAGCCTGAGC AACGCCACCC CTTGCGCTGT GCTGCGGCCC TCTGGGGCTG 780
TGGTCACCCCT CGAATGCGTG GAGAAGCTGA TTCGGAAGGA CATGGTGGAC CCTGTGACTG 840
50 GAGACAACT CACAGACCGC GACATCATCG TGCTGCAGCG GGGCGGTACC GSTTCGCGGG 900
CTCCGGAGTG AAGCTGCAAG CGGAGAAATC ACGGCCGGTG ATGCAGGCCT GAGTGTGTGC 960
55 GGGAGACCAA ATAAACCGC TTGGGTGCGC AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1020
AAAA 1024

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(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 983 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

10 CGACACGGCT GCGAGAAGAC GACAGAAGGG CCCGACCGCG AGCCGTCCAG GTCTCAGTGC 60
TGTGCCCCC CCAGAGCCTA GAGGATGTTT CATGGGATCC CAGCCACGCC GGCATAGGA 120
15 GCCCCTGGGA ACAAGCCGGA GCTGTATGAG GAAGTGAAGT TGTACAAGAA CGCCCGGGAG 180
AGGGAGAAGT ACGACAACAT GGCAGAGCTG TTTGCGGTGG TGAAGACAAT GCAAGCCCTG 240
20 GAGAAGGCCT ACATCAAGGA CTGTGTCTCC CCCAGCGAGT ACACTGCAGC CTGCTCCCGG 300
CTCCTGGTCC AATACAAAGC TGCCTTCAGG CAGTCCAGG GCTCAGAAAT CAGCTCTATT 360
GACGAATTCT GCCGAAGTT CCGCTGGAC TGCCCGCTGG CCATGGAGCG GATCAAGGAG 420
25 GACCGGCCCA TCACCATCAA GGACGACAAG GGCAACCTCA ACCGCTGCAT CGCAGACGTG 480
GTCTCGCTCT TCATCACGGT CATGGACAAG CTGCGCCTGG AGATCCGCGC CATGGATGAG 540
30 ATCCAGCCCG ACCTGCGAGA GCTGATGGAG ACCATGCACC GCATGAGCCA CCTCCCACCC 600
GACTTTGAGG GCCGCCAGAC GGTCAGCCAG TGGCTGCAGA CCCTGAGCGG CATGTCGGCG 660
TCAGATGAGC TGGACGACTC ACAGGTGCGT CAGATGCTGT TCGACCTGGA GTCAGCCTAC 720
35 AACGCCTTCA ACCGCTTCCT GCATGCCTGA GCCCGGGGCA CTAGCCCTTG CACAGAAGGG 780
CAGAGTCTGA GCGATGGCT CCTGGTCCCC TGTCCGCCAC ACAGGCCGTG GTCATCCACA 840
40 CAACTCACTG TCTGCAGCTG CCTGTCTGGT GTCTGTCTTT GGTGTCAGAA CTTTGGGCC 900
GGGCCCCCTC CCACAATAAA GATGCTCTCC GACCTTCAAA AAAAAAAAAA AAAAAAAGR 960
45 KSGGCGCGGT CCCCANTCCC CCC 983

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 2421 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

60 CCGGCTGATC GCTGCCGCTC CGCCAATACA ATAGAGCCAK CCACTACCAG CAGCCTGGCC 60

	CTCTTCTCC TTCTCCAGAG AGACCAATCC AGCCGAACTC GGGGTTTGCC TGAGGAGAAG	120
	GAGGAAGTGA CCATGGACAC AAGTGAAAAC AGACCTGAAA ATGATGTTCC AGAACCTCCC	180
5	ATGCCTATTG CAGACCAAGT CAGCAATGAT GACCGCCCGG AGGGCAGTGT TGAAGATGAG	240
	GAGAAGAAAG AGAGCTCGCT GCCCAAATCA TTCAAGAGGA AGATCTCCGT TGTCTCAGCT	300
	ACCAAGGGGG TGCCAGCTGG AAACAGTGAC ACAGAGGGGG GCCAGCCTGG TCGGAAACGA	360
10	CGCTGGGGAG CCAGCACAGC CACCACACAG AAGAAACCTT CCATCAGTAT CACCACTGAA	420
	TCACTAAAGA GCCTCATCCC CGACATCAAA CCCCTGGCGG GGCAGGAGGC TGTGTGGAT	480
15	CTTCATGCTG ATGACTCTCG CATCTCTGAG GATGAGACAG AGCGTAATGG CGATGATGGG	540
	ACCCATGACA AGGGGCTGAA AATATGCCGG ACAGTCACTC AGGTAGTACC TGCAGAGGGC	600
	CAGGAGAATG GGCAGAGGGA AGAAGAGGAA GAAGAGAAGG AACCTGAAGC AGAACCTCCT	660
20	GTACCTCCCC AGGTGTCAGT AGAGGTGGCC TTGCCCCCAC CTGCAGAGCA TGAAGTAAAG	720
	AAAGTGACTT TAGGAGATAC CTTAACTCGA CGTTCCATTA GCCAGCAGAA GTCCGGAGTT	780
25	TCCATTACCA TTGATGACCC AGTCCGAAC TCCAGGTGC CCTCCCCACC CCGGGCAAG	840
	ATTAGCAACA TTGTCCATAT CTCCAATTG GTCCGTCCTT TCACTTTAGG CCAGCTAAAG	900
	GAGTTGTTGG GCGCACAGG AACCTTGGTG GAAGAGGCCT TCTGGATTGA CAAGATCAAA	960
30	TCTCATTTGCT TTGTAACGTA CTCAACAGTA GAGGAAGCTG TTGCCACCCG CACAGCTCTG	1020
	CACGGGTCA AATGGCCCCA GTCCAATCCC AAATTCTTTT GTGCTGACTA TGCCGAGCAA	1080
35	GATGAGCTGG ATTATCACCG AGGCCTCTTG GTGGACCGTC CCTCTGAAAC TAAGACAGAG	1140
	GAGCAGGGAA TACCACGGCC CTGCAACCC CCACCCAC CCCCCTCCA GCCACCACAG	1200
	CACCCCGGG CAGAGCAGCG GGAGCAGGAA CGGGCAGTGC GGAACAGTG GGCAGAACGG	1260
40	GAACGGGAAA TGAGCGGCG GGAGCGGACT CGATCAGAGC GTGAATGGGA TCGGGACAAA	1320
	GTTGAGAAG GGGCCGTTT CCGATCAAGG TCCCGTRACC GCCCGCAA GGAACGTGCG	1380
45	AAGTCTAAAG AAAAGAAGAG TGAGAAGAAA GAGAAAGCCC AGGAGGAACC ACCTGCCAAG	1440
	CTGCTGGATG ACCTTTTCCG AAAGACCAAG GCAGCTCCCT GCATCTATTG GCTCCCCTG	1500
	ACTGACAGCC AGATCGTTCA GAAAGAGGCA GAGCGGGCCG AACGGGCCAA GGAGCGGAG	1560
50	AAGCGCGAA AGGAGCAAGA AGAAGAAGAG CAAAAGGAGC GGGAGAAGGA AGCCGAGCGG	1620
	GAACGGAACC GACAGCTGGA GCGAGAGAAA CGTCGGGAGC ACAGTCGGGA GAGGGACAGG	1680
55	GAGAGAGAGA GAGAAAGGGA GCGGGACAGG GGGGACCGAG ATCGGGATAG GGAAAGGGAC	1740
	CGAGAACGAG GCAGGAAAG GGATCGCAGG GACACCAAGC GCCACAGCAG AAGCCGGAGT	1800
	CGGAGCACAC CTGTGCGGGA CCGGGGTGGG CGCCGCTAGC TGGGAAAACA CTAGAGCTGC	1860
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AGGTACCAGC CACTCGGCCC CAGGGGGTTA TGGCCACAGA GGGATAGGCA CAGTCTCCAC 1920
 CACCCTGGAG CCAAGGGTCT TTCACATCAC CTATCCCTAC ATACATACCA AATGGAAAAG 1930
 5 TGGCCATCCT TTTCCCCCA AACACACCCC CTTAACCTAT CTCTTGGGAC TTAGCCCGAC 2040
 CCTCCCTCTC ATTTCCCAT T AAGTCTGAGA GGCAAGAGCT AGGTTAGGCA AGGAGGTGGT 2100
 TGGCCAGAGA TGGGGAACAG CCAGGTGCCC CAGTCCTCTG ATTTTTCCTC CATCCTGCTT 2160
 10 ACCACCTCCC TGGGTACTTA CAGCCTTCTC TTGGGAACAG CCGGGGCCAG GACTGGGTCA 2220
 CCTATGAGCT GAATCAGCAT CTCCTCCTGA GTCCAGGGC CCCTGCAGTT CCCAGTCTCT 2280
 15 TCTGTCTGAG AGCCCTTGCC TCTTTCCAC AGGTTCCACT TTATATCCAC CTTTTCCTTT 2340
 TGTCAATTT TTATTTTAT TTTTATTAT ATTAAATGAT GTGGTCTATG GAAAAAAAAA 2400
 TAAAAATCTG ACTTAGTTTT A 2421
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25 (2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 840 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

CTCAAATCC TGAGCTGAAG CGATCTACCT GCCTCAGCTA GGATTACAGG TGTGAGCCAC 50
 35 CGCACCCAAC CTCAATAAGC KTATTTGATA AAKATATGC AAGCTCCCTT TATKCACTTT 120
 TCATTCAGAA TGTTTAGTAA TTTGTATTGT TTTTCAGATT TTCAGCCAA TATATCTCTT 180
 40 TGCCCACTGT GTCACTGTAT TCTACCTAWA CATCATCAGG TGTTCCTGCT ATTGGCTGTA 240
 TGATGGAACA CTGGGGCTCA TTTTCCTGAA AACTGCCGAT AGTGCATAGA RTGCTGGGAT 300
 GGAAACCAGA ARCTTTGAAT TCAAGCCTTG GTTCTGCCTT GTTTTTCCTT GGGTGGCCTT 360
 45 GAGTCAGCCA CATACCTTTT AAAATCTCAA TTTATTAGAA ATTATTCCAA ATCAAAATCA 420
 AATGAGAAGG TATATACAAA AGTGCTTTAT CCCACAATAA ACTATTCAAG AGAGAGCAA 480
 50 GGAGAGGACA TTTACTCAAC ACCTCCTAAA AGGCAGCCAG TGAAATTAGG CATTTTATTT 540
 AATCCTCTG GCAACTCTGA GAGTAAAGCA TTATTAATCC CATTTTGGCT GTTTAAAGAA 500
 ATTATTTGCA CTAGATTCCA GCTGTAGTTT AGYTTTCAGAA AAAAAATCC TGAGATGTCA 560
 55 ATTCACAGCT TTCTGGGTTT AAAGCCCAAG CTCTATCACA TCATGCTATT ATTGTTACAT 720
 TACTGCTAGT TCTATGAAAA GAAATACTAA TTTATGAAAT ACATCTTATC CAAAAAAAAA 780
 60 AAAAAAAAAAC TGGGAGGGGG GGCCCGTACC CAAATCGCCG GATAGTGATC GTAAACAATC 840

5 (2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 2432 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

15 GGCACGAGGC CCGGAACGCT GAGGAAGGGC CCGTCCCGCC TTCCCCGGCG CGCCATGGAG 60
CCCCGGGCGG TTGCAGAAGC CGTGGAGACG GGTGAGGAGG ATGTGATTAT CGAAGCTCTG 120
CGGTCATACA ACCAGGAGCA CTCCCAGAGC TTCACGTTTG ATGATGCCCA ACAGGAGGAC 180
20 CGGAAGAGAC TGGCGGASTG CTGGTCTCCG TCCTGGAACA GGGCTTGCCA CCCTCCCACC 240
GTGTCATCTG GCTGCAGAGT GTCCGAATCC TGTCCCGGGA CCGCAACTGC CTGGACCCGT 300
25 TCACCAGCCG CCAGAGCCTG CAGGCAYTAG CCTGYTATGY TGACATCTCT GTCTCTGAGG 360
GGTCCGTCCC AGAGTCCGCA GACATGGATG TTGTACTGGA GTCCCTCAAG TGCCTGTGCA 420
ACCTCGTGCT CAGCAGCCCT GTGGCACAGA TGCTGGCAGC AGAGGCCCGC CTAGTGGTGA 480
30 AGCTCACAGA GCGTGTGGGG CTGTACCGTG AGAGGAGCTT CCCCCACGAT GTCCAGTTCT 540
TTGACTTGCG GCTCCTCTTC CTGCTAACGG CACTCCGCAC CGATGTGCGC CANAGCTGTT 600
35 TCAGGAGCTG AAAGGAGTGC GCCTGCTAAC TGACACACTG GAGCTGACGC TGGGGGTGAC 660
TCCTGAAGGG AACCCCCAC CCACGCTCCT TCCTTCCCAA GAGACTGAGC GGGCCATGGA 720
GATCCTCAAA GTGCTCTTCA ACATCACCTT GGAATCCATC AAGGGGGAGG TGGACGAGGA 780
40 AGACGCTGCC CTTTACCGAC ACCTGGGGAC CCTTCTCCGG CACTGTGTGA TGATCGCTAC 840
TGCTGGAGAC CGCACAGAGG AGTTCCACGG CCACGCAGTA ASCCTCCTGG GGAAGTTGCC 900
45 CCTCAAGTGT CTGGATGTTT TCCTCACCTT GGAGCCACAT GGAGACTCCA CGGAGTTCAT 960
GGGAGTGAAT ATGGATGTGA TTCGTGCCCT CCTCATCTTC CTAGAGAAGC GTTTGCACAA 1020
GACACACAGG CTGAAGGAGA GTGTAGCTCC CGTGCTGAGC GTGCTGACTG AATGTGCCCCG 1080
50 GATGCACCGC CCAGCCAGGA AGTTCTTGAA GGCCAGGTG CTGCCCCCTC TCGGGGATGT 1140
GAGGACACGG CCTGAGGTTG GGGAGATGCT GCGAACAAG CTTGTCCGCC TCATGACACA 1200
55 CCTGGACACA GATGTGAAGA GGGTGGCTGC CGAGTTCTTG TTTGTCTGT GCTCTGAGAG 1260
TGTGCCCCGA TTCATCAAGT ACACAGGCTA TGGGAATGCT GCTGGCCTTC TGGCTGCCAG 1320
GGGCCTCATG GCAGGAGGCG GCCCAGGGGC AGTACTCAGA GGATGAGGAC ACAGACACAG 1380
60

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ATGAGTACAA GGAAGCCAAA GCCAGCATAA ACCCTGTGAC CGGGAGGGTG GAGGAGAAGC 1440
 CGCCTAAGCC TATGGAGGGC ATGACAGAGG AGCAGAAGGA GCACGAGGCC ATGAAGCTGG 1500
 5 TGACCATGTT TGACAAGCTC TCCAGGAACA GAGTCATCCA GCCAATGGGG ATGAGTCCCC 1560
 GGGGTCATCT TACGTCCCTG CAGGATGCCA TGTGCGAGAC TATGGAGCAG CAGCTCTCCT 1620
 CGGACCCCTGA CTCGGACCCT GACTGAGGAT GGCAGCTCTT CTGCTCCCCC ATCAGGACTG 1680
 10 GTGCTGCTTC CAGAGACTTC CTTGGGGTTG CAACCTGGGG AAGCCACATC CCACTGGATC 1740
 CACACCCGCC CCCACTTCTC CATCTTAGAA ACCCTTCTC TTGACTCCCG TTCTGTTCAT 1800
 15 GATTTCCTC TGGTCCAGTT TCTCATCTCT GGAAGTCAAC GGTCTTCTTG TGCTAGAACT 1860
 CAGGCTCAGC CTCGAATTCC ACAGACGAAG TACTTTCTTT TGTCTGCGCC AAGAGGAATG 1920
 TGTTCAGAAG CTGCTGCCTG AGGGCAGGGC CTACCTGGGC ACACAGAAGA GCATATGGGA 1980
 20 GGGCAGGGGT TTGGGTGTGG GTGCACACAA AGCAAGCACC ATCTGGGATT GGCACACTGG 2040
 CAGAGCMANT GTKTTGGGGT ATGTGCTGCA CTTCCAGGG AGAAAACCTG TCAGAACTTT 2100
 25 CCATACGAGT ATATCAGAAC ACACCTTCC AAGGTATGTA TGCTCTGTTG TTCCTGTCTT 2160
 GTCTTCACTG AGCGCAGGGC TGGAGGCTC TTAGACATTC TCCTTGGTCC TCGTTCACTG 2220
 GCCCCTGTA GTATCCACAG TGCCCGAGTT CTCGCTGGTT TTGGCAATTA AACCTCCTTC 2280
 30 CTACTGGTTT AGACTACACT TACAACAAGG AAAATGCCCC TCGTGTGACC ATAGATTGAG 2340
 ATTTATACCA CATACCACAC ATAGCCACAG AAACATCATC TTGAAATAAA GAAGAGTTTT 2400
 35 GGACAAAAAA AAAAAAAAAA AAAAAAAAAA AA 2432

40 (2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1742 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

50 GTCTGCAGG AGCTGCACGC GGCCGAGGTG CGCANGAACA AGGAGCAGCG AGAAGAGATG 60
 TCGGGCTAAG GGCCCGGSAC GRGSGCGGCC CATCCTGCGA CGGAACACGT TCGGGTTTTG 120
 GTTTGTGTTT GTTCACCTCT GTCTAGATGC AACTTTTGTT CCTCCTCCCC CACCCAGCC 180
 55 CCCAGCTTCA TGCTTCTCTT CCGCACTCAG CCGCCCTGCC CTGTCCTCGT GGTGAGTCGC 240
 TGACCACGGC TTCCCCTGCA GGAGCCGCCG GCGGTGRAGA CGCGGTCCCT CGGTGCAGAC 300
 60 ACCAGGCCCG GCGCGGCTGG GTCCCCGGG GGCCTGTGA GAGAGGTGGY GGTGACCGTG 360

	GTAAACCCAG GCGGTGGCG TGGGATCRG GGTCTTACG CTGGGCTGTC TGGTCAGCAC	420
	GTGCAGGTCA GGGCAGGTCC TCTGAGCCGG CGCCCCTGGC CAGCAGGCGA GGCTACAGTA	480
5	CCTGCTGTCT TTCCAGGGGG AAGGGGCTCC CCATGAGGRA GGGGCGACGG GGGAGGGGGG	540
	TGATGGTGCC TGGGAAGCCT GCKTGTGCAN CCGGTGCTTG TTGAACTGGC AGGCGGGTGG	600
10	GTGGGGGCTG CAGCTTTCCT TAATGTGGTT GCACAGGGGT CCTCTRAGAC CACCTGGCGT	660
	GAGGTGGACA CCTTGGGCCT TCCTGGAAGC CTGCAGTTGG GGGCCTGCCC TGAGTCTGCT	720
	GGGGAGTGGG CATTCCTGTC CAGGGACCCA TGAGCAGGCT GCATGGTCTA GAGGTGTGG	780
15	GCAGCATGGA CAGTCCCCCA CTCAGAAGTG CAAGAGTTCC AAAGAGCCTC TGGCCCAGGC	840
	CCCTCCGTGG GACAGCCCCG CCGCCCCTCC CCACCAGGGC TTTGCAGATG TCCTTGAAAG	900
20	ACCCACCCTA GAGCCCTTTG GAGTGCTGGC CCCTCCTGTG CCCTCTGCCC TGGTGGAAGC	960
	GGCASCACAA GTCCTCCTCA GGGAGCCCCA AGGGGGATTT TKTGGGACCG CTGCCCACAG	1020
	ATCCAGGTGT TGGGAAGGGA GCGGGTAAGG TTCCCAAGCC AGCCCCAACA CCCTTCCCAC	1080
25	TTGGCACCCA GAGGGGGCTG TGGGTGGAGG CCTGACTCCA GGCCTCTCCT GCCCACACCC	1140
	TCTGGGCTGA GTTCCTTCTT TCCCTTGGAC GCCCAGTGCT GGCCTTGGAG GACGGTCAGC	1200
30	TGGAGGATGG CGGTGGGGGA GGCTGTCTTT GTACCACTGC AGCATCCCCC ACTTCTCCAC	1260
	GGAAGCCCCA TCCCAAAGCT GCTGCCITGGC CCCTTGCTGT AAAGTGTGAA GGGGGCGGCT	1320
	GAGTTCTCTT AGGACCCAGA GCCAGGGCCC TCAACTTCCA TCCTGCGGGA GGCCTTGGCC	1380
35	GGGCACTGCC AGTGCTTCC AGAGCCACAC CCAGGGACCA CGGGAGGATC CTGACCCCTG	1440
	CAGGGCTCAG GGTTCAGCAG GGACCCACTG CCCCATCTCC CTCTCCCCAC CAAGACAGCC	1500
40	CCAGAAGGAG CAGCCAGCTG GGATGGGAAC CCAAGGCTGT CCACATCTGG CTTTGTGGG	1560
	ACTCAGAAAG GGAAGCAGAA CTGAGGGCTG GGATATTCCT CATGGTGGCA GCGCTCATAG	1620
	CGAAAGCCTA CTGTAATATG CACCCATCTC ATCCACGTAG TAAAGTGAAC TTAAAAATTC	1680
45	AATCAAATGA ACAATTAAAT AAACACCTGT GTGTTTAAGA AAAAAAAAAA AAAAAAACTG	1740
	CG	1742
50		

(2) INFORMATION FOR SEQ ID NO: 50:

- 55 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1487 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- 60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

	GGCACGAGCC TCCGCGAACT GTGGAGTCGG CGGAGGGCTG GAATCAGCGT GGGCTCCAGG	60
5	TCGCTGGCAG CCGGGTGGCA GAACTCTTCC GAGGCTCCTT GGAAGAAGC TACACCCGAG	120
	GGAGCCCGAT GGGCTCGAA AACCTGGCCC GCTCTGGTTC TGTACCATTG CAAGGGGAAC	180
10	CGTAAACTGA GCTTTTCTAA CGTGGGTTTC TGCCAAGTAC TTTTCCAGCT GCCCCCTTCC	240
	CCCCAGCACA CAGGAGAGCC TCTGTGTAGC CAGCGCTTGA CAGTCGTTAG GTAGGTTGTA	300
	CTGTGTAGGG AGGAGCTCAA GATCATGAAT GGTGTGCACA GGAGAAAGCG GTTGCATCTT	360
15	TGCAAAACTA TATACCTGCT GTGGTTTGTG TTTTCTTTTC TGCTGAGTAA TGAAGTTGTA	420
	AGTTCACACT GGCACATTCT CAGGGCTGTG CAGATTATTT GCACTTTATT TCATAGGTGR	480
20	ATAAGTGCTT TTTAGCTTTC TTTGTATATT GAGTTGCTTT TGAATTGCTT CCCATATTTT	540
	TATTTTCATAC AAAGTGAACA ATTGTGGCCC CTCTATTTTA TTTATAAAGG TTCAGTGTAT	600
	CTTTCCTGTC CTACATCAAT CTGCAAGGGA GTTGCAGAAA GCCTCATGTT CATCGAGCCG	660
25	TGAGTCACAA CCAATTTCTA AGCTGTTATA AAAAAAAGT GTTGTCTTTT TTTACAAGT	720
	AACTTTAAAA GTGTACTTTA GAAAGAAAAC ATTTTCAATA AAAAGACACT ACATTAATCC	780
30	TGGATGCTTG CAAATCCTAA AATMTATTCC TCCTCTAGCG TTGCACAGCT CTGTGTGTGA	840
	TACACAGACT AGCTTTAAAA TTTGTCACAT ACCACTTTAC CTTTACTTTT ATGTATCAAT	900
	CCCCCGACTT CCTTACTGCA GGTGTGGGCA AGAAAACCTT TCCTTTAACA CTTTCAACA	960
35	GCGGCATAA AATTCTGCAG CTGAGGTCTT GAAGAATGCA GATGGGTACA GTATGTGTTG	1020
	GAGCTCACAG TGTGTATTGA CTAACCTAGT TCCTTTTTTG CTTTTTTTGG TATTGTCTTG	1080
40	TTAAAAGTGA CTCCCAGGTA GCAACTCTCT TTTTAAGGG TGGGAACGAA AGGGACCTAG	1140
	GAAGAATAGA TCTAGATTAT TTAACAGTCT TCGATAGAGT TTGAAAGCTT TCTTCTCAT	1200
	TCAATTTTGG GCAAAATACT GCCTCTGCAT TTGTTTCATA CAAAAGATT AGATTAATAA	1260
45	GTAGCTTTTG TTGGTGGAAA TTACCAGCTC TATAAGTCAC CCTTGGTGGT TCATGGACCT	1320
	CTGATTAGCT TGGGTTTTCG AGTCTCATTG CCACATGTAT ATGTGGAGCC AATGGCCTTT	1380
50	TGGTGCTCAG CTGTTTACGT CTGACTCCTT GACTTCTTTG GTACAGTGAT GGAGTCAGAT	1440
	CTCATTAAGT GTGATTCTCC ATGGATATAA CCAGCCCCAA AAAAANG	1487

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(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1328 base pairs

(B) TYPE: nucleic acid

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(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

5 GGCACGAGCT CGTGCCGAAT TCGGCACGAG AGAAGATTTC AAGAAGCCAG ATCCAGCTTC 60
CCTGCGGGCT GCTTCTTGTC GGAAGGGAA AAAGAGGAAG GCCTGTAAGA ACTGCACCTG 120
10 TGGCCTTGCC GAAGAACTGG AAAAAGAGAA GTCAAGGGAA CAGATGAGCT CCCAACCCAA 180
GTCAGCTTGT GGAACTGCT ACCTGGGCGA TGCCTTCCGC TGTGCCAGCT GCCCCACCT 240
TGGGATGCCA GCCTTCAAAC CTGGGAAAAA GGTGCTTCTG AGTGATAGCA ATCTTCATGA 300
15 TGCTAGGAG GTCTCTGACA TGGGACCCAT CTGCTCCTCC AGCCAACCTC TGTCCCTCAC 360
ATCCACCAT GGTGGCTCCT CCCACCTCCT CTGGATTGTG TCACTCTGAG ATCTGTTTGC 420
20 AGAGTGGGTG CTTAGCAGAC AGAGTGAAGC TGGCTGGGGG GCACAGTGGT GTGTAGTGCT 480
GCTGTGTATC AAAAGACCAA GGTATTATGG GACCTGGTTT CAGAATGGGA TGGGTTTCTT 540
CACCTCATGT TAAGAGAAGG GAGTGTGTCC TGAAGAAGCC CTTCTTCTGA TGTAAAATG 600
25 CTGACCAGAA CGCTCTTGAG CCCAGGCATC GTTGAGCATT AACACTCTGT GACAGAGCTG 660
CAGACCCCTG CTTGAGTCT CATCTCAGCA ATGCTGCCAC CCTCTGTGCT TTCAGAGTTG 720
30 TTAGTTTACT CCATTCTTTG TGACACGAGT CAAGTGGCTC ACAACCTCCT CAGGGCACCA 780
GAGGACTCAC TCACTGGTTG CTGTGATGAT ATCCAGTGTC CCTCTGCCCC CTTCCATCCC 840
CAACCACATT TGA CTGTAGC ATTGCATCTG TGTCTGTTG TCATTATGT TAACCTTCAG 900
35 GTATTAACT TGCTGCATAT CTTGACATAT CTTGAGATTC TGCATGCTTT GTAAAGAGAG 960
GGGATGTGCA TTTGTGTGTG ATGTTGGATA GTCATCCACG CTCAGTTTGG ACCATTGGAG 1020
40 GAACTTAGTG TCACGCACAA ATGGGGCTAT TCCTACGCTT AGAATAGGGC TTGTCTGCCC 1080
ACTTTAGAAG AGTCCCAGGT TGGTGAGCAT TTAGAGGAA GCAGGGCAGA ACTCTGAACG 1140
ACAATACGTC TCTCTGAGCA GAGACCCCTT TGTCTTGTG ATCCACCCAT ATGGACTTGG 1200
45 AATCAATCTT GCCAAATATT TGGAGAGATT GTGTGGATTT AAGAGACCTG GATTTTATA 1260
TTTTACCAGT AAATAAAAGT TTTCAATTGAT ATCTGTCCTT GAAAAAAAAA AAAAAAAAAA 1320
50 AAACGCA 1328

55 (2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1856 base pairs

(B) TYPE: nucleic acid

60 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

5	GAATTGGCA CGAGCTCTGC AACATTGCAA ATGAAGTTGG AGTCGAGGGT TCCGCTGCCC	60
	CCTAGATTAA ATTCCCGGG CTGAAGTGA GTTGCAGAT TACATATCA TATTTTAAAT	120
	TGCTGTCTTC AATTAAACCA TTTATGACCA TAACTAATT TCAGGATGC GATGCATGCT	180
10	TTTCCAGGCC TTCTTCTTT GTACAAAGT AATGTCCAT AAACGTTTC ACTTATATTC	240
	TTCAAACATG ATGCTAATTT AAATTAATTA CTTCCTATGA TATGTTATTA TTCCTATGAT	300
15	TTTGCCACTG TTATTAGTTC TCTCAAAAT ACATCTAGGG AAGAGGATTA TTTTAAGTAA	360
	TTTGATTATC TTCTATCTC TTTTATTTAT TTCTCAATTA CTATAGAAAT TCGTTCCAT	420
	GGTTGGCATT GATACAGTAA ATTGTAAAT GAGGAGACAA TATAAAAAT CTAAATTACT	480
20	TGTGCTTAAT GACTGTAGCA GAATSCCTTT TCTCAAAAT AATGTCTTT TCTTGCAGTT	540
	TAGTTTGATA GATTGCAAG CTATGCTGCT TCCATGAAT TATGTCCGT GGTAGGAACG	600
25	CAGGCTTCTT TGTCTCTGGT TGTAGCTTGC ATGATCCTCC CATTAGGCCA ACAACGTAGC	660
	CGGAGATCAC AAATCAGGCC CTGGTGTAG TTCTATGTT GTGGAGGTGC AGAGAGGTTG	720
	GCAGAACTG ACCTCACTGG GCAAGGCTGG CCATGGACCT GATCTTTAA TGCACCTAT	780
30	GTGTTTCAGGA AGCCACAGGC CATATTGAC TCTGAGGAG AAAACAAGAG GAAAAACCCC	840
	ACAAAGTATA ACAACCCCTT AAGATACATC TATTTTAAAG TGAATTAAT TTTCAGTTT	900
35	ATACCATTGG CCATTACAA GATAAATAG TTCAATTCTC TATAGATCC TTGTTGACT	960
	TGCTTTTCA TCTCTGCTA TTTATATTTG TCACTGTAG TCAACAAAGT CTTATTGCT	1020
	GAGGAAGGAC TTTCTGCAC TTAAGTATCC ACATCAACA CTGGGAGGG TGGTGTAA	1080
40	CTTTTAAAAA AATGTTATTC TGATTAAAT AATAATATG GCTTTTTC TGAAGAGGC	1140
	GCCACCTGCG AAGTTTAGT GAGATTATG GAAATTAAAT AACTAGCAG GAATTGCTGC	1200
45	TAGCTCCAAA AATTGCGAA GCAAAAGCTA GCCCAATG GTTGGGAAGT TTGAACTGA	1260
	TTAACAGATT TGCATTGAA GTGACTCAG ACATTAGGT CAGCATTAG TTAATAATAG	1320
	AAAGAGGAAT AAGACATCT YTTCTCTCTA GAATGATAA CACCCCAAT AATAATCCTT	1380
50	CCCACCTTCA TTGAGATCAG CTGTCTGAT AACCTGATA GATGTGATA ATGATAAACA	1440
	TGATAAATAGT GGTACTTTTG TAATTTTCTT GGTGCATTAA AATAGATAGT AAKGATGAG	1500
55	TTCACTTTT CTGCAACAT YCCTATCTCT AGATGATGTT CACCTCAAT TGGGAATTAT	1560
	AACTGTCTTA ATTTTGTG TGTACCTGTA TGCCCTTTT GCTTTAATAC CCACAGTGA	1620
60	ACAATTAAAT ATCACTAT GACATATGAT TTAGTAGGA TATTTAATG ATAAATTTTA	1680

GGGGTAAATG TTTACTTCAA AATGACTCCA TATTTCAAAT ATCTGTTTAG ACTGTGAAGG 1740
CCAAATAATT TTAAAGAAAA CATTGAAGA GTAGTGTGTT TGCATTTGTG AATAATCTTA 1800
5 CTCACAGCAA GTAAACGTAA TAAAAGCCAA CATTTAAGCC AAAAAAAAAA AAAAAA 1856

10 (2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1558 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

20 TGGGTATCCA TTCCTGNAAT TACTTTACTT AGGATAATGG CCTCCAGCTC CGTCCAAGTT 60
GCTGCAAAAG GTATTATTTT GTTCCTTTTT GTGGCTGAGT AGTATTCAT GGTGTATATA 120
TACCACATTT TCTTTATCCA CTCATTGCTT GATGGGCAGT TAGGTTGGTT CCACATCTTT 180
25 GCAATTGTGA GTGTGTGTC TCCAGATATC ATCTTTAACT CCTTTGCCTT CTCCACATAC 240
ATTTCCAAGT CCTGTTCAAT CTACCTCCAA AATGTATCTT GTATCCATTC ATCTCTCTCC 300
30 ATCTTCAATC TATTTCAATG CCCATCATC TCTTGCATGG AGGAGTGTA TAATTGGCTA 360
ACTGGCCTGT TCTTACATTT TAAAATCAAA AGATGTGACA GGTGAAATGC CTATTTCACT 420
GTCCATTGAT GGTTCCTGCTT ACACACCACC TGGCTGCCTG GTGTCGCAGT GGCAGAGTTG 480
35 AGCAGTGTGA AAAAGACTGC TTGGCCCTTT ACAGGGAAAG CAGGTCCACT GTGGCCTGTG 540
AGGACGAGAG CTCTGGGCAG GCTCGGACAC TGGCAGACCC TGGTCTTGGC TGGCCAAGGC 600
40 AGCAGGGTAT GTGTTTCGGG TCACTCACAG GGCTCAGCAC CACTCCTCAT GGCTTCCTTA 660
CTGTTTCGGC AGAGGCTGAC CCGCGGCTGA TTAGTCCCT CTCCCAGATG CTGTCCATGG 720
GCTTCTCTGA TGAAGGCGGC TGGCTCACCA GGCTCCTGCA GACCAAGAAC TATGACATCG 780
45 GAGCGGCTCT GGACACCATC CAGTATTCAA AGCATCCCCC GCCGTTGTGA CCACTTTTGC 840
CCACCTCTTC TCGTGCCCC TCTTCTGTCT CATAGTTGTG TTAAGCTTGC GTAGAATTGC 900
50 AGGTCTCTGT ACGGGCCAGT TTCTCTGCCT TCTTCCAGGA TCAGGGGTTA GGTGCAAGA 960
AGCCATTAG GGCAGCAAAA CAAGTGACAT GAAGGGAGGG TCCCTGTGTG TGTGTGTGCT 1020
GATGTTTCCT GGGTGCCCTG GCTCCTTGCA GCAGGGCTGG GCCTGCGAGA CCCAAGGCTC 1080
55 ACTGCAGCGC GCTCTGACC CTTCCCTGCA GGGGCTACGT TAGCAGCCCA GCACATAGCT 1140
TGCCTAATGG CTTTCACTTT CTCTTTTGTT TTAAATGACT CATAGGTCCC TGACATTTAG 1200
60 TTGATTATTT TCTGCTACAG ACCTGGTACA CTCTGATTTT AGATAAAGTA AGCCTAGGTG 1260

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TTGTCAGCAG GCAGGCTGGG GAGGCCAGTG TTGTGGGCTT CCTGCTGGGA CTGAGAAGGC 1320
TCACGAAGGG CATCCGCAAT GTTGGTTTCA CTGAGAGCTG CCTCCTGGTC TCTTCACCAC 1380
TGTAGTTCTC TCATTTCCAA ACCATCAGCT GCTTTTAAAA TAAGATCTCT TTGTAGCCAT 1440
CCTGTTAAAT TTGTAAACAA TCTAATTAAA TGGCATCAGC ACTTTAACCA AAAAAAAAAA 1500
AAAAAAAAA AAANAAAAA AAAAGGGGGC CGCTCTAGAG GTCCAAGTTA NGACGNGG 1558

15 (2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 948 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

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TAAAAATCAT GCTCTGTACC ATCCTCACCG TAGTCATCAT CATCGCCGCG CAGACCACGA 60
GAACTACTGG GATCCCTAAA AACGCCCCTG GTCCGGCCCC ACTCTGCGCC CCTCGATCTC 120
CCAGGCTCTT TCTGCAGWCA TACCGCGGAC CCAATGGGCG CCCTGCACAC CCGTTTCTGG 180
GGCCGTCAGA CTTGGATACA TCGTAAACTC CGCCTCCACG GAACGTCTCG CCTKGCGAGC 240
AAGMTCGGAA TCCAGTTCCT CAGGAACCCC TCCAAAACCC ACACCCCCAG GGACGCGGCT 300
TTCCGGGATC CCGGSCAAAC GCCGGACCCT CAGTCGCTCC AGGCCCCCTC ACCCTCAAAG 360
TGTAGCGCCC CCAACCGAGC AACCTCGGTT TGGTCCCTAA AACCCCGCCT CCTCTATAAG 420
CACCGCCCCA GCTCTGACAA AACCCCGCCT CCAGGTCGGC AGGCTCCGCT TCTTTTCTTC 480
TCCGCGGGGT GATTCACTCC AGTGATTGGG TTTGTGGCTC CAGGCCTCGC CCACAGACGG 540
ACAGACCCCT CCCTTTCTTC CGGCAAAAGG ACCGAGCCCT GGGGTAGTAA GGSCCCCACA 600
CTCCTGTTTT TTGCAAGTAC ATTTTGTGCC YTCCTCCACC CAGGTATCTG CCTATTTTCT 660
TGCTAATCCC AGAACCTTTC CTTTGTCTTT TTTTAAGGAC ATTTGGGAAG TTCCTGGTGT 720
AGGACCCCTC TCCCTGGGAT AAGAAACCTG CCTGTAAACG CTCTGTAAAT ACTCCCTTCC 780
ACCCATCCCA GCCCCTGGGC AGCCGGGCAG AAGGGAATCC AGGCTATGGA CCTCCCAAGT 840
CCCCGCTCCC CGCTCCCCTC GGCGGCCCCG CCTGTGTTCTG ATCTGTGTGT GAGTGTGTGT 900
GAACTTCTGA AAGACAATAT TAAAGAGACT TAGTTGAAAA AAAAAAAAAA 948

60 (2) INFORMATION FOR SEQ ID NO: 55:

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(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 990 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

10 GGGGAACTGC AGTGACAGCA GGAGTAAGAG TGGGAGGCAG GACAGAGCTG GGACACAGGT 60
ATGGAGAGGG GGTTCAGCGA GCCTAGAGAG GGCAGACTAT CAGGGTGCCG GCGGTGAGAA 120
TCCAGGGAGA GGAGCGGAAA CAGAAGAGGG GCAGAAGACC GGGGCACTTG TGGGTTGCAG 180
15 AGCCCCCTCAG CCATGTTGGG AGCCAAGCCA CACTGGCTAC CAGGTCCCCCT ACACAGTCCC 240
GGGCTGCCCT TGGTCTGGT GCTTCTGGCC CTGGGGGCCG GGTGGGCCCA GGAGGGGTCA 300
20 GAGCCCGTCC TGCTGGAGGG GGAGTGCCTG GTGGTCTGTG AGCCTGGCCG AGCTGCTGCA 360
GGGGGGCCCG GGGGAGCAGC CCTGGGAGAG GCACCCCTG GCGAGTGGC ATTGYTGCG 420
GTCCGAAGCC ACCACCATGA GCCAGCAGGG GAAACCGGCA ATGGCACCAG TGGGGCCATC 480
25 TACTTCGACC AGGTCCTGGT GAACGAGGGC GGTGGCTTTG ACCGGGCCCTC TGGCTCCTTC 540
GTAGCCCCTG TCCGGGGTGT CTACAGCTTC CGGTTCATG TGGTGAAGGT GTACAACCGC 600
30 CAAACTGTCC AGGTGAGCCT GATGCTGAAC ACGTGGCCTG TCATCTCAGC CTTTGCCAAT 660
GATCCTGACG TGACCCGGA GGCAGCCACC AGCTCTGTGC TACTGCCCTT GGACCCTGGG 720
GACCGAGTGT CTCTGCGCCT GCGTCGGGG NAATCTACTG GGTGGTGA AATACTCAAG 780
35 TTTCTCTGGC TTCCTCATCT TCCCTCTCTG AAGGACCCAA GTCTTTCAAG CACAAGAATC 840
CAGCCCCTGA CAACTTTCTT CTGCCCTCTC TGGCCCANAA AACAGCANAA GCAGGANANA 900
40 NACTCCCTCT GGCTCCTATC CCACCTCTTT GCATGGGAAC CTGTGCCAAA CACCCAAGTT 960
TAAGAAAAAA ATAAACTGT GGCATCTCCA 990

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(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1603 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

GGTCGACCCA CGCGTCCGGC CCGCCGGCTC CGGAGCGGCT CTGCCTTCCC GAGCGCGGGA 60
CCGCGCCCTG GGGGAGGAGG GCGAACGACG CGGCGATGGC TCCGCGGGCA CTCCCGGGGT 120
60

	CCGCCGTCCT AGCCGCTGCT GTCTTCGTGG GAGGCGCCGT GAGTTCGCG CTGGTGGCTC	180
	CGGACAATGG GAGCAGCCGC ACATTGCACT CCAGAACAGA GACGACCCG TCGCCCAGCA	240
5	ACGATACTGG GAATGGACAC CCAGAATATA TTGCATACGC GCTTGTCCCT GTGTTCCTTA	300
	TCATGGGTCT CTTTGGCGTC CTCATTTNGC CAMCTNGCTT NAAGAAGAAA GGCTATCGTT	360
	GTACAACAGA AGCAGAGCAA GATATCGAAG AAGAAAAAGG TTGAAAAGWT AGRATTGAAT	420
10	GACAGTGTA ATGAAAACAG TGACACTGTT GGGCAAATCG TCCACTACAT CATGAAAAAT	480
	GAAGCGAATG CTGATGTYTT AAAGGCGATG GTAGCAGATA ACAGCCTGTA TGATCCTGAA	540
15	AGCCCCGTGA CCCCCAGCAC ACCAGGGAGC CCGCCAGTGA GTCCTGGGCT TTGTCACCAG	600
	GGGGGACGCC AGGGAAGCAC GTCTGTGGCC ATCATCTGCA TACGGTGGGC GGTGTWGTCC	660
	AGAGGGATGT GTGTCATCGG TGTAGGCACA AGCGGTGGCA CTTTATAAAG CCCACTAACA	720
20	AGTCCAGAGA GAGCAGACCA CGGCGCCAAG GCGAGGTCAC GGTCTTTCT GTTGGCAGAT	780
	TTAGAGTNAC AAAAGTGGAG CACAAGTCAA ACCAGAAGGA ACGGAGAAGC CTGATGTCTG	840
25	TTAGTGGGGC TGAAACCGTC AATGGGGAGG TGCCGGCAAC ACCTGTGAAG AGAGAACGCA	900
	GTGGCACAGA GTAGCAGGTG AGCCGTGGTT TTGGTGACAT TGGGGGAGA GTGGTGCAGG	960
	GTGAGGAGAA GGTACTTGA GCCTCCCAGG TGCTGTGGCA GCATAGGAAT GGTATTTGAC	1020
30	AGGGAAGTGG GAGAGCTTTC CTTGACCCAG GAAGACTGAG GGGGACTGAA CATGATTACT	1080
	TGTCTGCCTA GAGCTTCTTG TAAAGAAGTC ACAAACTTAG TGCCTCCAGG GGCTTGGCTG	1140
35	TGTGATAATG AGGATAGAGG ATTACTTGTG AGGCAATGTG GCATGGTGGG GATTGTGGCA	1200
	AACTAGAATT CACATCACCC ACCATATAGG GCTTGCAATTA CCACGAGGCA GAAAGCACCT	1260
	AGTGTGTGCTG CATCTTCITA CGCAAAAAG ACAAAATCCA GACTTCTAAA ATGTAAAATC	1320
40	ACTGATTTTC GATATTGGCA GCTTACTTTT TTTTMTTAAA CAACCATGCA GGCCAAATGA	1380
	CTTGTAATCT TGTCACCATT TTTAGGTAAA CTGTGACTTG AAAAAGTCTG GAGCAAACAA	1440
45	ACCAATGCTT TTTCTTTTA TTCTGTTGGR AACCAGTTT CTTTGTGTCA CAGTTYTGAA	1500
	ACCTCAATAC GAATATTCT CTTCACCA AATATTTTGA GGCAATTGAA AAGCCACAGT	1560
50	GATTTATTTT TTGATTGGC AATTTTAATT TTGCAAGACA ATT	1603

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1052 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

5 TACAGCTCAG GATGCCTGTA ACATGTGCAT CTCTGGGCTT CTGGGTCCTG CTTAGCCTGC 60
 TTTTTCCTG GAGGACTGAC CAGGGATGCG GCCCAGCAAC ATGTTACTAA ATCATACTCT 120
 CCTCCCTACC TTTCAGAC CTCTCACTCC TGCTGGTGT TCCAACCCGT TCTGTGGCCA 180
 10 GAGTATACAT TTGGAACCT CTTGAGGCC ATCCTGCAGT TCCAGATGAA CCATAGCGTG 240
 CTTGAGCAGN AAGGCCCGAG ACATGTATGC AGAGGAGCGG AAGAGGCAGC AGCTGGAGAG 300
 15 GGACCAGGCT ACAGTGACAG AGCAGCTGCT GCGAGAGGGG CTCCAAGCCA GTGGGGACGC 360
 CCAGTCCGA AGGACACGCT TGCACAACT CTCGGCCAGA CGGGAAGAGC GAGTCCAAGG 420
 CTTCTGCAG GCCTTGAAC TCAAGCGAGC TGAAGGCTG GCCCGTCTGG GCACTGCATC 480
 20 AGCCTGAATG AGGCTGGCCA CTGCCACTT TGCCCTGCCC TCTGCCTCCA GGGCTCCMCT 540
 MYCCTTCCTT TTCTGGTGA AAGGCACCTC CTTCTCTGAT AATGAATGGT GTTCCCTTTG 600
 25 CTTGGCTGGG GAGCCCCCA GGCCAGGTTT GCTGGCCATA GATACCTTTG GGCTGCCTGR 660
 GACAGGCTCC TGAGGAGGAT TGAGGGTGAA AGTCTCCAC GAGTACACTA AACCTAGGTC 720
 TGGTCACCAA TAGGTTTGG AGAGCAAAGG GCCACAATC ATCAGCTGCC TGTCTCTTAG 780
 30 ATGCACTTTC TTTTCCACC AGCACATCCT TCAACACACA GAATTCAGG GAAGAGTTCT 840
 CCCCCAAC CTAGCTCTTT ACCCTCCAT TTTAGCCTTC CACCCAGCTT CCACAAAAGA 900
 35 TTGGCTCTA CTTGGATCT GCTAGTAAAT AACTAATAGG CAGGCAGTTA TTTGGGTAAG 960
 GAAAAAGGG GTGGGAGAGA CAGAAAATTT GCCCACTGCT GCTCCTCCCC TTGGSTYTCC 1020
 ACCTGGGATT TGCTATTGAA TCTCTACCCT NN 1052
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(2) INFORMATION FOR SEQ ID NO: 58:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 814 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

55 ACNCGNTGGC GGCCGCTCTA GAACTAGGGG ANCCCCGGG CTGCAGGAAT TCGGCACGAG 60
 CATAGACTTT TAAACTGGTA CGGTTCTTAG AGATGGTCCT TGGCCTCTG TTGTTGTTGT 120
 KGTPTTTTC TTTTCTTCT TCTCCTCTC CTTCTCTTC TCTCTCCTT CTTTCTTCTT 180
 60 TTTTTCCTCA GAGTCTTGCT CTGTACCAA GACTGGAGTG AAGTGATGTG ATCTCGGCTT 240

ACTGCAACCT GGGAGGCAGA GGTTCAGTG AGTCGAGATG GTGCCATTGC TCTCGTTTGG 300
 GCAACAAGAG TGAAACTCTT GTCTCAAAAA AAAAAAAAAA ATGAGGTTTA AGACAGTTTT 360
 5 GTCATTACTG GTGGGATCTG GTCACACAAG ATAGCATTAA ACGTGACATG GCACATAAAA 420
 TTGGTTAAAA AATTTTGTMT TTTAATTACG TAATGTAAAA GCCCAACAAA CACTTTATGC 480
 AAGATTGGAA TGTATCTTCA AATTCAGATT TAATAACAT GTAAAGATCC TCTGTATATA 540
 10 AAAGTTGTAT TTAATCCCTT GTGCCCCAAG AATGCTATAA AAGATCCCAA GAATGTTATC 600
 TATGAAAAGA TAGCAATAGG GAATGGTGAA CAAATAATTT AATTTGCCAA TTCTAAAAAA 660
 15 CATGGACTTA AACCCCATGA AAAGTTGGTT CCATAGTTTT AACTGTITTA TGGTTCCAAT 720
 ACAAACCCAG AGTGGTTTAC ATTCCACAAT NACCAAATTT GCATCCAATN TTGGGGTAAT 780
 20 TTTNGGTATT TGCCATGGGA TACTATTCAT TTTT 814

25 (2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1215 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

35 AGAGGAAGTC TTTTGCCAAG CCTGTTCTCT GGAATAACGC CATCCAGGCT GGGAGGGGAA 60
 GAGTGCTCTG CTACACTCGT CCCCCTCCTG CCTCATCTTC CTCTCAGCC TTGGTTCCTG 120
 ATGGGAACAG AATGGAGGGC CTGAGAACAT ACTTTCTAAA TGCCTTTGAC CCAGGAACCG 180
 40 ATTATCTATA TTTGTTCCCA TTTTCCTTCA CCGTGACATT CCAGCATTGT CTGACTGTGA 240
 GGTGGGCCTT TGAGAGCCTC CAGGTTCCTC AAAACAGGCC TGAGCGATGG GCATCACACC 300
 CTCTGCCTAC CCACRTGCCT GCTTACCTGC CAGATAACCA AGTGNAGATG TCTGCGAGTG 360
 45 GCTAGTTTTT ACATTCTTAC TAGTGTITGG YTCACCTTTG GGCAAAGGCC CCCTCTAGGC 420
 CTTGCCCCAC CTCCATCAAA CGCAGACACT GTAGTCAGAC CTCAGYAATA TAGGAGGCAA 480
 50 TAATCTTTTA ACAGTGTMTT GCAAACAAAC AAAAAAGAGAA AAATCCCAGC CAGGGGAAC 540
 CGCCACCTGC CCACGCTAGT TCCATCCACG CTCAAGACCC GCCCTTAGAC CAGGCAGGCA 600
 AAGGCCCCCA TCACACTCGG CCACTAGTGG GGTCTTGAGG CCAAGAAAGA AACCAGACCC 660
 55 TGTATGACAA GPTGGGKTCT TTCCAGAACA CGACAGAAAC AGGGGGGGCC CCTGTTAAT 720
 GCCACTCCAT ACTCCAGAAG CATTATTCCT TATTTGGGAC AGCCAAGGGC AGATTACAG 780
 60 GTTATTGTAG GAATAAAGAC TAGTTTACAA AGGARAAGA GSCCCTGGAC TTCCCMAGGA 840

5 AAGGTCAGGT TAGGGCTCCT GTACCCATTC TGTTCACCA CTGTTTGATC TCTCTGGCCT 900
CCCACCAGGA ATGCCGTTTC CTTTTTATGG ATCTGTTGGG AACCAGAGAG AATCAACAGA 960
TCAATGACAT AGGATCCGAA GTGCAATGAT AGTCACTTCT AGTTTGGCAT TTCACAAACT 1020
CTGNACAGCA AGGTATTGGT AGGTACTCA ATTTCAAAG GGCCCCATGG CCAAATATGT 1080
10 TTAGGAACCG CTGTTTGNAT TTCTTTTTTT GGAGACGCAT TGTATATAAT ATATGTCAAA 1140
GGCTTTCGGA ATTCCTGCAG GAAAGAAATC AGCTTGTGA AATCCNAAA AAAAAAAAAA 1200
AAAAAATAG ACTCG 1215

20 (2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 478 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

30 ATTTCTTATG ACATGGGGGT TTGAATTGGT TGGCAAATGT TTAATTTTAA TATCCATAAT 60
CAGTGAGGTC CTGCTGGCTG TAATCATTA TGTGAAATC TAAGGAGCTT AGTTCATGGC 120
TCTAGAATTT CACAGAAAAR TGYGMTATGA TACGAGCATT AAGTTTATTT CTTCTGATCT 180
35 TTGATGCAGC TTTGTTTCA GTTATCTGTTT TTGTATTTAT TGGTCATCTA CTTCCCATGC 240
CAAAAGGGAC TGGTCTACAT AGCTGCGCTA AACACCTGAT CAAATCACTA AAAGAAAATG 300
TGTTACCTCT AATGAATTAT CCTGATTGTA AGTTAAAAAT CAATATTTCC CCGTAGTGAG 360
40 GTTTGCTTTT TAAAAAGAAK KCTTAAAAA AAAAAAAAAA AAACGAGTTN AAGAAAAGGA 420
AGCAAGCTCA GGTAAGGTGC ACACATTGGG CTAAGGAAGC TAGAGCCTGT GGAGANGC 478

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(2) INFORMATION FOR SEQ ID NO: 61:

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 618 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

TATGACCTTG ATAACCCCAA GTTNGAAATT AACCTTCANT AAAGGGAACA AAAGCTGGAG 60
60 TTCGCGCGCT TGCAGTTTGA CACTAGTGA TCCCAAAGAA TTCGGCACGA GTCATAATGA 120

5 GCTACTAGGT AAGCCTTCTG GGACTTTCAG ATATTTTGGG GAAGATTGAT TTTTGTCTT 180
 ACATGCTGTG GACCCCTGGC CATCAAATGG TATGGGGAAG CTCATCCGTC TGTCTGTGAT 240
 GGTCAATGTCA GTCAGGCGTC TTTTGTAGTAT TTACTGGGTG CTCAGTACTG TGCCAGATGC 300
 TGTCCGGAGC CGTGGTGGTA TGGAGGAGGA GTGCTCCAGA GGACTCTGCT GTGTGGCAGG 360
 10 CCAGCATAAA CAAGCCAAGG GGAAGGCA GGCATGGAAT AAAGGGGAG AATACCAGTG 420
 TGTGACTTAC TGCTGACTGT GTGGATTAGC CTATCAGCAG TAATCAAGCA GGGCGGAGGG 480
 CATTATCTTT GAGCCAGAAG AGTGAGCACT GGSCCGAGGG TGGAGCATCA AGAGGGGGTG 540
 15 TAGGACCNCA AGGCTTCTTN CNGGGGAGAC AACGTCAATA AGCNGTCAGT AGTCACCGAC 600
 AGTTTGGGA AGCAAGG 618

20

(2) INFORMATION FOR SEQ ID NO: 62:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 751 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

TCGACCCACG CGTCCGAGGA GCTGGACTTC TGAGACAGCC ATTCTCCTTG CATAGCACTG 60
 35 TCTGCTGCTA CAGCTCATAG AAGTCAACAA TTTTCTTCAA CACTGGTAGG CAGCCTCTAA 120
 ATGGCCCTGA TCACCCTCAC CTCCTGCCAT TCACACCNNT GTAAATTC ACCCCTGGAC 180
 40 CTAGTGACTC ACTTCTAACA ANGAGAATAC AGCAAAAGTA ACATCGCTTC TGAGGTGAGG 240
 CTACAAGGAG ACTACGATGC CTGCCTTGGT CACCCCTCTC CTGCTCTTTC CATTGCTCCC 300
 TCTGATGGAA GCCAGTTGCC ATGTGATGAG GTGCCCTATG GAGAGGCCCA CGTGACAAGG 360
 45 TATTGTAAAA AGCCTCTGAC CAATAGCCAT CTAGAAACGG AGGCCAGTC CAGCAGCCTC 420
 TGAGATGAAT CCTGCCAACC TGAGCTTGGG GACAGATTCT CTCCCTATCC TGCCTTGGGA 480
 TGATCACAGC CACCACCAAC ACCTTCACTG CCTGGTGAGA GGCCAAGCCA GTGAACCCAA 540
 50 GGTAAACTGG ACAGAATCCT GACCCACAGA AACTGAGATA ATGTTTGTTA TTTTAAGCTG 600
 CTCAGTTTGT TACAGAGCAA TAGATAACTA ACTCAAACAC CATAAAATTC TAATATTTTA 660
 55 TTCTATCACA CAAACCAGGT AATACCAAGT AAATGCCATT ACTATACACA TATTTTGTGTA 720
 ACACAATTAC ATGTGATTTT TTAAGAAGGC T 751

60

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 780 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10 (ii) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

CNGNCACTCA CNGTCCCCGA TTCCCGGGTC GACCCACGCG TCCGGGTGG CAACTCCTGA 60
GGCCTGCATG GGTGACTTCA CATTTCCTA CCTCTCCTTC TAATCTCTTC TAGAGCACCT 120
15 GCTATCCCCA ACTTCTAGAC CTGCTCCAAA CTAGTGAATA GGATAGAATT TGATCCCCTA 180
ACTCACTGTC TGCCGTGCTC ATGCTGCTA ACAGCATTGC CTGTGCTCTC CTCTCAGGGG 240
20 CAGCATGCTA ACGGGGCGAC GTCTTAATCC AACTGGGAGA AGCCTCAGTG GTGGAATTCC 300
AGGCACTGTG ACTGTCAAGC TGGCAAGGGC CAGGATTGGG GGAATGGAGC TGGGGCTTAG 360
CTGGGAGGTG GTCTGAAGCA GACAGGGGAT GGGAGAGGAG GATGGGAAGT AGACAGTGGC 420
25 TGCTATGGCT CTGAGGCTCC CTGGGGCCTG CTCAAGCTCC TCCTGCTCCT TGCTGTTTTT 480
TGATGATTTG GGGGCTTGGG ATCCCTTTG TCCTCATCTG AGACTGAAAT GTGGGGATCC 540
30 AGGATGGCCT TCCTTCTCTT TACCCTTCCT CCTCAGCCT GCAACCTCTA TCCTGGAACC 600
TGCTCTCCCT TTCTCCCCAA CTATGCATCT GTGTCTGCT CCTCTGCAA GGCCAGCCAG 660
CTTGGGAGCA GCAGAGAAT AACAGCATT TCTGATGCCA AAAAAAAAAA AAAAAAACC 720
35 GCGGCCGAAA GCTTATNCC CTTTAAGTAA GGGGTTAATT TTAGCTTGG CCACTNGGCC 780

40

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 588 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50 (ii) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

TTCCGAATTA ATCGACTCAC TATAGGAATT GCGCTCGCCA TGACCCGCGG TAACCAGCGT 60
GAGCTCGCCC GCCAGAAGAA TATGAAAAG CAGAGCGACT CGGTTAAGGG AAAGCGCCGA 120
55 GATGAGGGGC TTTCTGCTGC CCCCCGCAAG CAGAGGGACT CGGAGATCAT GCAGCAGAAG 180
CAGAAPAAGG CAAACGAGAA GAAGGAGGAA CCCAAGTAGC TTTGTGGCTT CGTGTCCAAC 240
60 CCTCTTGCCC TTGGCTGTG TGCTGGAGC CAGTCCCACC ACGCTCGCGT TTCCTCTGT 300

322

AGTGCTCACA GGTCCCAGCA CCGATGGCAT TCCCTTTGCC CTGAGTCTGC AGCGGGTCCC 360
TTTTGTGCTT CCTTCCCCTC AGGTAGCCTC TCTCCCCTG GCCCACTCCC GGGGGTGAGG 420
5 GGGTTACCCC TTCCCACTGT TTTTATTCC TGTGGGGCTC ACCCCAAAGT ATTAAAAGTA 480
GCTTTGTAAT TCCAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 540
AAAAAAAAA AAAAAAAAAA AAAANNCGGG GGGGGGCCCC CCCCCCCC 588
10

(2) INFORMATION FOR SEQ ID NO: 65:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 774 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

20

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

TTTAAAGATG AAGAAATGAC AAGGGAGGGA GATGAGATGG AAAGGTGTTT GGAAGAGATA 60
25 AGGGGTCTRA GAAAGAAATT TAGGGCTCTG CATTCTAACC ATAGGCATTG TCGGGACCGT 120
CCTTATCCCA TTTAATTAAT TTCTCTGACA ATTCAATTAT TTTCTGTTAT TAATGTTGCC 180
30 ACTGCTTTCT GTTTGTCTGC ACTTCTTGA TAAATATTTG CTATCGTTTT ACTCCAGTCA 240
TTGATGTTG CTGAGATTTA CATATGACTC TTGTCAACAT CTCATCTTTT GACCCAATCT 300
TATTCATTTA ATAAGAGGTC TCATTCATTT GCATGGAAAA ATGCTCATTG TATATTGCAA 360
35 AGTGAAATA ACGAGTTGCA AAACAGTGA TACATATATG TGTGTATATA TGTACACTTT 420
ATTTGTACAT TTCTATGTGA CATAATGCAA AGGAAAGTGT CTGATTTTAT TATACACCAA 480
40 AGGTTAACAG TGAATCTCTG TGTGATCTCT TTTTTTTTCT TTTTGCCTAT CTGCATCTTC 540
TCACTTGCCA AAAAATGAAT ATATGTTTAT GTGTGTATAT TACTTGTGTC ACAAAAAACC 600
CTAAAGTAGA CAGTAAAAGA ACTTGTCAAT CGCCTTTGGA AGGCAATGAA ACACTTAATA 660
45 AACTCTCAAT AACAGAAGCG TAAAAATGAA ATGTAACCT CCAATTACCT CTGGATCTCT 720
TAGCCAGAGT AATAAACTGG TAATTATTAC AGATAAAAAA AAAAAAAAAA AANA 774
50

(2) INFORMATION FOR SEQ ID NO: 66:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1866 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

	ACCCACGCGT CCGGTCCTCT TCTTCAGCAC ATGCCAAAGC TGTTCCTCAC GGCCTGTGAG	60
5	ACAAGAGCAT CTTGGATGTA GGACAATGGA AGAGTTAGAT GCCTTATTGG AGGAACTGGA	120
	ACGCTCCACC CTTCAGGACA GTGATGAATA TTCCAACCCA GCTCCTCTTC CCCTGGATCA	180
10	GCATTCCAGA AAGGAGACTA ACCTTGATGA GACTTCGGAG ATCCTTCTTA TTCAGGATAA	240
	CACAAGTCCC TTGCCGGCGC ATTCGTGTAT ACTACCAATA TCCAGGAGCT CAATGTCTAC	300
	AGTGAAGCCC AAGAGCCAAA GGAATCACCA CCACCTTCTA AAACGTCAGC AGCTGCTCAG	360
15	TTGGATGAGC TCATGGCTCA CCTGACTGAG ATGCAGGCCA AGGTTGCAGT GAGAGCAGAT	420
	GCTGGCAAGA AGCACTTACC AGACAAGCAG GATCACAAGG CCTCCCTGGA CTCAATGCTT	480
20	GGGGTCTSG AGCAGGAATT GCAGGACCTT GGCATTGCCA CAGTGCCCAA GGGCCATTGT	540
	GCATCCTGCC AGAAACCGAT TGCTGGGAAG GTGATCCATG CTCTAGGGCA ATCATGGCAT	600
	CCTGAGCATT TTGTCTGTAC TCATTGCAAA GAAGAGATTG GCTCCAGTCC CTTCTTTGAG	660
25	CGGAGTGGCT TGGNCTACTG CCCCACGAC TACCACCAAC TTTTCTCTCC ACGCTGTGCT	720
	TACTGCGCTG CTCCCATCCT GGATAAAGTG CTGACAGCAA TGAACCAGAC CTGGCACCCA	780
30	GAGCACTTCT TCTGCTCTCA CTGCGGAGAG GTGTTTGGTG CAGAAGCCTT TCATGAGAAG	840
	GACAAGAAGC CATATTGCCG AAAGGATTTC TTAGCCATGT TCTCACCCAA GTGTGGTGGC	900
	TGCAATCGCC CAGTGTGGA AACTACCTT TCAGCCATGG AACTGTCTG GCACCCAGAG	960
35	TGCTTTGTTT GTGGGACTG CTTACCACT TTTCTACTG GCTCCTCTT TGAAGTGGAT	1020
	GGACGTCCAT TCTGTGAGCT CCATTACCAT CACCGCCGGG GAACGCTCTG CCATGGGTGT	1080
40	GGGCAGCCCA TCACTGGCCG TTGTATCAGT GCCATGGGGT ACAAGTTCCA TCCTGAGCAC	1140
	TTTGTGTGTG CTTTCTGCCT GACACAGTTG TCGAAGGGCA TTTTCAGGGA GCAGAATGAC	1200
	AAGACCTATT GTCAACCTTG CTTCAATAAG CTCTTCCCAC TGTAAATGCCA ACTGATCCAT	1260
45	AGCCTCTTCA GATTCCTTAT AAAATTAAAA CCAAGAGAGG AGAGGAAAGG GTAAATTTTC	1320
	TGTTACTGAC CTTCTGCTTA ATAGTCTTAT AGAAAAAGGA AAGGTGATGA GCAAATAAAG	1380
50	GAAGTTCTAG ACTTTACATG ACTAGGCTGA TAATCTTATT TTTTAGGCTT CTATACAGTT	1440
	AATCTATAA ATTCTCTTTC TCCCTCTCTT CTCCAATCAA GCACTTGGAG TTAGATCTAG	1500
	GTCTTCTAT CTCGTCCCTC TACAGATGTA TTTTCCACTT GCATAATCA TGCCAACACT	1560
55	GGTTTCTTA GGTTTCTCCA TTTTCACCTC TAGTGATGGC CCTACTCATA TCTTCTCTAA	1620
	TTTGGTCTG ATACTTGTTC CTTTTCAGT TTTCCATTT CCCTGTGGCT CACTGTCTTA	1680
60	CAATCACTGC TGTGGAATCA TGATACCACT TTTAGCTCTT TGCATCTTCC TTCAGTGTAT	1740

TTTTGTTTTT CAAGAGGAAG TAGATTTTAA CTGGACAACT TTGAGTACTG ACATCATTGA 1800
TAAATAAACT GGCTTGTGGT TTCAATAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1860
5 AAAAAA 1866

10 (2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1152 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

20 CTCAAGGATG TAAAGGCTCT GCAGATTTTCG GGAGGCCTGT CTCCCAGCAC CTGATGGGAC 60
ACTTTTIGCC CCACTGTAAA TTCTGGGTGT ATCCTCCACT GTATGCTGTC ACCCCAAGGG 120
CAAGCACTGC ATCTGCTTAG TGAAGGATTT ATTGTTCCGA AGATACATTT TCCCCTTKAG 180
25 CAGAGAGTGG CGTATCCTGG CAGTCTTCGG TGAGCCAGTT GTACCAGGAT TATGAAATGC 240
AGATGTTTAC TGTGTCATIG TTGCTGTCAT TGCTACTGAG GAGTACTGAC CAGAATCATC 300
30 TGCAACTYTT AGTTGGCAGA GAGGACCACT ATGGCGGGTA GCTCTTTTCT TTCCTGCCAT 360
TGTGGGGATG ATTCCAGGCC AAAGATGATG GARAAGTATG GAAATCATCT GAAAGGTTGA 420
AGCTTGGCAC GTGAAGCCAT TCATGACTTT GTAAGGCAGT TTGCTGAAG GCCAGTTCTG 480
35 CCCTGGGAGG GACGGAGGTG AATCCTCCTG AGTACCTGTG GTTTTCITTAC TTCCTGCTGA 540
ATTTACCTAA GTGCCTGTTG TTGCTTGCT GTGGAGGCTT TCTGGTATTT CATTTAGGT 600
40 GCAGATGCCT TCACTTTCCC ACCRAAAAAA CCCMACCAA ACCTAAGACC TTAATGCAAC 660
TAAGTYTNCC AAGTACTTTT TAACCCAATG GGATGAACAG CCTGTGGTCT GCTCAGATCA 720
CCCTGAGTGC GTGTGAGAAG GCMINGGCTT TGCCAGGAAA TCCAGGAAGG CAGGGCCGGG 780
45 CTGTGTTGGA AGCTGGCTTA GCTGGTGGGG CAGCCTTATT TCAATTAAAA GGGCATTGAC 840
TGGGAGCAGC AGTCTCGGAG TTGTTGCAT TTCCTATTGC CCTCAAAATG AGAAACCAGG 900
50 AAAATAGCAG ATTGGAGCCT TCGAGAAGGC AGTAAATGGC TGTTTTTATT GACAAAAGGA 960
AAACATTTTA CTGCCATCTC ACTGATGGCA TCTCACTGAC TTAAAATGAA GGCANGTTGT 1020
AGTAAAAAAA AAAGTCTACA TTTTCCACC GCCACGTTCT TATATCCTGT TTGTCAGCCA 1080
55 CTGCTCANAA GGGCATGTTG TCTTGCGGAN TANAGGCGCT CTCCTTCCCT CGTTTCCCT 1140
ATAGGTTGGG TG 1152

(2) INFORMATION FOR SEQ ID NO: 68:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2483 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

AGCAGGCGGT GCGCTGGGG CGGGAGCAGC GCGKAGCCCG GCTCGGCCAC ACCGATCGCC	60
CGCCGCCATG GGCTCCTCGC AAAGCGTCGA GATCCCGGGC GGGGGCACCG AGGGCTACCA	120
CGTTCTGCGG GTACAAGAAA ATTCCCCAGG ACACAGAGCT GGTTTGGAGC CTTTCTTTGA	180
TTTTATTGTT TCTATTAATG GTTCAAGATT AAATAAAGAC AATGACACTC TTAAGGATCT	240
GCTGAAASCA AACGTTGAAA AGCCTGTAAA GATGCTTATC TATAGCAGCA AAACATTGGA	300
ACTGCGAGAG ACCTCAGTCA CACCAAGTAA CCTGTGGGGC GGCCAGGGCT TATTGGGAGT	360
GAGCATTCGT TTCTGCAGCT TTGATGGGGC AAATGAAAAT GTTTGGCATG TGCTGGAGGT	420
GGAATCAAAT TCTCCTGCAG CACTGGCAGG TCTTAGACCA CACAGTGATT ATATAATTGG	480
AGCAGATACA GTCATGAATG AGTCTGAAGA TCTATTCAGC CTTATCGAAA CACATGAAGC	540
AAAACCATTG AAAGTGTATG TGTACAACAC AGACACTGAT AACTGTCGAG AAGTGATTAT	600
TACACCAAAT TCTGCATGGG GTGGAGAAGG CAGCCTAGGA TGTGGCATTG GATATGGTTA	660
TTTGCATCGA ATACCTACAC GCCCATTTGA GGAAGGAAAG AAAATTCTTC TTCCAGGACA	720
AATGGCTGGT ACACCTATTA CACCTCTTAA AGATGGGTTT ACAGAGGTCC AGCTGTCCTC	780
AGTTAATCCC CCGTCTTTGT CACCACCAGG AACTACAGGA ATTGAACAGA GTCTGACTGG	840
ACTTTCTATT AGCTCAACTC CACCAGCTGT CAGTAGTGT CTGAGTACAG GTGTACCAAC	900
AGTACCGTTA TTGCCACCAC AAGTAAACCA GTCCCTCACT TCTGTGCCAC CAATGAATCC	960
AGCTACTACA TTACCAGGTC TGATGCCTTT ACCAGCAGGA CTGCCCCAACC TCCCCAACCT	1020
CAACCTCAAC CTCCCAGCAC CACACATCAT GCCAGGGGTT GGCTTACCAG AACTTGTAAG	1080
CCCAGGTCG CCACCTCTTC CTTCCATGCC TCCCCGAAAC TTACCTGGCA TTGCACCTCT	1140
CCCCCTGCCA TCCGAGTTCC TCCCGTCATT CCCCTGGT CCAGAGAGCT CTTCTGCAGC	1200
AAGCTCAGGA GAGCTGCTGT CTTCCCTCCC GCCCACCAGC AACGCACCCT CTGACCCTGC	1260
CACAACTACT GCAAAGGCAG ACGCTGCCTC CTCCTCACT GTGGATGTGA CGCCCCCAC	1320
TGCCAAGGCC CCCACCACCG TTGAGGACAG AGTCGGCGAC TCCACCCAG TCAGCGAGAA	1380
GCCTGTTTCT GCGGCTGTGG ATGCCAATGC TTCTGAGTCA CCTTAACTTT GAACATTCT	1440

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326

TTGGAATTGG CGTGGTATAT TTAACCACGG GAGCGTGTCT GGAAACGCAA ACTATCATTA 1500
 ATTTTCATACT AGTTTGTACC GTATCTGTAG GCATCCTGTA AATAATTCCA AGGGGAAAAC 1560
 5 TAAACGAGGA CGTGGGTTGT ATCCTGCCAG GTTGAGTGGG GCTCACACGC TAGGGTGAGA 1620
 TGTCAGAAAG CGCTTGTATT TTAACAACCC AAAAAGAATT GTAAGGGTGG CTGCTGCCA 1680
 GGCTTGCACT GCCGTTCTTG GGGGTGTGCA TCTTCGGGAA AGGTGGTGGC GGGGCGTCCA 1740
 10 CTAGGTTTCC TGTCCCTGCG TGCTCCTTCC GTAAGAAAAT GAAATATTCT ATGCCTAATA 1800
 CTCACACGCA ACATTTCTTG TACTTTGTAA GTCGTTTGGC AGAATGCAGA CCACCTCACT 1860
 15 AAACGTGAAA CGGTAAAGAG ATTTTACTT TTGGTCTCCG TGAGTCGCAT CTCTACTAAG 1920
 GTTTACACAG GAATTCACCC TGAAGACTTG TGTTAAAGTT CTACAGCGCG CACTGTTAAC 1980
 TGAACGTCTT TTTCTTCAGC CTATACGCGG ATCCTTGTTT TGAGCTCTCA GAATCACTCA 2040
 20 GACAACATTT TGTAAGTCT GCTGTGCTT TCTACATACA CCTTATAAAG TGACATTTCA 2100
 AAAGAAATAA GGTGCCACAG TTTTAAACCA GAAGGTGGCA CTCTGTGGCT CCTGTAGTA 2160
 25 TTATAGCTAT ACTGGGAAAG CATAGATACA GCAATAAAGT ACAGTAATTT TACTTTTMTT 2220
 CTTGTGTTAC ATCTAAATTA CAACCCTTAA TTGCCACGTG TGCACCTACT ACTCTCCAGT 2280
 ATGTCTTATT ACTCTCCAGT ATGTCACGCA TCTTTAACTT TTCACGTCCT ATGTTTGCTT 2340
 30 TCTCCCATTT TTAAGAGATG GTAAGTTAAC TGAATTGAT TTAAGTAATG AAATTAATG 2400
 CAGATATCCC TGTTTTGTAA ATAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2460
 35 AAAAAAAAAA AAAAAAAAAA AAA 2483

40 (2) INFORMATION FOR SEQ ID NO: 69:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 536 base pairs
 (B) TYPE: nucleic acid
 45 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

50 GAGAAATGGA GCTTTGTTAG ATAAAAATTT TTTCAACGCA AACAGTCATT TTCCAGTGAA 60
 AGGAGAGCGT ATCCGCCGTA GGATGGACTT AGATCGTGTA AAAGCTGAGG CCACCGAGGA 120
 TATAACCTCC GGGGTCCTTT GCCTCCTTTT CCTTAGACTC CCTCCAAACT CGTGTATCTT 180
 55 TCCTTCAGCA GTACTGGGCT CCACGCGAAC CTAGTCCTTT GTCTTTACCC TATTACCTTT 240
 CATAACATCC TAGTTGAAAA GTATTATTC AACCGCGTTT GAAATGAGA ACAGGTTTAC 300
 60 AGARGCTAGG TTAAGTGGCA AGGTCGTTCA ATTAGTAACC AGTAACGCCA GGAAGTCCAG 360

327

TTTCTTGCTT CCGAATTCTC ATGGTAGCTT TCACCARGCT CCCCGTCMAA TGCTAACGTC 420
AACTACTGAA CTAGATTAGC AAAAAGGTCT TTAAACAGAA TTCCTGGTTT TCAGAGAGAG 480
5 TTTCTTTTCAT GAAGCGCCCC ATTTCTACAG AGGAAAATAA ACTCCAAGCA GCCAGT 536

10

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 865 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

20

CCACGCGTCC GGCCTTTCTT GGCCAGAGGC GCCGGTTGGA CTCACGGGCG GGGCATGATG 60
GGTAACAGGA CCGGTGGGGT CCCAGGAAG TCCTAGAGGG GGTCCGGGTT TGGGTGGACA 120
25 AGCTTTCTCTC GTCCTCTCCC GACAGAGCTG ACGTGTCTTG GGTTCACCG GGAGCGGGCA 180
TTTCCACCGG ACGGGAGGGT TCGGGGTGTC CGGGGCTGGG GAATACGTAG GGGTTGCCGC 240
GCGGTGTGGG GAGTTGGGGC GTGTGGCTGC AGTCCCGGA GTTCTTGAG GGGGTCCGCC 300
30 CACCGAGCTT CCGGACCGGC TGATCTGCCC GTAGCTTGCC GGANGGARGG CGGAGCTGAC 360
TCTCCGTCCC TTCTCCCATC CCCTCCAGTG GTGGGTACGG GCACCTCGCT GGCCTCTCC 420
35 TCCCTCCTGT CCCTGCTGCT CTTTGCTGGG ATGCAGATGT ACAGCCGTCA GCTGGCCTCC 480
ACCGAGTGGC TCACCATCCA GGGCGGCCTG CTTGGTTCGG GTCTCTTCGT GTTCTCGCTC 540
ACTGCCTTCA ATAATCTGGA GAATCTTGTC TTTGGCAAAG GATTCCAAGC AAAGATCTTC 600
40 CCTGAGATTG TCCTGTGCCT CCTGTGGCT CTCTTTGCAT CTGGCCTCAT CCACCGAGTC 660
TGTGTACCA CCTGCTTCAT CTTCTCCATG GTTGGTCTGT ACTACATCA CAAGATCTCC 720
45 TCCACCCTGT ACCAGGCAGC AGCTCCAGTC CTCACACCAG CCAAGGTCAC AGGCAAGAGC 780
AAGAAGAGAA ACTGACCCTG AATGTTCAAT AAAGTTGATT CTTTGTA AAAA 840
50 AAAAAAAAAA AAAAAAAAAA AAAAA 865

55

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

60

- (A) LENGTH: 932 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

5 TCATCATATA CAAAGTTTTT CGTCACACTG CAGGGTGA ACCAGAAGTT AGTTGCTTTG 60
 AGAACATAAG GTCTTGTCAG AGAGGAGCCC TCGCTCTTCT GTTCCTTCTC GGCACCACCT 120
 GGATCTTTGG GGTTCTCCAT GTTGTGCACG CATCAGTGGT TACAGCTTAC CTCTTCACAG 180
 10 TCAGCAATGC TTTCAGGGG ATGTTCAATT TTTTATTCCT GTGTGTTT TA TCTAGAAAGA 240
 TTCAAGAAGA ATATTACAGA TTGTTCAAAA ATGTCCCTG TTGTTTGGG TGTTTAAGGT 300
 AAACATAGAG AATGGTGGAT AATTACAAC GCACAAAAT AAAAATTCCA AGCTGTGGAT 360
 15 GACCAATGTA TAAAAATGAC TCATCAAATT ATCCAATTAT TAACTACTAG AAAAAAGTA 420
 TTTTAAATCA GTTTTCTGT TTATGCTATA GGAAGTGTAG ATAATAAGGT AAAATTATGT 480
 20 ATCATATAGA TATACTATGT TTTTCTATGT GAAATAGTTC TGTCAAAAAT AGTATTGCAG 540
 ATATTGGAA AGTAATTGGT TTCTCAGGAG TGATATCACT GCACCCAAGG AAAGATTTTC 600
 TTTCTAACAC GAGAAGTATA TGAATGTCCT GAAGGAAACC ACTGGCTTGA TATTTCTGTG 660
 25 ACTCGTGTG CCTTTGAAAC TAGTCCCTA CCACCTCGGT AATGAGCTCC ATTACAGAAA 720
 GTGGAACATA AGAGAATGAA GGGGCAGAAT ATCAACAGT GAAAAGGGAA TGATAAGATG 780
 30 TATTTTGAAT GAACTGTTTT TTCTGTAGAC TAGCTGAGAA ATTGTTGACA TAAATAAAG 840
 AATTGAAGAA ACACATTTTA CCATTTAAAA AAAAAAAAAA ACTNGAGGGG GGCCCGGTAC 900
 CCAAATCGCC GCATAGTGAT CGTAAACAAT CT 932
 35

(2) INFORMATION FOR SEQ ID NO: 72:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 996 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

45

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

50 CGCCTGGCAC CATGAGGACG CCTGGGCCTC TGCCTGTGCT GCTGCTGCTC CTGGCGGGAG 60
 CCCCOCGCCG CGGGCCCACT CCCCCGACCT GCTACTCCCG CATGCGGGCC CTGAGCCAGG 120
 AGATCACCCG CGACTTCAAC CTCTGCAGG TCTCGGAGCC CTCGGAGCCA TGTGTGAGAT 180
 55 ACCTGCCCAG GCTGTACCTG GACATACACA ATTACTGTGT GCTGGACAAG CTGCGGGACT 240
 TTGTGGCCTC GCCCCCGTGT TGGAAAGTGG CCCAGGTAGA TTCCTTGAAG GACAAAGCAC 300
 GGAAGCTGTA CACCATCATG AACTCGTTCT GCAGGAGAGA TTTGGTATTC CTGTTGGATG 360
 60

ACTGCAATGC CTTGGAATAC CCAATCCCAG TGA CTACGGT CCTGCCAGAT CGTCAGCGCT 420
 AAGGGAAGT AGACCAGAGA AAGAACCCAA GAGAACTAAA GTTATGTCAG CTACCCAGAC 480
 5 TTAATGGGCC AGAGCCATGA CCCTCACAGG TCTTGTGTTA GTGTATCTG AAAGTGTAT 540
 GTATCTCTCT ACCTTCTGGA AACAGGGCT GGTATTCCTA CCCNGGAACC TCCTTTGAGC 600
 ATAGAGTTAG CAACCATGCT TCTCATTCCT TGA CTACG TCTTGCCAGG ATGGTTAGAT 660
 10 ACACAGCATG TTGATTGGT CACCTAAAA GAAGAAAAG ACTAACAAGC TTCACCTTTA 720
 TGAACAATA TTTGAGAAC ATGCACAATA GTATGTTTT ATTACTGGT TAATGGAGTA 780
 15 ATGGTACTTT TATTCTTCT TGATAGAAC CTGCTTACAT TTAACCAAGC TTCTATTATG 840
 CCTTTTCTA ACACAGACTT TCTTCACTGT CTTTCATTTA AAAAGAAAT AATGCTCTTA 900
 AGATATATAT TTTAYGTAGT GCTGACAGGA CCCACTCTTT CATTGAAAGG TGATGAAAT 960
 20 CAAATAAAGA ATCTCTTCAC ATGAAAAA AAAAAA 996

25

(2) INFORMATION FOR SEQ ID NO: 73:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 785 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

40

GGCACGAGGG GCTTTGCGTA CACAATAGCT GCTAGGAGTA CCCAAGCCT GARTACARCC 60
 TGCTGGTGTG ATGGCCACGT GTGAGCAGG CAGCGTCAMA CGGCTCGCTG TGACCCGTCC 120
 40 CGRAGACTGA AATGGGCCTG GGTCTTCTCC TKGTCCTGTG ATWAAAGTCC TCTCTGAAA 180
 GTGAGAGCA AAGGCACACA GAGGTGCGG CTCACAAGAA TTCCTCCCGG TGACTGGGTA 240
 45 ATCAATGTTA CTGCTGTTTC CTTTGCAGGA AAGACCACAG CAAGATTCTT TCATTCTCT 300
 CCTCTAGCC TGGGGGACCA GGCTCGAACT GACCCTGGAC ATCAAAGGAG GGATTATGTG 360
 GCTGCTAAAG CCATCGGCC ACAGCCCTGT TCACRTCTTG GTGCTTCTCT TCCCAGAGG 420
 50 CTGGTCCCAG CCAGGCACAC ACAAAGGCA GATTCTCGTA AACSCAGCCT CCTCCCTGG 480
 AGGCTGCCTC CTGCCCTGGA TCTGGAGTGG AGCTGCTCTG AGATTTTGAG TTCTTCTGCA 540
 GAGATGATTA AATATATCCA AGAGACATTG GAAACCTGC TGAACATTTT ACATTGGTCT 600
 55 GCTCAGCACA TGGCTGGATG CGGATATTTC TATAATTCCA GAAAGTCACA CAGCTCCTCT 660
 GTATGAGACC AGTGGGCGCC ATTTAAAAA ACAGGATGAG AATCTAAGAT ATATTATTAA 720
 60 TAAATGTAAT GGATTTTTTT TTTGTAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 780

AAAAA

785

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(2) INFORMATION FOR SEQ ID NO: 74:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1069 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

TCCTCACCAT TCCCCTAGGN CAGGTCCCTG CAGGTCCAC ACTTCTCCCA GGTCCCTAAA	60
CTTGGGTCGG TCCTTTCCCT GGAGTAGCTG GNTCCTCCAG TCGAGGTCCC TGTTTCAGTCG	120
20 GTTCTTAGGC TCCTGCACAT GAAGGTGTGT GCCTGTGGTG TGTGGGCTGC TCTAGGAGCA	180
GATACAGGCT GGTATAGAGG ATGCAGAAAG GTAGGGCAGT ATGTTTAAGT CCAGACTTGG	240
25 CACATGGCTA GGGATACTGC TCACTAGCTG TGGAGGTCCT CAGGAGTGA GAGAATGAGT	300
AGGAGGGCAG AAGCTTCCAT TTTGTCCCTT CCTAAGACCC TGTTATTGT GTTATTTCTT	360
GCCTTTCCGA GTCCTGCAGT GGGCTGCCCT GTACCCTGAA CCTCATGAGC CTCTAAGGGA	420
30 AAGGAGGAAC AATTAGGACG TGGCAATGAG ACCTGGCAGG GCAGARTACA AGCCCAGCAC	480
CAGTGTCCCA GCCTTACTGG GTCCTTACCC TGGGCCAAAC AGGGAGGGCT GATACCTCCT	540
35 TGCTCTTCCT AGATGCCCAC CTCCTACAAT CTCAGCCCAC AAGTCCTCTC CACCCTAGGG	600
GGCTTGCTGC ATGGCAATAA CTCATAATCT GATTTGGAGG TTTGCCCTTT ACAGGGGCAG	660
ATTTTCTGCT CAGTTCAACA ATGAAATGAA GAGGAACTCC CTCCTTCTAC AGCTCACTTC	720
40 TATCAGAGGC CCAGGTGCCT CAGAGCCACA TTGAGTGTCT TTTTCTGGGA TGAGGAAGTA	780
GGGTAAACT CCCAGTTTC CTGAGGGAGG CTCCTGACAG GTGCCCTTTG TCAGACCCTA	840
45 CCACAGCCTG GATAGGCAGC CACATGGTTC CTCGCCCTTG CTCGGNACTC CGTGGTGGTC	900
CTGCCCTTCT CCCTGCATGC CTGTGGGTCT GCTCTGGTGT GTGAAGGTCG GTGGGTAAAC	960
TGTGTGCCTA CTGAACCTGG CAAATAAACA TCACCCTGCA AAGCCAAAAA AAAAAAAAAA	1020
50 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1069

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(2) INFORMATION FOR SEQ ID NO: 75:

- 60 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 831 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

5
GGACATTAGA TCACTGTGGA CCTAAAACAA ACAACAACCT ATAAGGAAAA TGGCATTAGA 60
AATGGTCTGG GGATCAGTTT ATCACTGCAG TTGTTACATC ACCCCATGGT CTAAAATACA 120
10 GAGCTTTAGT CTGTCTCTGT TTCAGTTCAT TTTACAGGAG GTGAACATCA CACTTCCAGA 180
AAACTCTGTC TGGTATGAAA GGTATAAAAT TGATATTCCT GTCTTTCAC TGAATGGCCA 240
GTTTCTGATG ATGCATCGAG TAAACACCTC AAAACTTGAA AAACAGCTCC TGAAACTTGA 300
15 GCAGCAAAGT ACTGGARGCT GACTGATGCC CTCATGATTT TCCACCCTCT CTTCCCATAA 360
AGCATCTTCC TAAGGAAATG AMCATGGCCT GATACTCATT TTGTCACTTG TACAGAGCCC 420
20 TAAGGATGTT CTGAATTCAG TGGTGCCAAA TAAATGTTGA CATTCCCCTT TTGGTTGATG 480
GAAGTATCAG TGTGGGAAC TTTTGCTTAA TGGCATTTTA TAAATAAKA AKAKCATATT 540
AGCAGGGAGG GAGATGATGG AGGGAGGGAG AAGTCCATTT GTCTTATTTA TCCTTTTGTG 600
25 ATTAATAGAG AAGCACTTCA CAGTCACTGG CAATGCCATT TATAGGAAGA AGGTTCTGCA 660
TTCTTGCTGC TCCCGGAGGG CTTAACTTTT TAATGAAAGA ATAAATGCTC TTCCACTCAG 720
30 TAGATAAAGT GAAATGTGAA TTGTTAATAA CTGTGCACGG TCAATAAAGC GATGTTTTAA 780
GGAATACAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAACTCG A 831

35

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:
40 (A) LENGTH: 590 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

TATATATAGA CNGTTAATAG TCGTGANTGN TGTGNACGAA CATTAACGGA AGTAGCATGT 60
AGCCAGTCGA ATAACNTATA AGGACAAAGT GGAGTCCACG CGTGCGGCCG TCTAGACTAG 120
50 TGGATCCCCC GGCTGCAGGA TTCGGCACGA GCTGCCAGGT GAGGAGCAGA GAGACTGTTC 180
CCTTGGGTGG AGAGGTGTGG GCATGAGAGC CACCCATTGC CAAGCAGCAA GAATGTTTCGT 240
55 GCTTTTTTCC CTTCCAAAT ATGCAGGGCT CAGGCTCCCA ATTCCGGGCC TGTCTGCTTT 300
GCTTGTGTTT CTCCTGTCCC TGTCTCCCG GAGGGCCAG GTGGAATCA CGACAGGGAG 360
GGAGACGCTT CCCAAAAACC TGCAGGGCTA TTTCCAGAA TTTGGTTTTT AAGTACAAAA 420
60

CTTTTGTGCC TGTAAGATAT ATGCAGCCTC ACAGAAGCAG CCTCTGCCCTC CACTTTACCA 480
 GCTACGTTTT TATCTTAAGC ACATGGGGCT CCCTTAGAAC TTACTCCACT GATTTAAAAA 540
 5 AAAAAAAAAA AAACGAGG GGGGCCCCG TACCCATTCG CCCTAAAAGT 590

10 (2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1274 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

20 GAGCCACCAC ACCTGGCCTG GAAGGAACCT CTTAAATCA GTTACGTCT TGTATTTTGT 60
 TCTGTGATGG AGGACACTGG AGAGAGTTGC TATTCAGTC AATCATGTCG AGTCACTGGA 120
 CTCTGAAAT CCTATTGGTT CCTTTATTTT ATTGAGTTT AGAGTTCCT TCTGGGTTTG 180
 25 TATTATGTCT GGCAATGAC CTGGGTATC ACTTTTCCTC CAGGGTTAGA TCATAGATCT 240
 TGGAACTCC TTAGAGAGCA TTTTGCTCCT ACCAAGGATC AGATACTGGA GCCCCACATA 300
 30 ATAGATTTCA TTCACTCTA GCCTACATAG AGCTTTCTGT TGCTGTCTCT TGCCATGCAC 360
 TTGTGCGGTG ATTACACACT TGACAGTACC AGGAGACAAA TGAATTACAG ATCCCCCGAC 420
 ATGCCTCTTC CCCTGGCAA GCTCAGTTGC CCTGATAGTA GCATGTTTCT GTTCTGATG 480
 35 TACCTTTTTT CTCTTCTCT TGCATCAGC CAATTCCTCAG AATTTCCCCA GGCAATTTGT 540
 AGAGGACCTT TTTGGGGTCC TATATGAGCC ATGTCCTCAA AGCTTTTAAA CCTCCTTGCT 600
 40 CTCCTACAAT ATTCAGTACA TGACCACTGT CATCTAGAA GGCTTCTGAA AAGAGGGGCA 660
 AGAGCCACTC TGCGCCACAA AGGTTGGGGT CCATCTTCTC TCCGAGGTG TGAAGTTT 720
 CAAATGTAC TAATAGGSTG GGGCCCTGAC TTGGCTGTGG GCTTTGGGAG GGGTAAGCTG 780
 45 CTTTCTAGAT CTCTCCCACT GAGGCATGGA GGTGTTTCTG AATTTTGTCT ACCTCACAGG 840
 GATGTTGTGA GGCTTGAAAA GGTCAAAAAA TGATGGCCCC TTGAGCTCTT TGTAAGAAAG 900
 50 GTAGATGAAA TATCGGATGT AATCTGAAAA AAAGATAAAA TGTGACTTCC CTGCTCTGT 960
 GCAGCAGTCG GGCTGGATGC TCTGTGGCCT TTCTTGGGTC CTCATGCCAC CCCACAGCTC 1020
 CCAGGAACCT TGAAGCCAAT CTGGGGGACT TTCAGATGTT TGACAAAGAG GTACCAGGCA 1080
 55 AACTTCCTGC TACACATGCC CTGAATGAAT TGCTAAATTT CAAAGGAAAT GGACCCTGCT 1140
 TTAAAGGATG TACAAAAGTA TGCTGCATC GATGCTGTA CTGTAAATTT CTAATTTATC 1200
 60 ACTGTACAAA GAAAACCCCT TGCTATTTAA TTTTGTATTA AAGGAAAATA AAGTTTGT 1260

TGT TAAAAAA AAAA

1274

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(2) INFORMATION FOR SEQ ID NO: 78:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1133 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

AGGATTTTTC	CTTGTTCAAC	CAAAATCTGA	GCATTCTTTC	TATGTTGAAA	ACACTGAAAA	60
ACTAATTTWA	GTTAATGAAC	TAGAAAGAAT	ATTGATTTTW	AAGAAACAGA	AAAATACTAC	120
TTATTTTCTC	TCTCAAATAA	CGTTTCTTTC	AAAAACTTCT	GGCTGAAGTA	TAACATGCTG	180
GTAGTTAACA	TAAATCTTGT	CTTCTCTTGT	TTCTTTATCT	TTCTTTGTTA	TTTAGATGCT	240
TGTATAAATG	TCTTTTGTTC	TTATTAAGTG	CCTAATTGAC	AGAGCTTAAT	TTGAAGAAGT	300
GCCCTAATTT	ATTGACCACT	TAAGAATTGC	CTTTATTGGG	GTATTTTATT	TGTCCTGCG	360
TCTTTTGTAT	GTGTTTCAGT	CTACTCATCC	CTGTGAGTAT	GTGTGGGGGA	CAGCTGATAG	420
AAGGGAGGAG	AGTGTGTCTA	TGCTCAGGAT	TGCCCTTTAG	CCACTCAGCC	AGAGATCCAC	480
AGGGAGCAAC	AAGGACAGTT	TCACATGCTT	AGACTTTCTT	GGAAGAAACA	GTGAGGAGGA	540
GTAAGTCGTG	AGTAGTGTC	AGCTGGATGT	AGAATTGTCC	TAAGGCAGTT	GACCCACCT	600
TCCAACATGT	TTTCACTTTA	TTTGCCCTTC	CCTACATTTG	GGTTAGGTTT	CATTTGGATT	660
TGCAGCAATA	ATGACTTTAT	TTCTCTCTTG	GTCAGGATTT	GGCACATAAA	ATCCTTTTAT	720
TATAGAACTA	GCTATTTTAG	TTACATAGTA	ATGTAATAA	TGGAGAGATT	TATAGAGAAT	780
TTTGKTTTTC	CTGTCATATA	TGTCCATTTT	GGAGACAGAT	ATGATAGAAC	TAGAAATTAA	840
GTTGCATTTT	TGCAAGTGCC	ATTTGAATGA	ACTTCAAGTA	TCTTCTTAAT	TATTAAATTT	900
TCTGATGAAG	GCATTGTAAC	AAATATATAG	TATTATTAAA	TCTAATTAAT	ATTTGGAAAT	960
ATTAATAAAT	AGGTATTTTA	TTTACTGTAA	AAAGTCAAAC	TTCATTATGT	AGATAAATCT	1020
TATTCCTTTC	ATTCCTTCCC	CTGTTTACAT	CCTTTTACAT	AAGCTTAGTC	ACCAATTAAA	1080
GCTTTCCTAT	CAAAAAA	AAAAA	ACTCGAGACT	AGTTCTCTCT	CCT	1133

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(2) INFORMATION FOR SEQ ID NO: 79:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 661 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

GAATTCGGCA CGAGGGGAAA AGGATGCTGA ACGAGAGCAG AAAGCCTCTT TCCTTTGCTT 60
10 CACGCCTTTC CAGTCTTTAT TTAAACTCG GGTTCCTTTT CTGTGGTGGC AGCAACCTTT 120
ACTCCACCTG CACTGCTGCT CCTGGGGGCT CCCAGGCCT CCTCTGCCT TTCTACCCAG 180
TGGCTGACGG GATGCCTGTC TTGCCTGGAC GCACCACTGC TCTCCTGTCC CTCACCTTGG 240
15 CTTTGTCTGT GCCCTGCTCT GGGGTTGAAG CTGGCCCATG TGTCCTCCCG AGTCATGGCT 300
GCTCCTCTG GGAGGCCTCT GTGTGCGTCA CGTCTTCCAC ACCTGGGGGC AGCTGGCGAG 360
20 CCCGTGCTCT GTTCCCTCG GCTGCTTGGC ACAGAGTGC AGCCTGGGAY TCTCCGTGGA 420
CCCAGACTGG GGATTTTGCC AGGGGGGCGA TGGGAGGAGC AGGTGCTTTG CCTGGCGGCT 480
GTGTCTGCAT TTCTGGACGC CCCAGAGCAC AGAAGTTGCC GGCACCTTGA GGTCTTCCTC 540
25 GGCATGTGCC AGATTACATG AGTGACGGCT GGAATATGT TTTCTTTTGT GTAATGGAGG 600
CGTGTTCAC ATATAGTAA GCTCACCAA AAGTAAAAA AAAAAAAAAA AAAAACTCG 660
30 A 661

35 (2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1378 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

45 ATTGGGTACC GGGCCCCCCC TCGAAGTTTT TTTTTTTTTT TTTAATGAA AGCTCTCAA 60
TAAGCGATT TATTCCTATC CATGATGCA GACATTTACA AAACCATAAC ATCTGAGTTC 120
ACCTTAAAA ATAACCTATA TAAAGCAGTG ATATACACAG CACAAAATAG TTCAGGGAGG 180
50 GGGCAGGAGC AACTTGTAAT AATTAAAATG TAAACGTGAA AAAAAGGATG GAATAAAAGT 240
CCCTACTTAT TTCTACTTAA GATGTCATGT GATAATATTT TACAATGTCC TGTGGGTCAA 300
TGTATGTATG TGTATATGTC TGTATAACAT ACACATATAC AGTACATTCT CTTTCCACA 360
CATATACATA CACACATAAT TATTTGCAGT TCAGTTTAGG GCAATTCTAA TATGCCACTC 420
60 CGTACAGTTG TTTGAATCAC ATTTGGACCC GCTTCTCTCA CAAAAGAGGG GAGAGAGCAG 480

5 GAAATAAAAA GGTGGTTTG GTGTGACTGA GATTCCCTTG TTAACTGTA CACTGTGATG 540
 AATAATTTTC TTCCGTAGTA GTTCTGTGAA GGGCTGACTC ACTGTGGTTT TCATGAGGAG 600
 10 ACTTGGTAAT GGATCACACG CTCATTGTCA TGCTAGGGGA GTAACTCTCA CTCTGAAAAG 660
 GATTTAAGAA ATTTCCCCC ATTTCCGCAT CATCCCTTGG AGTGCCCGGT TGATTACTCA 720
 GGCTCATATT ATTGGGAGAA TTCTTGAAA TACTGTCCAT ATCTCCTGAG CCTAAAGAGC 780
 15 CATTCATGTG ATGTGACTCC ATTCCTCCTA ATCCACCCAT GGGACCATCT GACCCAGGRC 840
 CCATTGAAA ATTAGGTCTG TTAGGTCCAG GAGGTACTGC ATTCATTAAA GTATACATGT 900
 TATCACCAGA GTTGGTTGAA TCTGCTGGAC TAGGCATGAT GGGTGTTCCT GGTGGCCCTC 960
 CACCTCCTGG AGGACCTACA TAATTCCCAG GAGATGCTGA GGAGTATGGT ATTGAATTGG 1020
 20 CATTTGTGTG GTTTGGCCAA GGCTACCAC CACCTGGACC CATGTTTCATT CCAGGCATTC 1080
 CAGGGCCACC TAAAGCAATC AGTGGGGGTC TCATTGCACC TCCATAGTTC TGTGGTCCTA 1140
 AGGGCACCAT TCCTCTTGA GAGTCATTC TCTGCATTGG CCCACCCATA TTTGGATGTC 1200
 25 CTTGTTGTCG AGTTGGATCC ATTCCACTGG GGAGTAATGG CTGACTTCCT GGGACACCTC 1260
 CAAGTGCTG ATTAGGTATC CTCAATGGG GCCTTGACC TCCAGGTAC CGAGGTGACA 1320
 30 TAAAAGGTA ATCATGGAAG GCTTTTGCTT CACTGAGTG TTCACATGTT TCACGTCT 1378

35 (2) INFORMATION FOR SEQ ID NO: 81:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1440 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

45 ACTTTGTCCA AATGTGTCTG TCACATGTAG TCAGCTGNAG NAATTTAAAA TGAATTGCCA 60
 AGTGAAGAGT CTGTGGATTA ATTGGCCGTT AATTAACAGG CTTTATCAAT GTGTCCTCAA 120
 GGGAGAGGCC CAACCCTAAT TAAGGAGCTA AACTTCCTGA GTGAGGGGCT GTGAGGATGG 180
 50 AGGTGGAGGA GGCATCTGGG GCGGGTGGTG GCCGGGCCAG CAGATGGCGC CTCCCTGGCT 240
 GAGCTGCCCG CACCGCCAGT TCCCTCATTT CCACTCAGGA AGGCAGAGAA GGCAGAGTGA 300
 TCTCCTCAAG GAAGAGCTTC CCCAGCCTTC GGGAGCAGCT GGCAGGGCGT CCGGAATAA 360
 55 GCCCTACACG CCGCCGCTG CCTCCAATC ACTAACCCTG CGCCTCTTGT CTTTCAGATT 420
 CAACGCGTTC AACAGAAGCC ATCCCAGCC CAGCTTAAAT TATAAAGATA GACAATAACT 480
 60 CTGTTCCAAT CTGCGTGGTG CTTCTTTAGT AAATACTGTA CAGATTTTAC CATGGAGAAC 540

5 TTTTITTTTA GTTTTACCT TTTCTAATT ACCCTTATTC CGAATGGACG AACACTTTCT 600
 ACCACTGCTG ACCATTGTAA AATACCGTGT ATATAAATCC CATTGAAATA ATGCCCTGGA 660
 ATAGAACATC TCAAATGCTG CTTAATTACA GACTCAGGTC GATTACTTGT ATTTTCATGTA 720
 ATGTCCTCC AAGTTAGACA TCTGGTGCAA GACCAACCGG GAGACCATGG AATTGTCAAA 780
 10 AGTACAAACT GACAGTGTGT ATATTTAATT TAAAGACTTA TTTAAAACT CACAAGCTCT 840
 CACCTAGACT TTGGAGAGCA GTCTGTTTTT TGTAAATGTCT GATACTAGAA ACTAATTGTC 900
 TTATTTTAGT TGTATTCAAG ATTTGAAGAT GTATTTTATA GACAAGTTCT GTTTTGAAC 960
 15 TTTGTGGAAC TGTTC AATCAATTTT CCAGTTATGA TGAGTATTTA CATTATGAAT 1020
 GTATAACCCA GACATGATTT GTAAAGCCGA CAGTATGTTT CTATTACACA ACACTTTTGT 1080
 20 ATACAGCGTC TCTGTCTTTC ACTGATACTG GAGTCTCCGT TGTCTGCNNG GTCCCTTGA 1140
 GTTCTTAGTT ACAGACACAA TCATACTGTG ATTTTATTTT TAATATGGAT ATGCTATCAA 1200
 ACTGTGATAC ACTTATAATT CACTGGTCCT GCATCAGGAG ATGGAGTGGG GAAAACGTGA 1260
 25 TTTAATACAG TTTGTATCTG AATAATCTGT ATGGTTTATA CAGTTTGTGT TGTTCAGAGA 1320
 TGTTTAAAGT TTGATCTTTG TTTTCTAAA GATTAAAAA GCACTTGCCC CACTGTAAAT 1380
 30 ATACAGCATG TAAATTTCT RTAGTATATA AATGGCAGCA AATCACAAA AAAAAAAAAAN 1440

35 (2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1381 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

45 CCCGGGCTGC AGGAATTCGK YACGAGGCCA GCAGTTGCTC CCAGTTCAGG AGGTGCTCCT 60
 GTACCCCTGGC CACAGCCCAA TCCTGCCACT GCTGACATCT GGGGAGACTT TACCAAATCT 120
 ACAGGATCAA CTTCCAGCCA GACCCAGCCA GGCACAGGCT GGGTCCAGTT CTGACCTGAG 180
 50 CACGGTTTTT CCTCATGTGA CTCTGGGAA GCGCTCCCT CATCTGGGCC AAAGGAAGGA 240
 GGACGAAGCC CTCCTCAGCT GGCTGTGTT TGGGGCATGA ATCTCTCCTC TCCTCCTTGT 300
 55 CTGGCTCTGT TGACAAACCG GGCATGTTG GCAGTAAAT GGCACCGTGT CACACTGTTT 360
 CCTGGGATTC AAGTATGCAA CCAGAACACA GGAGAAGAAA AGCTCCAGGA TCCCTGTCCC 420
 60 CATCTGTCCT CTTGATGTGA GAGAGACTCT GAGACTTCTT CCATCGCAAT GACCTGTATT 480

	AAACACAAGC CCCCCAAGCA AAAGAAGAGG TTGAGTTTGC TGCCAGGATT CAGATCAGCC	540
	CTTCCCAGGG TCTGCAGGTG TCACATGATC ACAGTTCAGC GGGAGGCTTT CCGTACCCAC	600
5	ACTGGCTGTA GCACTTCAGT CCATCTGCCC TCCAGAGGAG GGTTCCTTCC TGATTTTATG	660
	CAGGTTTAGA GGCTGCAGCT TGAGCTACAA TCAGGAGGGA AATTGGAAGG ATTAGCAGCT	720
10	TTTAAAAATG TTTAAATATT TTGCTTTGCT AATGTGCTGA TCCGCACTAA CTCATCTTTG	780
	CAAAAGGAAC TGCTCCCTCG GCGTGCCCCA GCTGGGGCCT CTGAAGGGAT TCCTCACTGT	840
	GGGCAGCTGC CCTGAGCTTC AGGCAGCAGT GTTCATCTCT GCCCAGTTGT CTGGTTTCCA	900
15	TGTATTCTAG GCCAGGTAGG CAACACAGAG CCAAGGCGGG TGCTGGAAGC CAGACGGAAC	960
	AGTGTGTTGGG CAGGAAGGTG GATGCTGTTG TCATGGAGCT GTGGGAGTTG GCACTCTGTC	1020
20	TGCTGGTGGC CCTCTCGGCT CACATGTTCA CAGTGCAGCT CCTGGCAGAC TTGGGTTTTC	1080
	TCTTTGGTGG TTTCTAAAGT GCCTTATCTG CAAACAACCT CTTTCTCTCT TCAGGAACTG	1140
	TGAATGGCTA GAAGAAGGAG CTCAGTAAAC TAGAAGTCCA GGGTTGCTTG GTTACTGGT	1200
25	TTATAAGAAA TCTGAAAGCA CCTCTGACAT TCCTTTTATT AACTCACCTC TCAGTTGAAA	1260
	GATTTCTTCT TTGAAAGGTC AAGACCGTGA ACTGAAAAAA GTGTTGCGCT TTTGCGGGA	1320
30	CCAGATTTTT AAGATAAAAT AAATATTTTT ACTTCTGTCA AAAAAAAAAA AAAAAAATNT	1380
	C	1381

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(2) INFORMATION FOR SEQ ID NO: 83:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1706 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

45

	ACTGCACCCAC TGCCAGGTC TCCCGGCTGG ATGAAGACGT GGTCCATGAG GAAGCTGGCT	60
	AGCTCAGACT GGAGAGTAGC TTCAGGAAAA AAGACAAGTG GCCTAAGGAA ATCACGCCCC	120
50	CCAACTATCA TCTGAGGGCT AAAGATGAGA AGTAGATCAC TTAATAAGAC AAAAGCCTGT	180
	AGGGGGAAAA GAAAGGATGT TTAAGAGGAC AGAATGTTTC CCAAGGTAGA AATGACACTG	240
55	TCAATTTCTC CTTGGAATGG GGGCAGGGAT ACTCGCCTTG TTGCTCCAC TTGAGTCAGT	300
	ACTCACCTGC TCCTGGATCT CAGTATCCAC ATCTGAGAGG CAACTCTGGC AGAGTTCACA	360
	GAAGGCCACC ATTCTGTCCC TCAAACCTGA CAGCTGCTTC TGTGGGCACA GTGGCTTGAA	420
60	GGGAAGAAT GAAGACACAG ACTCCTCTGT TCCCATATC CCATCTAAGA CCCCACTCA	480

CCTGGGAAG CATCTGATTT AGAAATGTGG GTTAGTGTCC AGAGAATGGA AAAATAGACA 540
 AGAGTCAAGG CTGGCAGGAT AACCTGTAAC AACAAAGGGT TTGAAAAATG AGGTTTGGGT 600
 5 TAGGAGAGGG AGAGACAGAT AGCCAGAAAC ACACCAGTGA AGAGGAGAGA AAATGAGTAA 660
 AGGGAGAGCT AATTCCTTTT CCAGTGGAAA ATGAGTGATA TTCTGGACAT TCTTCAGAGG 720
 10 CATCTACAG AAGTAGAAAT GTCACCGCTC CCTAATTAC TCTACGTCTT CTAGAATCCC 780
 TCAATATTAT CCTTGGCTTC CAGGAAATCC AAGAAGACCC TGGAAGTAGA GTCCACCTTC 840
 TAAGAGAGGA ATGTAAGAGG TGACCCCCAC CCACCTGATC TTCCTCGCTT TGTCCTCTCC 900
 15 ACGCACTGAG ACTTGACACA CCTAGTGGCC ACCTAGAACG TAGGTCCTTA AAATYTAGCC 960
 CCCCAGCCCC CAACCCATCT CTAGCCTGTC CACTCACCTG GTGAGGAACY TYTCCTGTGT 1020
 20 CCACAGCYTT CTGCAGGAGT TGGCAACATG GCTCATAGAG CTCCCAGCGA GTCAGGTCAT 1080
 GAGTGCTTTG GGGGAGAAAG GGAATGTTA TACTGGAAAA GAACAGAGGG AACCAACTCC 1140
 ACAGACACCA GTAAAAACGG GATGGGAAG AGGAGGAAAG CCACTCACTT GTAGAAGGCA 1200
 25 GAGAGGCGTT TCAGAGTGGC TGCCAGATTA TATACCTCAT CCTCATCTAG GAAGGACGAC 1260
 TGAGAAGGAA AGAAGATCCA CAATAGCATT TCCCCAGAA CTCATCAGTC CACATCCCCC 1320
 30 GTCTTGACG CCCTCCACC CTGTGTTGGG GTGTCCCATT GTCCAGCCCC AGCTCCTACC 1380
 TGTAACAGCT CTTCAAGCTC CTGCTGGAAR CGGTCAGTCA GCAAATCTAC TAGCTGGCTG 1440
 CGGGCAAAGT CCGCCCGGCT GAAGAAAGTG AATTCGGGAT TACAGAGCAG GTAAGAGCAT 1500
 35 GCGCCCCAGC CTCAAGCACC GCTGGCTCTG CATGCTTCAC CACCACCTCC TGGAGTTGCT 1560
 GCAGGAACAG CTCCAGGTGC TGAGAAGAAA AGGCAGAAGA TGGTGTGCTG TGGGATGGG 1620
 40 AGGAGGACAC TCTTCTGGCG GGAAGTGGA CGGGTTAAA AGCATTAAAC TTCAAGGATA 1680
 AGATGCCTAA RAAAAAAAAA AAAAAA 1706

45

(2) INFORMATION FOR SEQ ID NO: 84:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

GAATTCGGCA CGAGCTTGGT AGCCTTAGAA CTGCATGAGC TGCTTTACCA CTGGGAAACA 60
 CGAGCACAGC CTAGCTTGAT TTTGTATGTG GTATCAGATC TAAGGTGGAT GGAATTCAGG 120
 60

ACTTCCTGTC TACTCTTTGA TTTTGTTTTA TTTTGTAGAA TGTTTTATTT TGTTTTATTC 180
 ATTTATTCAT CTTCAGAGAC ATGGTCTGGC TCTGTGCCC AGGATGGAGT GCATGGTGTG 240
 5 ATCATAGGCC ACTGCAGTGT TGAGCTCCCG GGCTCAGGCG ATCCTCCTGC CTCAGCTYCC 300
 TTAGTAGCTG GGACTATAGG CACATGCCCT ACCATGCCCTG GCTTTGTCTA CTTTTGAAT 360
 GATGTCYCAA ACTAGAAGGT CTATTAATTT AAAAAATTAA GGATAGCATG CCATAATTAA 420
 10 AAATAATAAC AGTGGGAAAA GGCACCTTCC AATGATTCAG ACATCAACTT GTGATTTAAA 480
 AAAACGAAAA ATAAATAATA GAAAAAAG GGGAAAAAGT TAAATAAAAA TAAAATTAAA 540
 15 AAAAAAAAAA AAAAAGCTGA GGGGGGCCCC GTA 573

20 (2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 684 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

30 CTCTTTGGCT GTGTCTACCT CCTTCATCTG CTGCGCCGAC ATAAGCACCG CCCTGCCCCCT 60
 AGGCTCCAGC CGTCCCGCAC CAGCCCCCAG GCACCGAGAG CACGAGCATG GGCACCAAGC 120
 CAGGCCCTCC AGGCTGCTCT YCAGTCCCT TATGCCACTA TCAACACCAG CTGCTGCCCCA 180
 35 GCTACTTTGG ACACAGCTCA CCCCCATGGG GGGCCGTCCT GGTGGGGTTC ACTCCCCACC 240
 CACGCTGCAC ACCGGCCCCA GGGCCCTGCC GCCTGGGCCT CCACACCCAT CCCTGCACGT 300
 40 GGCAGCTTGT TCTCTGTTGA GAATGGACTC TACGCTCAGG CAGGGGAGAR GCCTCCTCAC 360
 ACTGGTCCCG GCCTCACTCT TTTCCCTGAC CCTCGGGGGC CCAGGGCCAT GGAAGGACCC 420
 TTAGGAGTTC GATGAGAGAG ACCATGAGGC CACTGGGCTT TCCCCCTCCC AGGCCTCCTG 480
 45 GGTGTCAATC CCTTACTTTA ATTCTTGGGC CTCCAATAAG TGTCCCATAG GTGTCTGGCC 540
 AGGCCACCT GCTGCGGATG TGGTCTGTGT GCGTGTGTGG GCACAGGTGT GAGTGTGTGA 600
 50 GTGACAGTTA CCCCATTTCA GTCATTTCTT GCTGCAACTA AGTCAGCAAC ACAGTTTCTC 660
 TGAAAAAAAA AAAAAAAAAA AAAC 684

55

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 1036 base pairs

340

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

TGGAGGCAGA TGCACAGGAG AAAGGTTCCC GTCCGCACCC TCTCAGACCT GAGGCTGAGC 60
TTGCAGTGAG GGCTTCTCCT CGGCCCTCG CCGCCCCCA GAGCTGCCAT CCCTGCTGTT 120
10 ACAAGCCAGA GGAGCCCGA TGTGAGGCC CAGATCACCT CCAGGACTT GGGGTTCCTCA 180
TCTGAAATCC TTTATTTTGG TACCATGGGG TGGGCCCGG GCTGAGAAGG AAGAAGCACC 240
15 CTCTCCCCGG CCTCCTCTGT CTGCACCCGT GGGGCTGTGA CTTACTCCTG CCTCCAGGGG 300
CGGGGCGGGG CCCCTTGGGA CCTCTTAAGG CCAAGGTGG GCGCCAGGAC CTYTGCGCAG 360
AGTGAYTGC TCATGGCAGA TGTGTGGCAA TGTCTGGCTG WGTCTTTCCG GCAMCTGCGT 420
20 YCCCTYTCCC GGGYTCCCT GCTGCATGGT GGATGTGCTC CTTCTGGCC CGGTCACATT 480
GCCTCCTTGA GCCTTAGTCC AGGGGGTCAC TYCTCCACC CCACCTACCT CACAGGGTTG 540
25 TTGTGAGGGT GCACAGAGGA GCAAAGTCCC TGAAGGCCCT CAGGCAGTAT ATAGGGGCGG 600
CCCACCTTCA GCTGCCCTGG GATGGGAAGG ACCCAGCCCG ACCCTGGGC ATAACACTGT 660
GTTTGCAAT GGAGATTGAG GTATTGGGA TGCAGGTTGT GGGGAGCTGG CCTGGCAGAG 720
30 TAGGGGTAGT TGGCTTGGCC TTCTCTTGG TGATCCACC CCCAGCCATT TGCATTGCTG 780
GCCCAGCGCC TGGCTTGGG GCGGGGAGA GGCAGAGAA GGGCTGGC AGGGGCGGTG 840
35 GAGGACTCAG GAACTGCCG GGGAGAGTGG GTATGGCGC TGAGCCAGG GCCCTCCTGT 900
GTTTGACTTC CCGGATGGG TCCTTGCTC TCAGCTGTGT CCGACCCAC CATGTAATAA 960
AACCCAAAGG AACAGCAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1020
40 CCCNGGGGGG GNCCCG 1036

45

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 908 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

55 TTAAACAAAT GGAATCATGC AATATGTGAC CTTTTCGTC TGGCTTATTT TATTTAGCAT 60
AATGTTTTTG AGGTTTCATCC AAGCTGTAGC ATGTATCAGC ACCTCATTTT TTTTCTGGC 120
60 TGAATATTAT TCCATTATAT GGATTACCA CAATTCAATT ACCTATTCAT CTTTGTGTTT 180

5 TGCTGTCTGG CTATTGTGAA TAATGCTTCG ATAAACATTC ATATACAAGT TTCTATGTGG 240
 CTTTATGTTT TCATTTCTCT TGGCTATCTA CATGGGAGTA GAATTCTAGG TCATAATATA 300
 ATTTTATGTT TAACTTCTCA AAGAATTGCC AAAAGGTTTT TCATAGTGGC TGCATCATTT 360
 ACATTCACCAC CGGCAATGTA CAAGGATTTT TATTTTCCA TATCCTTGCA CTTACCAACA 420
 10 CTTCTTTTTC GTWATWATTT TGTTTTTC TATTGCCAC CCTAGTGGAT GTGAAATGGC 480
 ATCTTATTGT TTTGATTGTC ATTTCTCTAA TGACAAATGA TATCATACTT TTTTATGTG 540
 CTTACGGATC AAAGGTATTT CCTTGGAGAA ATGTCCCTTC AAGTCCTTTG CCATTTCAAA 600
 15 ATTTGGTTAT TTGTCTTTTA TTATTCAGTT TTAAGAAATT CTGGCCAGGC GCAGTGGCTC 660
 ACCTGTAATC MTAGCACTTT GGGAGGCCAA GGCGGGCAGA TCACTTGAGK TCAGGACTTC 720
 20 GAGACCAGCC TGGCCAACAT GGTGAAACCC CATCTTACTA AAAATACAAA AATTAGCTGG 780
 GCGTGGTGGC AGGTGCATGT AATCNTATCT ACTCAGGAGG CTGAGGCAGG AGAATCGCTT 840
 GAACCCAGGA GGCGGAGGCT GCAGTGAGCC AAGATCACGC CATTGCACTC TAGCCTGGGT 900
 25 GACACAGA 908

30

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 655 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

40

TGCACTGGTT CCTTCTCCCC AGCAAATACT GCCTTCTTGT TTTTCTCTGA TGTGGCAGGT 60
 GACTACAAAA TCCGCCTTGG TATTCTTCAA ATGCATATAT ATTCCTTTCT TGTGAGCTCC 120
 45 CTCTCTTCCT AGATTAGAAA ACTGCCTCAT TTTCTGCTCA CTGGATGTGC AGTCCCAGCT 180
 TGTCTTCCTC TCCTCCCCC CTGTTGCAGG TGTCTTTTTT TTTTCTCTC TCTCCCCACT 240
 GGGCAGCAAA AGTTGTTCCA CAGTGAAAW TTAGGCATCC TCAAGTTTCY TCCCAGCTTC 300
 50 TGCTGTGTTT TCTTAGAGTA AATTGCCAAT TTCTGTTTTT ACAGGAAATC CTTTTTAAA 360
 AATGGAATCA GTGTGGTCCC CATCTACTCT GCAAAAATG CATTTTCTC TATTTTCAAA 420
 55 TGAGATTGT TCAAGTTTCA AAACACGTG AAATAATAAA TGTATAGTAG TTTTCTTTTC 480
 CTTGGGCATT GCTWGATATG TGAAATGGGT TTATGAAAA TAATAAATC ATAACGCTAT 540
 TTGTTTGACT TTCAATTTC TGGGAATTTT TCTCAGCTAA ACTCTAAATG GTGATTARGC 600
 60

AAAAAAAAA AAAAAAACY GRAGGGGGC CCGGTACCA TTCGCCCTAT AATGA

655

5

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 1102 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

15

TTTTTTTTT ACCATTTAAA ATAAATGAA AGTGACCTTC TGTTTATAAA AATCTTTGTC 60

TGCATCTCTG CTTATTTTCT TAGAAGAGAT TCCAAGAAGC GGTGAGTGAT TTCACGGCAG 120

20

CAGAGGGTTG GGACATATTA CGGGCGCGGA TCCCTCTTGG AGTGAGATGA CTCTCCGGAG 180

AGATTTAGTC GTCACCTCG CGTGTGAGGC TGCCTCACAC CCCAGGGATG TGTCTATCAA 240

GATGGAAGAT CTTTACACG CTCTTGATTT TGTGTGSCY TTTTCTATT ACTAGTGAGA 300

25

AKGAACTTT TTATATGATT ATTATCCATC ATAATCCAAC ACAAATTACT GCTTCATGTT 360

CTTTTACTTT CCTGTGAAGG TTTTAGTGCC TTTTAAAAAT TGCTATATAT TAAGCTTGTT 420

30

AATACTTCCA TGCTGTATTT GTGGSCATCA RTTCCCCCG GNACAGGCNT GCACATTTTG 480

CCTTCACAG CTGGGTGGTT TTTTATTTT AMTCTATTT CTCGTTCTTC TATCGTTTTA 540

TGTTTCAGAC GGTTCCTCCG TGTAGAAAGC AGTTTATGAA GATTTACTTT CGACAGTCTT 600

35

CTCTCTACTT TCTACAGTGA ATTCTCTGAT GTGCTGGGA GTTTGGGGT CTGGGTAAGA 660

RTCCTCCTCT CACCTATTC TCTATTACGA TCCACAGCCT CATGCTTTAT GARATTGGTG 720

40

GCCGGGARCG GGGGAGATTT GCGGATCCCC CAAGCCAGAC TTTATCCCC TATCCCTGCC 780

TCTGGATCCC ACGTACAGGC CTGGGAATC CCTGTGGTA GGGCCAATG GTCTCGCACT 840

CTCACCTGTA CCCCAGGGCT GGCACAGGAT GGTCAAGGAG AGAGGCTGCC CAAGCGCATC 900

45

CYTCTGGTGT CCCCCTGACA CGCCTCCAAA GTGAGCAGGT AGGTTTCAAC AGCCCCACGT 960

TGCAGGTGG AGATGAAGCT CAGGGTGGAG ACCAGTATCT CACAGTTCTC TTTGCATGGC 1020

50

CGGTACTTG TTAGTCAACT GATCAAGTGA AAATTCTAGC CCCAGAGGCA GGAGAATCCG 1080

GAACAAAATT AAACCAGCCA GG 1102

55

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 1533 base pairs

343

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

	GGCACGAGCC GNCACGGGCA GCGCCCCATA GCGCCAGGGA CCCCTGGCA GCGGGAGCCG	60
	CGGGTCGAGG TTATGGATCC AGCGGGCGGC CCCCGGGGCG TGCTCCCGCG GCCCTGCCGG	120
10	TGNTGTGTGC TGCTGAACCC GCGCGGCGGC AAGGGCAAGG CCTTGCAGCT CTCCCGAGT	180
	CACGTGCAGC CCCTTTTGGC TGAGGCTGAA ATCTCCTTCA CGCTGATGCT CACTGAGCGG	240
15	CGGAACCACG CGCGGGARCT GGTGCGGTGC GAGGAGCTGG GCCGCTGGRA CGCTCTGGTG	300
	GTCATGTYTG GAGACGGGCT GATGCACGAG GTGGTGAACG GGCTTCATGG AGCGGCCTGA	360
	CTGGGAGACC GCCATCCAGA AGCCCTGTG TAGCCTCCCA GCAGGCTCTG GCAACGCST	420
20	GGCAGCTTCC TTRAACCATT ATGCTGGCTA TRAGCAGGTC ACCAATGAAG ACCTCCTGAC	480
	CAACTGCACG CTATTGTGTG GCCCGCGGCT GCTGTCACCC ATGAACCTGC TGTCTCTGCA	540
25	CACGGCTTCG GGGCTGCGCC TCTTCTCTGT GCTCAGCCTG GCCTGGGGCT TCATTGCTGA	600
	TGTGGACCTA GAGAGTGAGA AGTATCGGCG TCTGGGGGAG ATGCGCTTCA CTCTGGGCAC	660
	CTTCTGCGT CTGGCAGCCC TGCGCACCTA CCGCGGCCGA CTGGCCTACC TCCCTGTAGG	720
30	AAGAGTGGGT TCCAAGACAC CTGCCTCCCC CGTTGTGGTC CAGCAGGGCC CGGTAGATGC	780
	ACACCTTGTG CCACTGGAGG AGCCAGTGCC CTCTCACTGG ACAGTGGTGC CCGACGAGGA	840
35	CTTTGTGCTA GTCCTGGCAC TGCTGCACTC GCACCTGGGC AGTGAGATGT TTGCTGCACC	900
	CATGGGCCGC TGTGCAGCTG GCGTCATGCA TCTGTTCTAC GTGCGGGCGG GAGTGTCTCG	960
	TGCCATGCTG CTGCGCCTCT TCCTGGCCAT GGAGAAGGGC AGGCATATGG AGTATGAATG	1020
40	CCCCTACTTG GTATATGTGC CCGTGGTCGC CTTCGGCTTG GAGCCCAAGG ATGGGAAAGG	1080
	TGTGTTTGCA GTGGATGGGG AATTGATGGT TAGCGAGGCC GTGCAGGGCC AGGTGCACCC	1140
45	AAACTACTTC TGGATGGTCA GCGGTGCGT GGAGCCCCG CCCAGCTGGA AGCCCCAGCA	1200
	GATGCCACCG CCAGAAGAGC CCTTATGACC CCTGGGCCGC GCTGTGCCTT AGTGTCTACT	1260
	TGCAGGACCC TTCCTCCTTC CCTAGGGCTG CAGGGCCTGT CCACAGCTCC TGTGGGGTG	1320
50	GAGGAGACTC CTCTGGAGAA GGGTGAGAAG GTGGAGGCTA TGCTTTGGGG GGACAGGCCA	1380
	GAATGAAGTC CTGGGTGAGG AGCCAGCTG GCTGGGCCCA GCTGCCTATG TAAGGCCTTC	1440
55	TAGTTGTTC TGAGACCCCC ACCCCACGAA CCAAATCCAA ATAAAGTGAC ATTCCCAAAA	1500
	AAAAAAAAA AAAAAAAAAA ANCCCGNGGG GGG	1533

60

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 575 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

ATCCTCTGGA ATCTAGGTGG AAGCCACCAA GCCTTCTTCA CACTTGCCTT CTGAGCATCT 60
 GCAGACTTAA CCCCATGTGG CAATCACCAA GGCTTATGGC TTGTGTCTTC CAGAACTGTG 120
 15 GCCAGAGCTG TACCTGGGCC CCTTTGAGCT GAGGCTGAAG CCAGAGTCTG AAGCTCAGCA 180
 GGGCAGTARG GCCCTGGGCC TGGCCCTGA AACCATCTTT TTCTCCTAAG CCTCTGGGCC 240
 20 TTTGATGGGA RGGGCTGTCC TCAAGATTTT TGAAATGCCT TTGGAGGGTT TTTGCCTTGT 300
 CTTGGATATT GGCTTCCTTT TAGTTATGCT CATCTCTCTA GCAAGTGAAT GTTTCACAAC 360
 CTGCTTGGAT TCTTTCTCTA CCACAGARCC AGGCTGCAAA TTTTACAAAC TTTTACACTC 420
 25 TGTTCCTCTT TTAAATATAA ATTTCAATGT TAAGTCACTT CTTTGCTCCC ATATCTGATT 480
 TAGGTTGCTG GAAGTAGCCA AGTCACCTCT TGAATGCTTT GCTGCTTAGA AATTTCTCTT 540
 30 ACTAGGTAGC CTGGGTCATC AACTTAAGT TCAAA 575

35 (2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 639 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

45 TCCTTTCATC TTAAGCACCA CCCGACAGG CAGGTACTAT TACCATCTCC GTTTGACAGA 60
 TNAGGAACCT GGCACAGGAA GCATTTAAGT GGATTCCCCA GGATCGCCCC ACTGTCAGGA 120
 GCAGANTCAG AATGGGCCTC AGCATCAGGC TCCCAATCCT GGCTTCTAAC TGCTGCGCTC 180
 50 TGCCCTTCYC TCWCCCCACC TCCCCACTCC AGTGCCTTTG GTCATGCCAC TGCAGCTTTC 240
 AGGCCAATAC TGGATTAGCC TCTTAGTGTT CTTGTCCCTG CAGCCATTTC CCCAGGCAGC 300
 55 AATTCCATGT GCCCTCACTG ATGTAGGTGG CTCTGTGTC ATTTGTCACA TCCTATTGAA 360
 TTGTTTATGC ATCTTGTCA CACTCACAGC ACCCTCCCTC TCACACGTCC TCCTTATAAA 420
 AATGTCCCTC AGTGTCTGCT ATGAGCCAGG TGCAGACTTA AGTGACAGGG CTGCTACGGG 480
 60

345

AAATAAAAAA TTAACAAGGA GCACCTGCCT CTTAATGCAC AGTAACAAAC TATGTTAAGT 540
GTCAGGAAGG AAAGGTTAAG GATGCCAGGA AGGCTTTTAA TAAATAACCT GACTTAGATG 600
5 GGCAGGTGGT GCTGARGATT AAGAACGTGT TCTTCTCGA 639

10 (2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 744 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

20 GAATTCGGCA CGAGAGTGGC TGGAGTCTGG CTGCAGAGGG AAGACATCAG CAGGGAGGGA 60
GCCAGGGCCT GTCACATCTT TCCTCTGGCC ATGTCTCTGG TCTTTGTAAG CCCAGAATCT 120
CCCCCTCCCT GAAGGGAGGC CAGCACCCCA GGAGGGCAGC AGGTGTGCTG TGAGGGTTGG 180
25 AGTAGTGTGA GAGGTCAGGG TACACTAGAA TGGCCATGGA CACCATGTGG GGGTGCTCTG 240
GGCTGGGCCA CAGAACAGTG TCCTTCCTGC TGCTCCTCCC CTGCAGCTTC CCCCACCTT 300
30 GTNGTTTATT TGGTTTGATA CCAATCAGCA GACCCTGCAA GGTGGAAGCT CCCAGGCTCT 360
CAGTCCCACS ACTCTCATGT GCCAGTCACC CNTACTGTAA CTGCCCAATG AGTACTTCTT 420
GCCCCACTGCC AAGATAGAGC CAGTTTACCA AGACAGGGGA ATTGCAGTAG AGAAAGAGTT 480
35 GAATATACAT AGAGCCAGCT AAATGGGAGA GTGGAGTTTT CTTATTACTT AAATCAGCCT 540
CCCYTAAAT TCAGAGGTGA GAATTTTTC AAGACAGTTT GGTGGSCAGG CCTAGGGAAT 600
40 GGATGCTGCT GATTGGCTAG GGATGCAATC ATAGGGGTGT AGAAAAGTWC CTGTGCACT 660
GAGTCCACTT TTGGTGAGAG CTACCAAGGA GCTGCTGGTC TGCTGGTCCC GGTAGAGCCA 720
45 TCTGGTGTCA GGAATGCAAA AGTG 744

50 (2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 526 base pairs
(B) TYPE: nucleic acid
55 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

60 GCAGGGGAAT TCGGCCACGG AGGGGTTTCA ACAGGGCCCG TGGGGTGAGG TGCARACACA 60

346

AAGCCCATAA GTGCTGGCCT GTTGGGACAA ATGAGAGAAA TCCCATAGGG TGGTGATGAC 120
AGCGCAYTCA GCCATCYTAY TCCTGGGGAA AATGAAACTT GTGCTCCTAT CAAATGCTCA 180
5 GTTGTA AAAC TGGAAAAAAA TTTAGAAGA CATCTGTCC AGCATCTGTG TTTATGTCTA 240
TAAAATGTAG AAAACTAAAG CACAGAGATG TTAAATGTTT TGTCCAAGGT CCAACAGCTG 300
10 GTTAGCARGC TTGGTCTGGT GACCTTTCTA CTGAACCACA GTGCCGCTGG GGAAGTCCT 360
CAGCACAGAT GGCTGCTGCT ATAGCTGGGG TATGGGCAGT ATTAGTAGTT AACCAGTCAA 420
CCCAAGTTCC CATAGTCTAG GTTCTGCTTC AGCTGGAGGT TAGGGAAAAA CACAAGAAAA 480
15 TCCCTTACCA CTCTACCAGT GCTGGGGGAT GACTAAGAG ATCCCC 526

20 (2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
(B) TYPE: nucleic acid
25 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

30 GGCACAGGC AGGAGAGACT TGGTCCATGG GGAGAAGCCT GCAGTATAGA TGGGACCTCC 60
AGGAGCCCAA GTAGCATAGA CCCTGCTGAT CCGGGCCAT TGAGCCAGAG GATTTGGGCT 120
35 GAATGTCCCC AGAGACAAAA GGGAAAGTA GATCCTTTCC CTTAAAGATG AAAGCCATCG 180
CCCGGGCTTG CTTATTGCTC TCTCTCCTGG TCCTTCCACA TGTGTTTCT GAACATTTGT 240
TCTGGCATCA CAATCCCCGT CATCTGTCA TCTGGCCCTT CCCACCTTTC CACCTTATCT 300
40 CTTGCAGTGT CTCGCGTCG ACCTGGCACC TGGGTGAARG CTTGCTCTTG CTGGTGCCCA 360
TAGCCCCCAG TGTATGGTCT TGAMCTCCCC AGCCATATGG ARACCCACCT CAGGAGGGCC 420
45 CCTCGA 426

50 (2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 844 base pairs
(B) TYPE: nucleic acid
55 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

60 GGCACAGCGG CACGAGATAG GAAGCTTGGC AGGGGCAGCT CCCCCAGTGC GCATTGCCCT 60

347

5 GTAACTCGAG CGCCTGGGAG TGGGGAGAGG CTTGGAAATG GAGCAGGGTG GTGGACCTCG 120
 TCTTCTCCTG CTCATCCCAG GCCTCCTCCA TAACACCTAC CTAGCACGGC CTGGGGACTT 180
 10 CCCAGCCCAA GGAACAACCTG AGAATACTGA GTGCCAGGGT AGCCCTAGCC CCATTTCACA 240
 CCTGGGCAAA GTGAGGTCAC TGGATTCAAA CACTCAGATT TAAACCTCCT CTGTGTCTGC 300
 AGCACCTGTA TATAACTGCC AGCCTCTGCT GCCCCTCTCC AAAAAGTCTC TGCCCTTGTC 360
 15 TTTGGCACCT GTCTCTGTCC TCCCCATTCT CTGCTCCTCC TTTCTCCAAC TCAGANTCAC 420
 CCTGTTAGTT CAGCAAATGT TCATCGAGCT CCATAATGTA GCAGGACAGG NCTGTCTAAC 480
 AGATTCTGGN CTTGCAAGGG TGAGACAAGT ACTCTCCATC TTTCTCTCAT CTTACAGAT 540
 GGTCTGCTCA ACAACTTTGC ACTGAATTGT AAATAATTGA TACTGCATAA AACATTGATG 600
 20 TTCTTTAAGG GTAGTCCAGC AAGGTGGCAA GTCTTATAAT GATAACTGCT CAAGGATCTC 660
 TCAGTGAAGC ATTGGGGST GCTAGCTCTG CCTATGGGTG AGGTCAGCTA TCTCACGCCA 720
 TCTACTTCCA CNTGCCCCCC CATGCCAGGC TCACCCTGAG CTGAGATGCC TGAGCAGGTG 780
 25 GCAGAAAGGA GCCACCTGGT TTATGCTTCG GGACCACAAA CTCCTCTATC CAGANGACAG 840
 TTTT 844

30

(2) INFORMATION FOR SEQ ID NO: 97:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1985 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

AGCCCTGCTG AAGTACAGGT TCTTCTATCA GTTCTGTGTG GGCAATGAAC GAGCAACAGC 60
 AAAGGAGATC AGGGATGAAT ATGTGGAGAC GCTGAGCAAG ATTTACCTGT CTTACTACCG 120
 45 CTCTTACCTG GGGCGGCTCA TGAAGGTGCA GTATGAGGAA GTCGCTGAGA AAGATGATCT 180
 AATGGGTGTG GAAGATACAG CAAAGAAAGG ATTCTYCTCA AAGCCATCGC TCCGCAGCAG 240
 50 GAACACCATT TTCACCCTAG GAACCCGCGG CTCTGTTCATC TCCCCCACTG AACTTGAGGC 300
 CCCCATCCTG GTGCCTCACA CAGCGCAGCG GNAGAGCAGA GGTATCCATT TGAGGCCCTC 360
 TTCCGCAGCC AGCACTACGS CCTCCTAGAC AATTCTTGCC GCGAATACCT TTTCATCTGT 420
 55 GAATTTTTCG TTGTGTCTGG CCCAGYTGCA CACGACCTGT TCCATGCTGT CATGGGCGGT 480
 AACTCAGCA TGACCCTGAA ACACCTGGAT TCTTATCTAG CTGACTGCTA CGATGCCATT 540
 60 GCTGTTTTTC TCTGTATCCA CATGTCTCTC CGGTTCCGTA ACATTGCAGC AAAGAGGGAT 600

	GTTCTGCCCC TGGACAGGTA CTGGGGAACA GGTGCTTGCC TTGCTATGGC CACGGTTTGA	660
5	ACTGATCCTG GAGATGAATG TTCAGAGCGT CCGAAGCACT GACCCCCAGC GCCTAGGGGG	720
	GTGGATACT CGGCCCCACT ATATCACACG CCGCTATGCA GAGTTCTCCT CCGCTCTTGT	780
	CAGTATCAAC CAGACAATTC CTAATGAACG GACCATGCAA TTGCTGGGAC AGCTGCAGGT	840
10	GGAGGTGGAG AATTTTGTCC TCCGAGTGGC AGCTGAGTTC TCCTCAAGGA AGGAGCAGCT	900
	TGTGTTTCTG ATCAACAACCT ATGACATGAT GCTGGGTGTG CTGATGGAGC GGGCTGCAGA	960
15	TGACAGCAAA GAGGTTGAGA GCTTCCAGCA GCTGCTCAAT GCTCGGACAC AGGAATTCAT	1020
	TGAAGAGTTG CTGTCTCCCC CTMTTGGGGG TTTAGTGGCA TTTGTGAAGG AGGCTGAGGC	1080
	TTTGATTGAG CGTGGACAGG CTGAGCGACT TCGAGGGGAA GAAGCCCGG TAACTCAGCT	1140
20	GATCCGTGGC TTTGGTAGTT CCTGGAAATC ATCAGTGGAA TCTCTGAGTC AGGATGTAAT	1200
	GCGGAGTTTC ACCAACTTCA GAAATGGCAC CAGTATCATT CAGGGAGCGC TGACCCAGCT	1260
25	GATCCAGCTC TATCATCGCT TCCACCGGGT GCTGTCCCAG CCGCAGCTCC GAGCCCTCCC	1320
	TGCCCCGGCT GAGCTCATCA ACATTCACCA CCTTATGGTG GAGCTCAAGA AGCATAAGCC	1380
	CAACTTCTGA TGTGCCAGAA ACCGCCCTGA GATCTGCCGG TCATCTCCAT GGACTTCTGC	1440
30	ACCCCATTC ATACCCTTCT TCACCTGGGG TACCCCTTCC AGTTTCCCC TTGCTTCCCA	1500
	GGCCCTTGAC ATGGCTTACC TGCCTTCACT CCCAGCACCT TGCCCAACAG GATAAGCTGG	1560
35	ATCCCTTGG CCTTCTGAAT ATCCCAGTGT CTTCAAGTTT CCCAAGACCA CTTCCTGTG	1620
	GGCTTCCAAA ATGGCCTTTA TCATTTCTCC AGTCTGTAC CCTCCTTCC TGCTCCATA	1680
	CACCCAAGGC TTGTTTCTTC CCTGTAAAA ACCACTGCCT CAATCTCTGG TTAACCTAAC	1740
40	TAGTCACCAT GTCCTGAGGC ATGAAGCTC CTCAGCTCTT GGAATTGCTG GCAAGGGTG	1800
	ACTGCCTCTG AGTCATTGTG TTTTCAAAG TGATTCTTT TCTGTAGCTT TTTGACCTAA	1860
45	GATCTCAGCA ATTTGAACAC TAACCTCTCC CCTCCTGGCT CAAGAATTAC TCCGAAGTCA	1920
	GTCTGCAGAA AATAAATATT TAGTATGACA TGAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1980
	AAAAA	1985

50

(2) INFORMATION FOR SEQ ID NO: 98:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1416 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

	ATATGAAGGG AAAGAATTTG ATTATGTTT CTCAATTGAT GTCAATGAAG GTGGACCATC	60
5	ATATAAATG CCATATAATA CCAGTGATGA CCCTTGGTTA ACTGCATACA ACTTCTTACA	120
	GAAGAATGAT TTGAATCCTA TGTTCCTGGA TCAAGTAGCT AAATTTATTA TTGATAACAC	180
10	AAAAGGTCAA ATGTTGGGAC TTGGGAATCC CAGCTTTTCA GATCCATTTA CAGGTGGTGG	240
	TCGGTATGTT CCGGGCTCTT CGGGATCTTC TAACACACTA CCCACAGCAG ATCCTTTTAC	300
	AGGTGCTGGT CGTTATGTAC CAGGTTCTGC AAGTATGGGA ACTACCATGG CCGGAGTTGA	360
15	TCCATTTACA GGAATAGTG CCTACCGATC AGCTGCATCT AAAACAATGA ATATTTATTT	420
	CCCTAAAAAA GAGGCTGTCA CATTTGACCA AGCAAACCTT ACACAAATAT TAGGTAAACT	480
20	GAAGGAACTT AATGGAACTG CACCTGAAGA GAAGAAGTTA ACTGAGGATG ACTTGATACT	540
	TCTTGAGAAG ATACTGTCTC TAATATGTAA TAGTTCCTCA GAAAAACCA CAGTCCAGCA	600
	ACTTCAGATT TTGTGGAAG CTATTAAC TGCTGAAGAT ATTGTCCTTC CTGCACTTGA	660
25	CATTCTTCGG TTGTCAATTA AACACCCAG TGTGAATGAG AACTTCTGCA ATGAAAAGGA	720
	AGGGGCTCAG TTCAGCAGTC ATCTTATCAA TCTTCTGAAC CCTAAAGGAA AGCCAGCAAA	780
30	CCAGTGCTT GCTCTCAGGA CTTTGTGCAA TTGTTTGTGTT GGCCAGGCAG GACAAAAACT	840
	CATGATGTCC CAGAGGGAAT CACTGATGTC CCATGCAATA GAACTGAAAT CAGGGAGCAA	900
	TAAGAACATT CACATTGCTC TGGCTACATT GGCCCTGAAC TATTCTGTTT GTTTTCATAA	960
35	AGACCATAAC ATTGAAGGGA AAGCCCAATG TTTGTCACTA ATTAGCACAA TCTTGGAAGT	1020
	AGTACAAGAC CTAGAAGCCA CTTTGTAGCT TCTTGTGGCT CTTGGAACAC TTATCAGTGA	1080
40	TGATTCAAAT GCTGTACAAT TAGCCAAGTC TTTAGGTGTT GATTCTCAAA TAAAAAAGTA	1140
	TTCTCTAGTA TCAGAACCAG CTAAAGTAAG TGAATGCTGT AGATTTATCC TAAATTTGCT	1200
	GTAGCAGTGG GGAAGAGGGA CGGATATTTT TAATTGATTA GTGTTTTTTT CCTCACATTT	1260
45	GACATGACTG ATAACAGATA ATTAAAAAAA GAGAATACGG TGGATTAAGT AAAATTTTAC	1320
	ATCTTGTAAG GTGGTGGGGA GGGGAAACAG AAATAAAATT TTTGCACTGC TGAAAAAAA	1380
50	AAAAAAAAA AAAAGGAAAC TCGAGGGGGG GCCCGG	1416

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1935 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

5	NTCTACCCTA ATCAAGATGG GGACATACTT CGCGACCAGG TTCTTCATGA ACATATCCAG	60
	AGATGTGTCTA AAGTAGTGAC TGCAAATCAC AGAGCTCTTC AGATACCAGA GGTTCATCTT	120
	CGAGAAGCAC CATGGCCATC TGCACAATCA GAAATCAGGA CAATAAGTGC TTATAAAACC	180
10	CCCCGGGACA AAGTGCAGTG CATCCTGAGA ATGTGCTCTA CGATTATGAA CCTCCTGAGC	240
	CTGGCCAATG AGGACTCTGT CCCTGGAGCG GATGACTTTG TTCCTGTGTT GGTGTTGTG	300
	TTGATAAAGG CAAATCCACC CTGTTTGCTG TCTACTGTGC AGTATATCAG TAGCTTTTAT	360
15	GCTAGCTGTC TGTCTGGAGA GGAGTCCTAT TGGTGGATGC AGTTCACAGC AGCAGTAGAA	420
	TTCATTAAAA CCATCGATGA CCGAAAGTGA CCAAGACCAA GGGCCACCAA GGCAGCAGAC	480
20	TGTTAATCAG ACAAACAGAT CTCTGAGAAG GTGCATCAGC TGCTTTGAAG GCTGAAGATT	540
	GTTTGTATG ATACTGCACA GCATCAGGCA TTTTAAAGCA GATCTTTACT AAACAGGTTA	600
	ATGAGCTAAC AAGCAGGTTT TCTCGTCTTT GGGCTCTTTC CTTTCTGAGT TGCATATTCT	660
25	ATTTTCTTGT CCCCAGTAG AGACTAGTAC TACAAAAAGG GACCACATTT TTCAAGTATT	720
	TCTAAGTATA AAAAACAAAA CAAAAATCTC TTAGGAAATG TCTAGACCTC CATCTCTGGA	780
30	TTCCCTTTCT TTCCTTTTAT TTTAAAAAAG AACAGTACCC CTCCTTTAAG ATGCTGTCTT	840
	ACATTAAATGA GCATCTAATG GAAAGAAGGT ATGAGTTGCA CTGAGGATTA GAATAGTGGT	900
	GCGTTAGTGG CATATCTAT AAATACACTC ACCTAAATTG AAAGCTAAGA AGGAAATGTA	960
35	AATATAATAT ATATTTATAT TTGATGTAAT ATGGACATCT GCAGATTCTA ATAAACAAGG	1020
	ACTATTGCTG ATAGTAGGCT GTGACATACT GTCTGTGAA ATGGTTTCCT TGACAAAATT	1080
40	TAAGCTGAGC TTAAGCAAA AAAACAAAA AGTACACAGA AATATTTATT AAAATGTAAT	1140
	ACAGTTTATT GAACTTTCTA GGTATGGAGT TTGATGGACA GGGCTGCCTY TAATGAGTGT	1200
	GAAGGTCAC T AAGTCACTTA GACATCTCAC CGTGGAGTT TGTGAGCCTG CATTAGGAGA	1260
45	TAGACTGATT ACCATACATG ACATAAAAAG GAACAGTGA TAGCTCATAC TTTATGGTGG	1320
	TTCTTCTCCT CCGAAATAAT ATACTGCAGA AATCCCAGAC AGAGCTCCTT ACAAACCTTT	1380
50	AATTGTAATA TATTTTGTAT GATTATTCAC ATTGAATGCA CAGACCAAGA ATTCAGTGAA	1440
	TGTCATTTTT TAAAAACTA ATTTGTATTG TCTGCTCTAG TGATACAAGT TTTACTAGTG	1500
	ATAAACTATT TTAATCAACC ATACTATTCT TATGGAAAA AATATCTATT TTGGCAGGTT	1560
55	TCTGTGCCTT TATTTCCCTC TTCTGAAAA AAGTCTGTGT TTTCATAGTT TGGTTTGCAT	1620
	TGTATATCAA TAATTAATCA GGAATGGGTT TTGGTGCCTG AAAAATTGGC CATGGAGGCA	1680
60	CACCAAAGCT TCAAGCACAA GTCTTGTA CA TGGGCCATCA CTGTCTGGTT TCACTTCGTG	1740

5 TGTTCCTAA ACACATTAG CTGCTTTT AACAACTCA GCCCCATACT TGAGTCCCTT 1800
GTGTTGGGA GCATTCCAG GCATCTTTA AGGGAAGTGT GACAAACAGC CTCGGGCAGA 1860
TGAACACGGA GGCTCTCTGT TGTCTGCTC TGAGATCTTT GTGTCTGGGA ATGCCTAAAG 1920
NTTTGNITT TTTT 1935
10

(2) INFORMATION FOR SEQ ID NO: 100:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 599 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

GAATTCGCCA CGAGCGTCCA CGCAGCCGCC GGCCGGCCAG CACCCAGGGC CCTGCATGCC 60
25 AGGTCGTTGG AGGTGGCAGC GAGACATGCA CCCGGCCCGG AAGCTCCTCA GCCTCCTCTT 120
CCTCATCCTG ATGGGCACTG AACTCACTCA AGACTCCGCT GCCCCCGACT CCCTGCTGAG 180
AAGTTCAAAG GGCAGCACGA GGGGGTCTTT GGCTGCTATT GTCATCTGGA GGGGAAGAG 240
30 TGAGAGCCGG ATAGCCAAGA CCCAGGCAT TTTCAAGGT GGCGGGACCT TAGTCCTACC 300
CCCAACACAC ACCCCTGAGT GGCTCATCCT CCCTTTGGGC ATAACGCTGC CCTTGGGGGC 360
35 TCCAGAAACA GGCGGTGGGG ATTGTGCCGC TGAGACCTGG AAGGGCAGCC AGCGTGCCGG 420
CCAGCTGTGT GCATGCTGG CTTAATATGC AGGGCTTGGG GGGCTGTGGC CACATGCCCG 480
GCAGGAGGTG AGTGAGGAGC CTTGTGGCGT GCTGGTGTGG GGATCGTGGG CATTTCAAAC 540
40 GGGCTTGTCG TACCCTGAAC AATGTATCAA TAGAGAAAAA AAAAAAAAAA AAAACTCGA 599

45 (2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 784 base pairs
50 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

55 GAATTCGCCA CAGAAAAAAA AGAGAGACTG GGTCTTACTG TGTGCCCAG ACTTGTCTTG 60
AACTCCTGCC TCAGCCTCTC AAGTACTTGG GATTATAGGC CAAGAAGCCA CCATGCCTAG 120
60 CTCTTCTCTG TCATTGATCC AGACTAATAC TCTGGGTCA GCCTCATTTT TTCTCTTCT 180

	CACTTTGCAC ATCCACTGT CACCAAATCK RGTTCATCT GCATCCTAAG TAAGTCCTTT	240
5	GATTCCTCCA GTTGTTCATT AGTAATGTCT CAARTGTAAT TTTTCTAGT AGTTTTCAGC	300
	CTGTCTTTCC KGCCTTCAGT CTTAACTTCT CCAGTACATA KGCCACATTG TTGTCAGCAK	360
	GATCAWATTT TATTTAAAAA TACTTTACAW AKGTTTATKG CCAAATATTA GRAAATACAG	420
10	ATTCATGGAA AGAAAAATCA CTGTCCCAAG GAGGTCACTG GCATGGTGAG GTTAAGGGGT	480
	GATTTTAATT TTTAAAAATG TATATTTTTT CCTGTGTAGA GTAGTAACAC CCTTGAAAAC	540
15	ACAWTCCCTT GTAAAGTCTC TAATTCTGTA CTCCGCATCT AGSTGRTCTC TTCTTTCTCA	600
	GATATTTTAC AATTTTATTT ATCACCACCT TTCTCTAGCC TTTACCCGTC TCTTCAATAT	660
	TWACATATGC AGAAGTTTCT CCTAACAAAC ACCTGCCCTCT GCCTCAGTTC TGCTACCACC	720
20	CTGTTGCTTT CTTTCCCTTC ACAATCAAAT TTAAGAGTGT CAAAAAAAAA AAAAAAAAAAC	780
	TCGA	784

25

(2) INFORMATION FOR SEQ ID NO: 102:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1035 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

	AGAGGCCTGG CTGCGTGGCC CTATCTCCGT CTCGCCACC CACTTAGCGT TTTAGGCATC	60
40	AATTACCAGC AGTTTCTCCG CCACTATCTG GAAAATTACC CGATTGCTCC CGGCAGAATA	120
	CAAGAGCTTG AAGAACGCCG CAGTTGCGTG GAAGCCTGCA GAGCAAGGGA AGCAGCGTTT	180
	GATGCCGAAT ATCAGCGAAA TCCTCACAGG GTGGACCTCG ATATTTTAAC CTTTACGATA	240
45	GCTCTGACTG CCTCTGAAGT TATCAACCCT CTGATAGAAG AACTTGGTTG CGATAAGTTT	300
	ATCAATAGAG AATAGTTAGG TGGTGACACT ACTTCAAGAG AACCTCTGCA TTCCAGTCAT	360
50	ACCAATCCTG CAACTTGATT TTCAGAAGTC AAGAGTATAT CGCGATAAGA CAGTGCACAG	420
	GTGGAGGGGA AAAAAAGGGG GAGGGGGAAG CTTATCTTGA AAAAGCATCA CAGAAGTAGA	480
	AAAAAATGTC GAAAGCATT AACTGTAAAC GTTCTTTGAG TTTGTGATTG ATCCACATTT	540
55	TTCCCCCTGC ATTATGGAAA ATGTCTCTCA GCATTGCTTT ATTACAAAGT AAAGGATGGT	600
	TTTATAAAAT TGAGACTGAT GAAACATCAA TACTAGAGCC CATGAGGATG AAAGAAATTA	660
60	TCAAATAGTG CTGAACAGAA TAAGATGTTA ACGCTGAGTT ATTAGGACTG GAAGGCTATG	720

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AAAAGAACTT GAAATTGTG GAATATGTGC TCTCTTCATG TCATATTCAA TAGAAGTTTC 780
 TAGTTTAAGA TTGATTTTGT GTTTTCTTAG GCATTTCAAG TGACAAGCAA AGTAAATGTA 840
 5 TATATTATGT GATAAATCAT GTTTTCAAGA ACGTCAAATT TCTGGACTTT TTTCTTTCAA 900
 TTTTAAATTT TTAAAGTTTT TTTGGTATTA AAAAATCYAT TCACAAGCCA AAAAATWIWT 960
 WAAATWIWCM GCGAAAAGCC AAAAAAAAAA AAAAMMAGGG GGGGCCGGGC CCCATCCCCC 1020
 10 CAAGGGGGTC CNGNT 1035

15

(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2218 base pairs
 20 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

AGGTATTAGG CCCTTTTGTG GGAGCCCCAT GTTTTGTMTT TCTGAGTTGG TGGGGAGGGA 60
 SGGAGGGGGA GGGCTGAATT GTTTTGCAGA GGAAGATGGC ATCTGTGCTT TAAATTTCTC 120
 30 ATTACTGGGT TAGAAAAACA AGAGGGAATG CCCTGCACAT TTTCTTTTGT GCTTTTAAAT 180
 GTTCTTAAG TTGGAACAGG TTTCTCGGG CCGTTTMTGA CTGATGCTG GAGTGCATTT 240
 GATAGTTAAA AATTACTAAT TGGTTTATTT TCCCTTCACA CTCTGCCTCC CCACTTCTCC 300
 35 CCCCGTTACT GAAAAATAAC CATTTTAGTG TCAGGCTAGA AATTGAATG CTGAGTTTGT 360
 TGTATCCTTT AAATTAATAA CCACAAGTGT TTATTGTAGT GGTAAACTG TAGCATCTCA 420
 40 GCATCTGGGT GGAAGCTGCC TATATTTCTT CCCAGTTTAA CTGGGGACCA TCTGTGAAAT 480
 TAATTTTCCA TCCAGACAGC TGCTGTGAGC AAATGAACAT AAATGCTCGC TGGAAATTTA 540
 CTAACCAGTT TTTATATTGA CCTGCAGTGT AAAAAGCACA TTTAATTATA AACATATAT 600
 45 TCAAAATGGG CAAATTTTAT TTTCAAATGC AGTGTAGAGC TAGATTAAAA GCAACTCTTT 660
 GCCACCTACT CTGCCCTTTT GGCAAAGTTA CCTTGAACAA AGAATCTTAA GGGTTTATTA 720
 50 AGAACTCTTT ATTTTCTTCA TACCCTGTTT TCTGCAGTGC TTTCTAACAG CTCTGGGTG 780
 CAGATTTTCT TCGGCATCCT TTTGCACTCA GCTTATTACA GGTAGGTAGT GCTTAAGAAA 840
 AGTCATGGAG GACTAAAGCC TAAGTCCTTT TCACTTTTCC TCCATCTGAA GGTAGGTGAG 900
 55 TTCATCTCTT TCATAGTAAT GCTGTTTAC CAAGACTTTA TAGCAGATGG ACCCAGAAAG 960
 AATTTTCTGC TATTGTGTTT ACTACAACAG GATAGGGACA TCAGACAGCC CCAGAAACCC 1020
 60 CTTCCAGATC TGATATGGGA CTATTAATTT TTATGCTGTT AATTGGTATT CATTACAAT 1080

	GCAGTTGAAG GGGGAAGGCT CCACTGCATT CTTTGGCTAA GGCCTGAATG CTTGCTCATC	1140
5	TGTAAGATCT ATACTCGAGG TTTTGTTCCT CTTTAAAAAT TCTTTAGGGA GAGAGGGATG	1200
	GTCTCTGAGG GGTCTGAAA GTATGATTCA ATGTGCAACA TACAGGTAGG TCTTCAGCAT	1260
	AAGCTGAAAT ATATGCATGT AAAAAGTTTG ACATCTTTTT TTTTAATTTT CCACTTTCTT	1320
10	CTTAACTTTA CTCTCTTTTT TGTCCCCCCC CCATCTTACA GAAGTTGAGG CCAAGGGAGA	1380
	ATGGTAGGCA CAGAAGAAAC ATGGCAAACCT GCTCTGTGCT TTCAAACCAA AGTGTTCCCC	1440
15	CCAACCCCAA ATTTGTCTAA GCACTGGCCA GTCTGTGTGT GGCATTTGTT TCTACAACCA	1500
	AATTCTGGGT TTTTTCTTC TTTCTTTAAA CATAGAGGTA CCACCACAAG GGATGCCCTA	1560
	CTCTCTCGCA GCTCTGAAA GCATCTGTTT GAGGGAAAGG TCTCTGGGCA AGCAAGTGGT	1620
20	TATTTGGATT GCTTGCTTCC CTTTTCACAC CTGGGACATT GYAATCATAA AATAACAGTA	1680
	AATTCCAAAC CTCAAAAACT ATTATGGCCT GAGCACAGCT GAAATCTAGC AGAGTTTAAC	1740
25	TCTTCTGCCT CCATGTCTGT CACTTATAAT TCAGGTTCTG CTGTTGGCTT CAGAACATGA	1800
	GCAGAAGAAT CGTTTTATGC TAGTTATTGC ATTCATGGTT GAAACTCAAC TTAGGGAAAG	1860
	GGTCCAATG TATTAAGCAA TGGGCTGCTT CTCCCAATC CTCCTAACA ATTCGTTGTG	1920
30	TGGACTTCTC ATCTAAAAGG TTAGTGGCTT TTGCTGGGA TCAGTGTCTT CTATTGATGT	1980
	TCTTGCTGGT CTCCAGACAC ATTCCTGTG CATTAAAGCT TGAAAGACTT GTAGATGTGT	2040
35	GATGTTCAAG CACAGGATGC TGAAAGCTAT GTTACTATTC TTAGTTTGTA AATTGTCCTT	2100
	TTGATACCAT CATCTGTTT TCTTTTGTGA GGTATAAATA AAAACACTGT TGACAATAAA	2160
40	AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	2218

(2) INFORMATION FOR SEQ ID NO: 104:

- 45 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1351 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

	CTTCACAGAC TGACAGAATG GTTTTGTTTT GTTTTGTTTT GTTTTGTTTT GTTTTGAGA	60
55	TGGACTCTAG CTCTGTCACC CAGGCTGGAG TGCAGTGGTG CGATCTCGGC TCACTGCAAG	120
	CTCCGCCTCC CGGGTTCTCA CCATTCTCCT GCCTCAGCCT CCCGAGTAGC TGGGACTACA	180
60	GGCGCCCAAC ACCACGCCCG GCTAATTTTT TGTATTTTTT AGTAGAGACG GGGTTTCACC	240

	ATGTTAGCCA GGATGGTCTC GATCTCCTGA CCTCGTGATC CGCCCGCYTC GGCCTCCCAA	300
	AGTGCTGGGA TTACAGGCGT GAGCCACCGT GCCTGCCCCA GAATGGTTTT TAAAGCCACA	360
5	GTTGAGARGC CACCCATTGC CCGGCGCCTG GACAGTGATC ATCTTGTTCA TCTTGTTTCA	420
	TCCTTTCTTG TGTGATTGGA ATTATTCATC CCCTTTGAAA GATGAGAAGG TTGAGATGCA	480
10	AAGAGTCTAC CTTTCCAAGT TCTCACTGCT GGAAAGARCT AGAAGCACAG TTCAAAGTTC	540
	TGGNITCTGG ACTCTGCAGT CCAGGTYTCC CTTYTCCCAC TTGCCTACCC TCAATGCCAC	600
	ACTGTTTTTG AAGTGGCCCA TAACTGAAG GRAAAGTTTA AAGACAGTTC AATTTAATCA	660
15	TCAGRATGCA TTCTTTTTTT TTTCGGARAC GGAATTTTAC TCTTGCTGCC CAGCTGGAG	720
	TGCAATGGTG CAATGATCTC GGCTCACTGC AACCTATGCC TCCTGGGTTT AAGNGATTAT	780
20	CCAGCCTCAG CCTCCCGAGT AGCTGGGATT ATGGGCGCCC ACCACCATGC CCAGCTAATT	840
	TTTGTATTTT TTTTTTTAGT AGAGATGGGG TTTCGCCAGG TTGGCCAGGC TGKTCTTG TG	900
	AAATCCTGGC YTCAGGTGAT YTGCCACYT CATCYTCCAA AAGTGCTGGG ATTACAGGCA	960
25	TGAGCCACTG CGCCTGGCYT CAGAATGCAT TCTTACACAT CTATCCTAGA CATTTATAAG	1020
	CACTCTAATG GATAACAATC CAAGAATAAA TGATTGTAAA AGATGATGCC GAAGAGTTGA	1080
30	TGTCAATCTT TTTTTCCTAA GAAAAAAGT CCGCGAGTAT TAAATATTTA GATCAATGTT	1140
	TATAAATGA TTACTTTGTA TATCTCATTA TTCTATTTT GGAATAAAAA CTGACCTTCT	1200
	TTAATCATAT ACTGTCTTT TGTAATAGC AGCTTTTG TGTCATCTCCC CACTTTATTA	1260
35	GTAAATTTAA ATTGGA AAAA ACCCTCAAAC TAATATCTCT GTCTGTTCCA GTCTTATAAA	1320
	TAAACTTAT AATGCATGTA AAAAAAAAAA A	1351

40

(2) INFORMATION FOR SEQ ID NO: 105:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2066 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

- 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

	GGCACGAGGC GGCGGAGGGC CACAATCACA GCTCCGGGCA TTGGGGGAAC CCGAGCCGGC	60
55	TGCGCCGGGG GAATCCGTGC GGGCGCCTTC CGTCCCGGTC CCATCCTCGC CGCGCTCCAG	120
	CACCTCTGAA GTTTTGCAGC GCCCAGAAAG GAGGCGAGGA AGGAGGGAGT GTGTGAGAGG	180
	AGGGAGCAAA AAGCTACCC TAAACATTT ATTTCAAGGA GAAAAGAAAA AGGGGGGGCG	240
60	CAAAAATGCG TGGGGCAATT ATAGAAAACA TGAGCACCAA GAAGCTGTGC ATTGTTGGTG	300

	GGATTCTGCT CGTGTTCCTAA ATCATCGCCT TTCTGGTGGG AGGCTTGATT GCTCCAGGGC	360
	CCACAACGGC AGTGTCTTAC ATGTCGGTGA AATGTGTGGA TGCCCGTAAG AACCATCACA	420
5	AGACAAAATG GTTCGTGCCT TGGGGACCCA ATCATTGTGA CAAGATCCGA GACATTGAAG	480
	AGGCAATTCC AAGGGAAATT GAAGCCAATG ACATCGTGT TTCTGTTCAC ATTCCCCTCC	540
10	CCCACATGGA GATGAGTCCT TGGTTCCAAT TCATGCTGTT TATCCTGCAG CTGGACATTG	600
	CCTTCAAGCT AAACAACCAA ATCAGAGAAA ATGCAGAAAT CTCCATGGAC GTTCCCCTGG	660
	CTTACCGTGA TGACGCATTT GCTGAGTGGG CTGAAATGGC CCATGAAAGA GTACCACGGA	720
15	AACTCAAATG CACCTTCACA TCTCCCAAGA CTCCAGAGCA TGAGGGCCGT TACTATGAAT	780
	GTGATGTCCT TCCTTTTCATG GAAATTGGGT CTGTGGCCCA TAAGTTTTCAC CTTTAAACA	840
20	TCCGGCTGCC TGTGAATGAG AAGAAGAAAA TCAATGTGGG AATTGGGGAG ATAAAGGATA	900
	TCCGGTTGGT GGGGATCCAC CAAAATGGAG GCTTCACCAA GGTGTGGTTT GCCATGAAGA	960
	CCTTCCTTAC GCCCAGCATC TTCATCATTA TGGTGTGGTA TTGGAGGAGG ATCACCATGA	1020
25	TGTCCCGACC CCCAGTGCTT CTGGAAAAAG TCATCTTTCG CCTTGGGATT TCCATGACCT	1080
	TTATCAATAT CCCAGTGGAA TGGTTTTCCTA TCGGGTTTGA CTGGACCTGG ATGCTGCTGT	1140
30	TTGGTGACAT CCGACAGGGC ATCTTCTATG CGATGCTTCT GTCCTTCTGG ATCATCTTCT	1200
	GTGGCGAGCA CATGATGGAT CAGCACGAGC GGAACCACAT TGCAGGGTAT TGAAGCAAG	1260
	TGGACCCAT TGCCGTGGC TCCTTCTGCC TCTTCATATT TGACATGTGT GAGAGAGGGG	1320
35	TACAACCTAC GAATCCCTTC TACAGTATCT GGAATACAGA CATTGGAACA GAGCTGGCCA	1380
	TGGCCTTCAT CATCGTGGCT GGAATCTGCC TCTGCCTCTA CTTCTGTCTT CTATGCTTCA	1440
40	TGGTATTTCG GGTGTTTCGG AACATCAGTG GGAAGCAGTC CAGCCTGCCA GCTATGAGCA	1500
	AAGTCCGGCG GCTACACTAT GAGGGGCTAA TTTTATAGGT CAAGTTCTTC ATGCTTATCA	1560
	CCTTGGCCTG CGCTGCCATG ACTGTCATCT TCTTCATCGT TAGTCAGGTA ACGGAAGGCC	1620
45	ATTGGAAATG GGGCGGCGTC ACAGTCCAAG TGAACAGTGC CTTTTCACA GGCATCTATG	1680
	GGATGTGGAA TCTGTATGTC TTTGCTCTGA TGTCTTGTA TGCACCATCC CATAAAAACT	1740
50	ATGGAGAAGA CAGTCCAAT GGAATGCAAC TCCCATGTAA ATCGAGGGAA GATTGTGCTT	1800
	TGTTTGTTTC GGAACCTTAT CAAGAATTGT TCAGCGCTTC GAAATATTCC TTCATCAATG	1860
	ACAACGCAGC TTCTGGTATT TGAGTCAACA AGGCAACACA TGTTTATCAG CTTTGCAATT	1920
55	GCAGTTGTCA CAGTCACATT GATTGTACTT GTATACGCAC ACAAATACAC TCATTTAGCC	1980
	TTTATCTCAA AATGTTAAAT ATAAGGAAAA AAGCGTCAAC AATAAATATT CTTGAGTATA	2040
60	AAAAAAAAA AAAAAAAAAA AAAAAA	2066

5 (2) INFORMATION FOR SEQ ID NO: 106:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1705 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

15 AATTCGGCAK AGGGCAGCTG TCGGCTGGAA GGAAGTGGTC TGCTCACACT TGCTGGCTTG 60
CGCATCAGGA CTGGCTTTAT CTCTGACTC ACGGTGCAAA GGTGCACTCT GCGAACGTTA 120
AGTCCGTCCC CAGCGCTTGG AATCCTACGG CCCCCACAGC CGGATCCCCT CAGCCTTCCA 180
20 GGTCTCTAAC TCCCGYGGAC GCTGAACAAT GGCCTCCATG GGGCTACAGG TAATGGGCAT 240
CGCGCTGGCC GTCCTGGGCT GGCTGGCCGT CATGCTGTGC TGC GCGCTGC CCATGTGGCG 300
25 CGTGACGGCC TTCATCGGCA GCAACATTGT CACCTCGCAG ACCATCTGGG AGGGCCTATG 360
GATGAACTGC GTGGTGCGA GCACCGGCCA GATGCAGTGC AAGGTGTACG ACTCGCTGCT 420
GGCACTGCCG CAGGACCTGC AGGCGGCCCG CGCCCTCGTC ATCATCAGCA TCATCGTGGC 480
30 TGCTCTGGGC GTGCTGTGT CCGTGGTGGG GGGCAAGTGT ACCAACTGCC TGGAGGATGA 540
AAGCGCCAAG GCCAAGACCA TGATCGTGGC GGGCGTGGTG TTCCTGTTGG CCGGCCTTAT 600
35 GGTGATAGTG CCGGTGTCTT GGACGGCCCA CAACATCATC CAAGACTTCT ACAATCCGCT 660
GGTGGCCTCC GGGCAGAAGC GGGAGATGGG TGCTTCGCTC TACGTGCGCT GGGCCGCTC 720
CGGNTGCTG CTCCTTGGCG GGGGCTGCT TTGCTGCAAC TGTCCACCCC GCACAGACAA 780
40 GCCTTACTCC GCCAAGTATT CTGTGCCCCG CTCTGTGCT GCCAGCAACT ACGTGTAAAG 840
TGCCACGGCT CCACTCTGTT CCTCTCTGCT TTGTTCTTCC CTGGACTGAG CTCAGCGCAG 900
45 GCTGTGACCC CAGGAGGGCC CTGCCACGGG CCACTGGCTG CTGGGGACTG GGGACTGGGC 960
AGAGACTGAG CCAGGCAGGA AGGCAGCAGC CTTCAGCCTC TCTGGCCAC TCGACAACCT 1020
TCCCAAGGCC GCCTCTGCT AGCAAGAACA GAGTCCACCC TCCTCTGGAT ATTGGGGAGG 1080
50 GACGGAAGTG ACAGGGTGTG GTGGTGGAGT GGGGAGCTGG CTTCTGCTGG CCAGGATGGC 1140
TTAACCCTGA CTTTGGGATC TGCCTGCATC GGTGTGGGCC ACTGTCCCCA TTTACATTTT 1200
55 CCCCCTCTG TCTGCCTGCA TCTCTCTGT TCGGGTAGG CCTTGATATC ACCTCTGGGA 1260
CTGTGCCTTG CTCACCGAAA CCCGCGCCCA GGAGTATGGC TGAGGCCTTG CCCACCCACC 1320
TGCTTGGGAA GTGCAGAGTG GATGGACGGG TTTAGAGGGG AGGGGCGAAG GTGCTGTAAA 1380
60

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CAGGTTTGGG CAGTGGTGGG GGAGGGGGCC AGAGAGGCGG CTCAGGTTGC CCAGCTCTGT 1440
 GGCTCAGGA CTCTCTGCCT CACCCGCTTC AGCCAGGGC CCCTGGAGAC TGATCCCTC 1500
 5 TGAGTCCTCT GCCCCTTCCA AGGACACTAA TGAGCCTGGG AGGGTGGCAG GGAGGAGGGG 1560
 ACAGCTTCAC CCTTGGAAGT CCTGGGGTTT TTCCTCTCC TTCTTTGTGG TTCTGTITT 1620
 10 GTAATTTAAG AAGAGCTATT CATCACTGTA ATTATTATTA TTTTCTACAA TAAATGGGAC 1680
 CTGTGCACAG GRAAAAAAAA AAAAG 1705

15

(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 1167 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

25 TGCAGGAATT CGGCAGAGGT TTTCCGCTAG ACTCTGGCAG TTGGTGAGCA TCATGGCAAC 60
 CGTTACAGCC ACAACCAAAG TCCCGGAGAT CCGTGATGTA ACAAGGATTG AGCGAATCGG 120
 30 TGCCCACTCC CACATCCGGG GACTGGGGCT GGACGATGCC TTGGAGCCTC GGCAGGCTTC 180
 GCAAGGCATG GTGGGTCAGC TGGCGGCACG GCGGGCGGCT GGCGTGGTGC TGGAGATGAT 240
 CCGGAAGGG AAGATTGCCG GTCGGGCAGT CTTATTGCT GCCAGCCGG GCACGGGGAA 300
 35 GACGGCCATC GCCATGGGCA TGGCGCAGGC CTTGGGCCCT GACACGCCAT TCACAGCCAT 360
 CGCCGGCAGT GAAATCTTCT CCTGGAGAT GAGCAAGACC GAGGCGCTGA CGCAGGCCTT 420
 40 CCGGCGGTCC ATCGGCGTTC GCATCAAGGA GGAGACGGAG ATCATCGAAG GGGAGGTGGT 480
 GGAGATCCAG ATGATCGAC CAGCAACAGG GACGGGCTCC AAGGTGGGCA AACTGACCCT 540
 CAAGACCACA GAGATGGAGA CCATCTACGA CTTGGGCACC AAGATGATTG AKTCCCTGAC 600
 45 CAAGGACAAG GTCCAGCCCG GGGACGTGAT CACCATCGAC AAGGCGACGG GCAAGATCTC 660
 CAAGCTGGGC CGCTCCTTCA CACGCGCCCG CGAACTACGA CGCTATGGGC TCCCAGACCA 720
 50 AGTTCTGTCA GTGCCAGAT GGGGAGCTCC AGAAACGCAA GGAGGTGGTG CACACCGTGT 780
 CCCTGCACGA GATCGACGTC ATCAACTCTC GCACCCAGGG CTTCCTGGCG CTCTTCTCAG 840
 GTGACACAGG GGAGATCAAG TCAGAAGTCC GTGAGCAGAT CAATGCCAAG GTGGCTGAGT 900
 55 GCGCGAGGA GGGCAAGCG GAGATCATCC CTGGAGTGCT GTTCATCGAC GAGGTCCACA 960
 TGCTGGACAT CGAGAGCTTC TCCTTCCTCA ACCGGGCCCT GGAGAGTGAC ATGGCGCCTG 1020
 60 TCCAGCAGGT CTATGGGGAT GCCGTGAGGG CTCTGGTAGC TGGTGCCCCG GATTCCGGTG 1080

ATGCCACGGT TGGTGGCCTC GTGCCGAATT CCTGCAGCCC GGGGGATCCA CTAGTTCTAG 1140
 AGCGGCCGCC ACCGCGGTGG ANCTCCN 1167

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(2) INFORMATION FOR SEQ ID NO: 108:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1907 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

GGCACAGGGG AATCATCGTG TGATGTGTGT GCTGCCTTTG TGAGTGTGTG GAGTCCTGCT 60
 20 CAGGTGTTAG GTACAGTGTG TTTGATCGTG GTGGCTTGAG GGAACCCCTT GTTCAGAGCT 120
 GTGACTGCGG CTGCACTCAG AGAAGCTGCC CTTGGCTGCT CGTAGCGCCG GGCCTTCTCT 180
 25 CCTCGTCATC ATCCAGAGCA GCCAGTGTCC GGGAGGCAGA AGGTACCGGG GCAGCTACTG 240
 GAGGACTGTG CGGGCCTGCC TGGGCTGCCC CCTCCGCCGT GGGGCCCTGT TGCTGCTGTC 300
 CATCTATTTC TACTACTCCC TCCCAAATGC GGTGCGCCCG CCCTTCACTT GGATGCTTGC 360
 30 CCTCCTGGGC CTCTCGCAGG CACTGAACAT CCTCCTGGGC CTCAAGGGCC TGGCCCCAGC 420
 TGAGATCTCT GCAGTGTGTG AAAAAGGGAA TTTCAACGTG GCCCATGGGC TGGCATGGTC 480
 35 ATATTACATC GGATATCTGC GGCTGATCCT GCCAGAGCTC CAGGCCCGGA TTCGAACCTA 540
 CAATCAGCAT TACAACAACC TGCTACGGGG TGCACTGAGC CAGCGGCTGT ATATTCTCCT 600
 CCCATTGGAC TGTGGGTGTC CTGATAACCT GAGTATGGCT GACCCCAACA TTCGCTTCCT 660
 40 GGATAAACTG CCCAGCAGA CCGGTGACCG TGCTGGCATC AAGGATCGGG TTTACAGCAA 720
 CAGCATCTAT GAGCTTCTGG AGAACGGGCA GCGGGCGGGC ACCTGTGTCC TGGAGTACGC 780
 45 CACCCCTTG CAGACTTTGT TTGCCATGTC ACAATACAGT CAAGCTGGCT TTAGCGGGGA 840
 GGATAGGCTT GAGCAGGCCA AACTCTTCTG CCGGACACTT GAGGACATCC TGGCAGATGC 900
 CCTTGAGTCT CAGAACAACCT GCCGCTCAT TGCCCTACCAG GAACCTGCAG ATGACAGCAG 960
 50 CTTCTCGCTG TCCAGGAGG TTCTCCGGCA CCTGCGGCAG GAGGAAAAGG AAGAGGTTAC 1020
 TGTGGGCAGC TTGAAGACCT CAGCGGTGCC CAGTACCTCC ACGATGTCCC AAGAGCCTGA 1080
 55 GCTCCTCATC AGTGAATGG AAAAGCCCCT CCTCTCCGC ACGGATTTCT CTTGAGACCC 1140
 AGGGTCACCA GGCCAGAGCC TCCAGTGGTC TCCAAGCCTC TGGACTGGGG GCTCTCTTCA 1200
 GTGGCTGAAT GTCCAGCAGA GCTATTTCTT TCCACAGGGG GCCTTGCAGG GAAGGGTCCA 1260
 60

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GGACTTGACA TCTTAAGATG CGTCTTGTC CTTGGGCCA GTCATTTCCC CTCTCTGAGC 1320
 CTCGGTGTCT TCAACCTGTG AAATGGGATC ATAATCACTG CCTTACCTCC CTCACGGTTG 1380
 5 TTGTGAGGAC TGAGTGTGTG GAAGTTTTC ATAACTTTG GATGCTAGTG TACTTAGGGG 1440
 GTGTGCCAGG TGTCTTTCAT GGGGCTTCC AGACCCACTC CCCACCTTC TCCCTTCCT 1500
 10 TTGCCCCGGG ACGCCGAAC CTCTCAATGG TATCAACAGG CTCCTTCGCC CTCTGGCTCC 1560
 TGGTCATGTT CCATTATTGG GGAGCCCCAG CAGAAGAATG GAGAGGAGGA GGAGGCTGAG 1620
 TTTGGGTAT TGAATCCCC GGCTCCCACC CTGCAGCATC AAGGTTGCTA TGGACTCTCC 1680
 15 TGCCGGCAA CTCTGCGTA ATCATGACTA TCTCTAGGAT TCTGGACCA CTCCTTCCC 1740
 TGGCCCTTA AGCCTAGCTG TGTATCGGCA CCCCCACCC ACTAGAGTAC TCCCTCTCAC 1800
 TTGCGGTTTC CTTATACTCC ACCCTTTCT CAACGGTCCT TTTTAAAGC ACATCTCAGA 1860
 20 TTAATAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAGGG CGGCCGC 1907

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(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 611 base pairs
 30 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

35 ATGAATTAAC GCCAAGCTNT NAATAGGGAC TCACTATGGG GGAAAGNTGG GTAACGCCTG 60
 CAGGTACCGT TCCGGAATTC CCGGTCGAC CCACGCTCC GATGGGGCTT TAGTAAATCA 120
 40 GGCTGTCAGG CTCAAAGCTG CAATCTGCCC ACTCTCAGGT ACTGAGACTT TGTGGGCCTC 180
 AGACACCAGG AAGAAAGTTG GGATACAGTC ATTTGAGTTA AAAAGGGAAT GACCCCTCAG 240
 AAACCCGCAT TAGCAGTGTT ACTCTGGAA GTGCCTTTAC TTTTAACGCT CTCTGTCTG 300
 45 AAAAAGAGGT GTTTGGTTAC GTGTGAGCCA ACATCACGTT TTGTTAGCTG TGATTACCT 360
 TTGTCGTTT AAAAGACTTC ACGGAGCCAT TCTGTATACA AGGTGTGCTC TTTCCAATGT 420
 50 AGAAGGGGTT ATGGAAAAGG GTGCGATCCT TTGCTGTAAA CTGGAGAGAC CAGTCCCAA 480
 CAGAGGGGAA TTTTAAGCCC TTCTCATCAC CCAATGGAT GTTTTGTCTT ATAGCAAATT 540
 55 CCTGCAAAAT AAATAAATAA ATATTGCAA AACTAAAAA AAAAAAAAAA AAAAAAAAAA 600
 GGGGGNCCN C 611

60

(2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2632 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

10 TCCCAGCTCT CAGGACAAGG GCCCTGGGCG ATCTTTTAAA AAAGCCGATT GGGTGTCTTT 60
CTAAAANTAC AACCAGTACT TCATCGTCAA GTTCTGGGA AGGGAGTCCC CTCCAGATTG 120
15 TCATGGAGTG ACAAATCTTG ACTCTGCTC CTGGAATTTT TCAGGCCCAA ACTAGCGTTT 180
CTACAATGAT TTATTGGCA AATTGTCTTT GATTATGGGT GGCTGATGAG GAACGTGCTT 240
20 TTGTTAGGAA CCGAACTGG GCGGCGGTGA GGGCGTGTAC GCAATGAGTC CGGAAGAGGG 300
TGAAATGCTT TCGGTAGGCA CTCACGGCT GTGAAGATGG CGGCGGTGC GTGGCTTCAG 360
GTGTTGCCTG TCATTCTTCT GCTTCTGGGA GCTCACCCGT CACCACTGTC GTTTTTCAGT 420
25 GCGGGACCGG CAACCGTAGC TGCTGCCGAC CGGTCCAAAT GGCACATTCC GATACCGTCG 480
GGGAAAAATT ATTTTAGTTT TGGAAAGATC CTCCTCAGAA ATACCACTAT CTCCTGAAG 540
TTTGATGGAG AACCTGTGA CCTGTCTTTG AATATAACCT GGTATCTGAA AAGCGCTGAT 600
30 TGTTACAATG AAATCTATAA CTTCAAGGCA GAAGAAGTAG AGTTGTATTT GGAAAACTT 660
AAGGAAAAAA GAGGCTTGTC TGGGAAATAT CAAACATCAT CAAAATGTGT CCAGAACTGC 720
35 AGTGAACCTT TTA AACACA GACCTTTTCT GGAGATTTTA TGCATCGACT GCCTCTTTTA 780
GGAGAAAAAC AGGAGGCTAA GGAGAAATGA ACAACCTTA CCTTTATTGG AGACAAAACC 840
GCAATGCATG AACCATTGCA AACTTGGCAA GATGCACCAT ACATTTTAT TGTACATATT 900
40 GGCATTTCAT CCTCAAAGGA ATCATCAAAA GAAATTCAC TGAGTAATCT TTTTACCATG 960
ACTGTTGAAG TGAAGGTCC CTATGAATAC CTCACACTG AAGACTATCC CTTGATGATT 1020
45 TTTTTCATGG TGATGTGAT TGTATATGTC CTGTTGGTG TTCTGTGGCT GGCATGGTCT 1080
GCCTGCTACT GGAGAGATCT CTTGAGAATT CAGTTTGGGA TTGGTGCTGT CATCTTCCTG 1140
GGAATGCTTG AGAAAGCTGT CTTCTATGCG GAATTCAGA ATATCCGATA CAAAGGARAA 1200
50 TCTGTCCAGG GTGCTTGAT CCTTGCAGAR CTGCTTTCAG CAGTGAAACG CTCCTGGCT 1260
CGAACCCTGG TCATCATAGT CAGTCTGGGA TATGGCATCG TCAAGCCACG CCTGGAGTCA 1320
55 CTCTTCATAA GGTGTAGTA GCAGRAGCCC TCTATCTTTT GTTCTCTGGC ATGGAAGGGG 1380
TCCTCAGAGT TACTGGGGCC CAGACTGATC TTGCTTCCTT GGCTTTATC CCCTTGGCTT 1440
TCCTAGACAC TGCCTTGTC TGGTGGATAT TTATTAGCCT GACTCAAACA ATGAAGCTAT 1500
60

	TAAAACTTCG GAGGAACATT GTAAACTCT CTTGTATCG GCATTTCACC AACACGCTTA	1560
	TTTTGGCAGT GGCAGCATCC ATTGTGTTTA TCATCTGGAC AACCATGAAG TTCAGAATAG	1620
5	TGACATGTCA GTCGGA CTGG CGGGAGCTGT GGGTAGACGA TGCCATCTGG CGCTTGCTGT	1680
	TCTCCATGAT CCTCTTTGTC ATCATGGTTC TCTGGCGACC ATCTGCAAAC AACCAGAGGT	1740
10	TTGCCTTTTC ACCATTGTCT GAGGAAGAGG AGGAGGATGA ACAAAGGAG CCTATGCTGA	1800
	AAGAAAGCTT TGAAGGAATG AAAATGAGAA GTACCAACA AGAACCCAAT GGAAATAGTA	1860
	AAGTTAACAA AGCACAGGAA GATGATTGA AGTGGGTAGA AGAGAATGTT CCTTCTTCTG	1920
15	TGACAGATGT AGCACTTCCA GCCCTTCTGG ATTCAGATGA GGAACGAATG ATCACACACT	1980
	TTGAAAGGTC CAAATGGAG TAAGGAATGG GAAGATTGTC AGTTAAAGAT GGCTACCATC	2040
20	AGGGAAGAGA TCAGCATCTG TGTCACTCTT CTGTACGGCT CCATGGGATT AAAGGAAGCA	2100
	ATGACATCCT GATCTGTTCC TTGATCTTTG GGCATTGGAG TTGGCGAGAG GTGTCAGAAC	2160
	AAAGAGAACA TCTTACTGAA AACAAGTCA TAAGATGAGA AAAATCTACG AGCTTCTTAT	2220
25	TTACAACACT GCTGCCCCCT TTCCTCCCAG ACTCTGACAT GGATGTTTAT GCAACTTAAG	2280
	TGTGTTGTTT CTGAACCTTC TGTAAATGTTT CATTTTAA ATCTGACAAA CTAAAAAGTT	2340
30	TAACGTCTTC TAAAAGATTG TCATCAACAC CATAATATGT AATCTCCAGG AGCAACTGCC	2400
	TGTAATTTTT ATTTATTTAG GGAGTTACAT AGGTGATGGG GGAAATGTTT AACTACCTTT	2460
	CATTTTCTG GGAAGTCAAG GTTACATCTT GCAGAGGTTG TTTTGAGAAA AAAGGGCCCT	2520
35	TCTGAGTTAA GGAGCCATAG TTCTATCAAT GATCAAAAGA AAAAAAAAAA AACTCGATCG	2580
	GCACGAGGGG GGGCCCGGTA CCCAATTCGC CCTATGGGAN TCGAATGAGA CC	2632

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(2) INFORMATION FOR SEQ ID NO: 111:

- 45 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2249 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

	GAATTCGGCA CGAGCTCACC GTGCTGCGTG ACACAAGGCC AGCCTGCGCC TACGAGCCCA	60
	TGGACTTTKT RATGGCCCTC ATCTACGACA TGGTACTGSW TGTGGTCACC CTGGGGCTGG	120
55	CCCTCTTCAC TCTGTGGGGC AAGTCAAGA GGTGGAAGCT GAACGGGGCC TTCCTCTCA	180
	TCACAGCCTT CCTCTCTGTG CTCATCTGGG TGGCCTGGAT GACCATGTAC CTCTTCGGCA	240
60	ATGTCAAGCT GCAGCAGGGG GATGCCTGGA ACGACCCAC CTTGGCCATC ACGCTGGCGG	300

	CCAGCGCTGG	GTCTTCGTCA	TCTTCCACGC	CATCCCTGAG	ATCCACTGCA	CCCTTCTGCC	360
	AGCCCTGCAG	GAGAACACGC	CCAACTACTT	CGACACGTCG	CAGCCCAGGA	TGCGGGAGAC	420
5	GGCCTTCGAG	GAGGACGTGC	AGCTGCCGCG	GGCCTATATG	GAGAACAAGG	CCTTCTCCAT	480
	GGATGAACAC	AATGCAGCTC	TCCGAACAGC	AGGATTTCCT	AACGGCAGCT	TGGGAAAAAG	540
10	ACCCAGTGGC	AGCTTGGGGA	AAAGACCCAG	CGCTCCGTTT	AGAAGCAACG	TGTATCAGCC	600
	AACTGAGATG	GCCGTCGTGC	TCAACGGTGG	GACCATCCCA	ACTGCTCCGC	CAAGTCACAC	660
	AGGAAGAMAC	CTTTGGTGAA	AGACTTTAAG	TTCCAGAGAA	TCAGAATTTC	TCTTACCGAT	720
15	TTGCCTCCCT	GGCTGTGTCT	TTCTTGAGGG	AGAAATCGGT	AACAGTTGCC	GAACCAGGCC	780
	GCCTCACAGC	CAGGAAATTT	GGAAATCCTA	GCCAAGGGGA	TTTCGTGTAA	ATGTGAACAC	840
20	TGACGAACTG	AAAAGCTAAC	ACCGACTGCC	CGCCCTCCC	CTGCCACACA	CACAGACACG	900
	TAATACCAGA	CCAACCTCAA	TCCCCGAAA	CTAAAGCAA	GCTAATTGCA	AATAGTATTA	960
	GGCTCACTGG	AAAATGTGGC	TGGAAGACT	GTTTCATCCT	CTGGGGTAG	AACAGAACCA	1020
25	AATTCACAGC	TGGTGGGCCA	GACTGGTGT	GTTGGAGGT	GGGGGGCTCC	CACCTTATC	1080
	ACCTCTCCCC	AGCAAGTGCT	GGACCCAGG	TAGCCTCTTG	GAGATGACCG	TGCGTTGAG	1140
30	GACAAATGGG	GACTTTGCCA	CCGGCTTTGC	CTGGTGGTTT	GCACATTTCA	GGGGGGTCAG	1200
	GAGAGTTAAG	GAGGTGTGG	GTGGGATTC	AAGGTGAGGC	CCAACTGAAT	CGTGGGGTGA	1260
	GCTTTATAGC	CAGTAGAGGT	GGAGGGACCC	TGGCATGTGC	CAAAGAAGAG	GCCCTCTGGG	1320
35	TGATGAAGTG	ACCATCACAT	TTGGAAAGTG	ATCAACCACT	GTTCTTTCTA	TGGGGCTCTT	1380
	GCTCTAGTGT	CTATGGTGAG	AACACAGGCC	CCGCCCTTC	CCTGTAGAG	CCATAGAAAT	1440
40	ATTCTGGCTT	GGGGCAGCAG	TCCCTTCTTC	CCTTGATCAT	CTCGCCCTGT	TCCTACACTT	1500
	ACGGGTGTAT	CTCCAAATCC	TCTCCCAATT	TTATTCCCTT	ATTCAATTTCA	AGAGCTCCAA	1560
	TGGGGTCTCC	AGCTGAAANS	CCCTCCGGA	GGCAGGTTGG	AAGGCAGGCA	CCACGGCAGG	1620
45	TTTTCGCGA	TGATGTCACC	TAGCAGGGCT	TCAGGGGTTT	CCACTAGGAT	GCAGAGATGA	1680
	CCTCTCGCTG	CCTCACAAGC	AGTGACACCT	CGGGTCCTTT	CCGTGCTAT	GGTGAAAATT	1740
50	CCTGGATGGA	ATGGATCACA	TGAGGGTTTC	TTGTTGCTTT	TGGAGGGTGT	GGGGGATATT	1800
	TTGTTTTGGT	TTTTCTGCAG	GTTCCATGAA	AACAGCCCTT	TTCCAAGCCC	ATTGTTTCTG	1860
	TCATGGTTTC	CATCTGTCTT	GAGCAAGTCA	TTCTTTGTTT	ATTTAGCATT	TGGAACATCT	1920
55	CGGCCATTCA	AAGCCCCCAT	GTTCTCTGCA	CTGTTTGGCC	AGCATAACCT	CTAGCATCGA	1980
	TTCAAAGCAG	AGTTTAAACC	TGACGGCATG	GAATGTATAA	ATGAGGGTGG	GTCTTCTGTC	2040
60	AGATACTCTA	ATCACTACAT	TGCTTTTCTT	ATAAACTAC	CCATAAGCCT	TTAACCTTTA	2100

AAGAAAAATG AAAAAGTTA GTGTTTGGGG GCGGGGGGAG GACTGACCGC TTCATAAGCC 2160
 AGTACGTCTG AGCTGAGTAT GTTTCATATA ACCTTTTGAT ATTTCTCAAA AAAAAAAAAA 2220
 5 AAAAAACCCG GGGGGGGGGC CGGACCTGG 2249

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(2) INFORMATION FOR SEQ ID NO: 112:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 2193 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

GATACTATAA GCGAAGTAC TCACGGGTGC GCCGTTAGAC TAGTGGATCC CGGGTGCAGG 60
 AATTGGCCAG AGCGCCGCG GAGTCGAAGT GCTGGCGCCC CCGCGCCGC TGCTCCGCG 120
 25 GANCCCAAAA TCATGAAGT CACCGTGAAG ACCCCGAAGA AAAGGAGGAA TTCGCCGTGC 180
 CCGAGAATAG CTCGCTCCAG CAGTTAAGG AAGAAATCTC TAAACGTTTT AAATCACATA 240
 CTGACCAACT TGTGTTGATA TTTGCTGGAA AAATTTTGAA AGATCAAGAT ACCTTGAGTC 300
 30 AGCATGGAAT TCATGATGGA CTTACTGTTC ACCTTGTCAT TAAACACAA AACAGGCCTC 360
 AGGATCATTC AGCTCAGCA ACAATACAG CTGGAAGCAA TGTTACTACA TCATCAACTC 420
 35 CTAATAGTAA CTATACATCT GGTCTGCTA CTAGCAACCC TTTTGGTTTA GGTGGCCTTG 480
 GGGGACTTGC AGGTCTGAST AGCTTGGGT TGAATACTAC CAACTTCTCT GAACTACAGA 540
 GTCAGATGCA GCGACAACCT TTGCTAACC CTGAAATGAT GGTCCAGATC ATGGAAAAC 600
 40 CCYTTGTTCA GACCATGCTC CTCGAATCCT GACCTGATGN AGACAGTTAA TTATGGCCAA 660
 TCCACAAATG CAGCAGTTGA TACAGAGAA TCCAGAAAT TAGTCATATG TTGAATAATC 720
 45 CAGATATAAT GAGACAAACG TTGGAACCTG CCCAGGAATC CAGCAATGAT GCAGGAGATG 780
 ATGAGGAACC AGGACCGAC TTTGAGCAAC CTAGAAAGCA TCCCAGGGG ATATAATGCT 840
 TTAAGGCGCA TGTACACGA TATTCAGGAA CCAATGCTGA GTGCTGCACA AGAGCAGTTT 900
 50 GGTGGTAATC CATTTGCTTC CTGCTGAGC AATACATCCT CTGGTGAAGG TAGTCAACCT 960
 TCCCGTACAG AAAATAGAGA TCCACTACCC AATCCATGGG CTCCACAGAC TTCCAGAGT 1020
 55 TCATCAGCTT CCAGCGGAC TCCAGCACT GTGGGTGGCA CTA CTGGTAG TACTGCCAGT 1080
 GGCATTCTG GGCAGAGTAC TACTGCGCCA AATTTGGTGC CTGGAGTAGG AGCTAGTATG 1140
 TTCAACACAC CAGGAATGCA GAGTTGTGT CAACAAATAA CTGAAAACCC ACAACTTATG 1200
 60

365

CAAAACATGT TGTCTGCCCC CTACATGAGA AGCATGATGC AGTCACTAAG CCAGAATCCT 1260
 GACCTTGCTG CACAGATGAT GCTGAATAAT CCCCTATTTG CTGGAAATCC TCAGCTTCAA 1320
 5 GAACAAATGA GACAACAGCT CCCAACTTTC CTCCAACAAA TGCAGAATCC TGATACACTA 1380
 TCAGCAATGT CAAACCCTAG AGCAATGCAG GCCTTGTTAC AGATTCAGCA GGGTTTACAG 1440
 10 ACATTAGCAA CGGAAGCCCC GGGCCTCATC CCAGGGTTTA CTCCTGGCTT GGGGGCATT 1500
 GGAAGCACTG GAGGCTCTTC GGGAACTAAT GGATCTAACG CCACACCTAG TGAAAACACA 1560
 AGTCCCACAG CAGGAACCAC TGAACCTGGA CATCAGCAGT TTATTCAGCA GATGCTGCAG 1620
 15 GCTCTTGCTG GAGTAAATCC TCAGCTACAG AATCCAGAAG TCAGATTTCA GCAACAACCTG 1680
 GAACAACTCA GTGCAATGGG ATTTTGAAC CGTGAAGCAA ACTTGCAAGC TCTAATAGCA 1740
 ACAGGAGGTG ATATCAATGC AGCTATTGAA AGGTTACTGG GCTCCCAGCC ATCATAGCAG 1800
 20 CATTTCTGTA TCTKGAAAAA ATGTAATTTA TTTTGTATAA CGGCTCTTAA ACTTTAAAAT 1860
 ACCTGCTTTA TTTTCATTTG ACTCTGGAA TTCTGTGCTG TTATAAACAA ACCCAATATG 1920
 25 ATGCATTTTA AGGTGGAGTA CAGTAAGATG TGTGGGTTTT TCTGTATTTT TCTTTTCTGG 1980
 AACAGTGGGA ATTAAGGCTA CTGCATGCAT CACTTCTGCA TTTATGTAA TTTTTTAAAA 2040
 ACATCACCTT TTATAGTTGG GTGACCAGAT TTGTCTCTGC ATCTGTCCAG TTTATTTGCT 2100
 30 TTTTAAACAT TAGCCTATGG TAGTAATTTA TGTAAGATAA AAGCATTAAG AAGAAGCAAA 2160
 AAAAAAAAAA AAAAATTCCT GCGCCCGCGA ATTCTTCT 2198

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(2) INFORMATION FOR SEQ ID NO: 113:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1043 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

CTGAAGTGTA TGTGGTGAGG AAGAAGAGGC TCCTACTGTA GACAGCCTTG TTCTACAGAT 60
 50 CCTCCCAGAA ATCTCTGGGC CAGGTGGAAC CCAGGTCAG AGAGGGATGG GAGAGAGGTT 120
 TAATTTTCCA TGATAAATAA AAATCTATAA AATAATAAAC AAGAGAAAAG AGATTGGAAA 180
 55 CAGCCAGGTT GGAGCAGTGA GTGAGTAAGG AAACCTGGCT GCCCTCTCCA GATTCCCCAG 240
 GCTCTCAGAG AAGATCAGCA GAAAGTCTGC AAGACCCTAA GAACCATCAG CCCTCAGCTG 300
 CACCTCCTCC CCTCCAAGGA TGACAAAGGC GCTACTCATC TATTTGGTCA GCAGCTTTCT 360
 60 TGCCCTAAAT CAGGCCAGCC TCATCAGTCG CTGTGACTTG GCCCAGGTGC TGCAGCTGGA 420

366

5 RGACTTGGAT GGGTTTGAGG GTTACTCCCT GAGTGA CTGTGCCTGG CTTTGTGGA 480
 AAGCAAGTTC AACATATCAA AGATWAATGA AAATGCAGAT GGAAGCTTTG ACTATGGSCT 540
 CTTCCAGATC AACAGCCACT ACTGGTGCAA CRATTATAAG AGTTACTCGG AAAACCTTTG 600
 CCACGTAGAC TGTCAAGATC TGCTGAATCC CAACCTTCTT GCAGGCATCC ACTGCGCAAA 660
 10 AAGGATTGTG TCCGGAGCAC GGGGGATGAA CAACTGGGTT AGAATGGAAG KTTGCACTGT 720
 TCAGGCCGGC CACTCTTCTA CTGGCTGACA GGATGCCGCC TGAGATKAAA CARGGTGCGG 780
 GTGCACCGTG GARTCATTC AAGACTCCTG TCCTCACTCA RGGATTCTTC ATTTCTTCTT 840
 15 CCTACTGCCT CCACTTCATG TTATTTTCTT CCCTTCCCAT TTACAATAA AACTGACCAG 900
 AGCCCCAGGA ATAAATGGTT TTCTTGGCTT CCTCTTACT CCCATCTGGA CCCAGTCCCC 960
 20 TGGTTCCTGT CTGTTATTTG TAACTGAGG ACCACAATAA AGAAATCTTT ATATTTATCG 1020
 AAAAAAAAAA AAAAAAACT CGA 1043

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(2) INFORMATION FOR SEQ ID NO: 114:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 703 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

GAATTCGGCA CGAGTGC CGCACCG CGGTTTTCG ACGCTGGCGG TGGACGCAGG 60
 CAGCATGGAC CACGGTTGCT GGGCGGATGG GGAGCGTCTA TGGTCAGTTG CTTAGAAGT 120
 40 GGTGAGATGG GAAGCTGCAG TTGGAAGACC CTGGAGGATG CCTGACAAGG GGATGTCTGA 180
 CACATGATTG GAGCTCTTTT TGAAATGTTT CTGCCCCTTC CTGGAGCAGA GGAGCCATTA 240
 45 TTTATGCAGG TACATCGAAG TCTTTTGACC TCCATACAGT GATTATGCTT GTCATCGCTG 300
 GTGGTATCCT GCGGCGCTTG CTCCTGCTGA TAGTTGTCGT GCTCTGTCTT TACTTCAAAA 360
 TACACAACGC GCTAAAAGCT GCAAAGGAAC CTGAAGCTGT GGCTGTAAAA AATCACAACC 420
 50 CAGACAAGGT GTGGTGGGCC AAGAACAGCC AGGCCAAAAC CATTGCCACG GAGTCTTGTC 480
 CTGCCCTGCA GTGCTGTGAA GGATATAGAA TGTGTGCCAG TTTTGATTCC CTGCCACCTT 540
 55 GCTGTGCGA CATAAATGAG GGCCTCTGAG TTAGGAAAGG TGGGCACAAA AATCTTCATG 600
 AGCAATACTT CTTAGTAGAT TGTTTTGTGA TTCAAATCAA GTTCTAGTGT TTTTATGTGA 660
 GATTATATAA TTTACAGTGT TGTTTTATAT ACTTTTGAAT AAA 703
 60

(2) INFORMATION FOR SEQ ID NO: 115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3684 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

5 GGCAGAGGGG GCATGAGCAG GAGGAGGATT ACCGCTACGA GGTGCTCACG GCCGAGCAGA 60
 15 TTCTACAACA CATGGTGGNA ATGTATCCGG GAGGTCAACG AGGTCATCCA GAATCCAGCA 120
 ACTATCACAA GAATACTCCT TAGCCACTTC AATTGGGATA AAGAGAAGCT AATGGAAAGG 180
 20 TACTTTGATG GAAACCTGGA GAAGCTCTTT GCTGAGTGTC ATGTAATTAA TCCAAGTAAA 240
 AAGTCTCGAA CACGCCAGAT GAATACAAGG TCATCAGCAC AGGATATGCC TTGTCAGATC 300
 TGCTACTTGA ACTACCCTAA CTCGTATTTT ACTGGCCTTG AATGTGGACA TAAGTTTGTG 360
 25 ATGCAGTGCT GGAGTGAATA TTAACTACC AAAATAATGG AAGAAGGCAT GGGTCAGACT 420
 ATTTCTGTGC CTGCTCATGG TTGTGATATC TTAGTGGATG ACAACACAGT TATGCGCCTG 480
 30 ATCACAGATT CAAAAGTTAA ATTAAAGTAT CAGCATTTAA TAACAAATAG CTTTGTAGAG 540
 TGCAATCGAC TGTAAAGTG GTGTCCTGCC CCAGATTGCC ACCATGTTGT TAAAGTCCAA 600
 35 TATCCTGATG CTAAACCTGT TCGCTGCAAA TGTGGGCGCC AATTTTGCTT TAACTGTGGA 660
 GAAAATTGGC ATGATCCTGT TAAATGTAAG TGGTTAAAGA AATGGATTAA AAAGTGTGAT 720
 GATGACAGTG AAACCTCCAA TTGGATTGCA GCCAACACAA AGGAATGTCC CAAATGCCAT 780
 40 GTCACAATTG AGAAGGATGG TGGTTGTAAT CACATGGTCT GTCGTAACCA GAATGTGAAA 840
 GCAGAGTTTT GCTGGGTGTG TCTTGGCCCA TGGGAACCAC ATGGATCTGC CTGGTACAAC 900
 45 TGTAACCGCT ATAATGAGGA TGATGCAAAG GCAGCAAGAG ATGCACAGGA GCGATCTAGG 960
 GCAGCCCTGC AGAGGTACCT GTTCTACTGT AATCGCTATA TGAACCACAT GCAGAGCCTG 1020
 CGCTTTGAGC ACAAACCTATA TGCTCAGGTG AAACAGAAAA TGGAGGAGAT GCAGCAGCAC 1080
 50 AACATGTCCT GGATTGAGGT GCAGTTCCTG AAGAAGGCAG TTGATGTCCT CTGCCAGTGT 1140
 CGTGCCACAC TCATGTACAC TTATGTCCTC GCTTCTTACC TCAAAAAGAA TAACCAGTCC 1200
 55 ATTATCTTTG AGAATAACCA AGCAGATCTA GAGAATGCCA CAGAGGTGCT CTCGGGCTAC 1260
 CTTGAACGAG ATATTTCCCA AGATTCTCTG CAGGATATAA AGCAGAAAAGT ACAAGACAAG 1320
 TACAGATACT GTGAGAGTCG ACGAAGGGTT TTGTTACAGC ATGTGCATGA AGGCTATGAA 1380
 60 AAAGATCTGT GGGAGTACAT TGAGGACTGA GAATGGCCCT GCATAAAATG AACTCTGAAA 1440

	ACTTTACCAT CTAGAGTGCT CATGCAATTA AAACAAAACA AACACAAACA AGGAGGCACT	1500
5	AAGCCTATTC TGACACCACT GGTCTGTAGT ACCAGAATG TTTTGTTAAT GGAAAGTTTA	1560
	AGTAAATTAT ATTGTAATAA AAAGGTAGAT AAACCATTGT ACAACAGTAT TCTAGGCCGC	1620
	CAACAAAAGT GTGACAGACA CACTAAAAGC CCTCCAACCT TAACTTGTA CGTAGCTTCA	1680
10	TTCTCAAAGC TGACTCCTTT TTTTCTTTT TCCTTTTCCT GAGTGTAGTA CAGTTAAAAT	1740
	TTCAACAGC TCCTTGACAC TGCTTTTCAT GTTCAAACCA GCCATTTTGT TGTACTTTGG	1800
15	TAAAGGACCT CTCCCCCTC CTCCCCCTACA CATACAGATA CACCCACACA CAGACTGACT	1860
	CTCTTTCTCT CATACCCCAA GGTCAAGAGT GAATGATGCT TAGTTCCTTG TAAAGAAAAT	1920
	CTTGGGATGG GGAAAGGGT AGGCAGCAAG AGGATTCAAC AAACGAAAAA CATAAAAACT	1980
20	TTGTATATGA CTTTAAAC AAGAGGACAA CACAGTATTT TTCAAAATTG TATATAGCGC	2040
	ATATGCATGG ACAAGCAAG CGTGGCACGT GTTGCATAA TGTTTAATTA CAAAAAATA	2100
25	TTTATCTTT AAAAATCTTC AAGATTATGT CTATTTGCTG TGCAITTTCT TTCAGTTTGC	2160
	TTATCTTTCC CGGGTTGGGG TTGGGATAAA GGTGTGTCGG TTTAGCACCT CTGGAAGACC	2220
	TATCTAGAGC TCITTCACCT TCCTGAGGTT ATTTTGCCCY TTCTGGTGTT GGTATGTCTG	2280
30	TTGCCGGCCA TGGGCTNCAY GCCTTGAATT CCTGCTCTTG ATCAGGGACA AGGGAGGTCA	2340
	AGCTCTGACT AATGCCATGA CCTGATTAAG GGTACAGCA GGGAGTTTG TTGCTACAGC	2400
35	TCATGAATTA ACCTGTCCCA ACCTAATCCC CCTCCATGGC ATCATGCCTC TACCCAAGCC	2460
	TTTGCTGCC CATGTTATGC ACACAGCTGT AGGCATTCTT AAGTCCCCTG TCGCATCCAG	2520
	TGGAAGCATT TTAAATTTT TTTTACTTTT TGGTTTCCC TTAATTGCTG CTTTTCAGAT	2580
40	TTTAGTTATG GCTCGTCTGC TCACCCCTC TCTACATTAG GGTGTCAAAG AGAATGTTTT	2640
	GCTTTAAATA TAAATAGCCA TTCAITTAGT CTCAGATTGT GAATTTAAAA TGGTGGATAC	2700
45	CGAAATTGCT TGTGTGTGTT GCTGTGGGTT TGGTTTGAAG GCAAACACCC CTAGAACATG	2760
	ATATTCCCAT CTAGTGCAAT TAAATAGAAA TCACTGAGTT TGCTGCTTTT TTATGTGAG	2820
	CAGATAGGAG AATTAATAAT GCATTTTAGC TGTGATGTCC ATTTTATGA AATTCCTACT	2880
50	AAGAGCTATG TTAAAGTAA AGGATGGTGG TGGTTGTATT AACTATATAC CTGTTTAGGC	2940
	CATTCTGGCT GTGGTATTTT TCAATAGGTC AGCATCTGTA AATCTGTCAG TTTTATACAG	3000
55	GAGTGCAGAG TGAAGTAGG AACTAGATTA AGAGGTCTAA ATATGAAATA CCAGTTGAGG	3060
	CTGAGGACCT CTTCGTCTTC CTTTAAATGT CTTTTCCTA GGGAGTGTTT ACCATTTGTG	3120
	AGGCAGCTTT GTCTGCTCTT ACACGTGACA TCCTATTACT CCATITGGAA GTAGGTTTAC	3180
60	TTTCCTCTGG CCTTTTGCCT AAGTTAGGCT TTGCTGAATC AACCTACTT TTCCTTTTAG	3240

AAAAGGTTGT TACAGGAGAT TTAAGTGGCAA CTGTTCTTTT CCCATCAAAA ATCAGTGAAT 3300
 GTTTGCTGAG TATAAATGCT GCTTCCTTAA ACCACTTGTC GCTTTAGGAT CAACTTTACC 3360
 5 TGTACCTTTT CTCCTTTCTT CCCTTGCCAC CTCAGGTGCA AATCTGAACT CAGTGTCTGC 3420
 TTCTTCCATT TTCTCGTCTC TCTCCCTCTT TCCCCATTA TCCATATGAC ATTATTTTAC 3480
 10 TTCAAATGAC AGCATCAATC TTAATAAGAT ATACATTAAA ACTAAGGAGT TTTTTTAAAG 3540
 AAAGCCTGAA TAAGTTCCTT TCCCTGGTAA CTTTGAAAAG CAGTCAGAGT TGCTATATAG 3600
 ATATATGTGG CTCCTTTAAA ATGCTTTGTG TATGTGTGGT GTTTAAAAAA AAAAAAAAAA 3660
 15 TTCGGGGGGG GGCCCGGTNC CCAT 3684

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(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1965 base pairs
 25 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

30 AAGAAAGGGT ATTAATAATC TAGATCACAT ATGGACCCCG GAAGGTTTTT NACCCTCTGT 60
 TAGTGACATC GAGTCTCCCA CTAGACAAAA TAGGTGGAAG AATCTCTCGA GGGCTCACAT 120
 35 TGTTTTGTCA TCTTCAGGAA AAACACCACC AGGCCATACC ACAGCCTGCC CAGTGAGGCG 180
 GTCTTTGCCA ACAGCACCCG GATGCTGGTG GTGGCCTTTG GGCTGCTGGT GCTCTACATC 240
 CTCTCTGGCTT CATCTTGGA GCGCCAGAG CCGGGATCC TGACCGACAG ACAGCCCCTG 300
 40 CTGCATGATG GGGAGTGAAG CAGCAGGAAG GGGCTCCCAA GAGCTCCTGG TGGTGCAGCC 360
 TGTGCTCCCC TCAGAAGCTC TGCTCTTCCC AGGGCTCCCG GCTGGTTTCA GCAGGCGACT 420
 45 TTCTTCCAAT GCTGGGCCCA GACTTCTTGC CTGGGTGCTG GCCTGCCCTC TCCGGNCCGC 480
 TTGCTGCCTG TCTGCTTTCC TTGGTGGYTT TGCTGGGTGC TGGGCCTGCC CTCTCCGGCC 540
 GCTGCTGCC TGTCTGCTTT CCTTGGTGGC TTTGCTGGGT GCTGGGCCTG CCTTCTCTGG 600
 50 CTGCTTGCTG CCTGTCTGCT TTCTTGGTG GCTTTGGCTT CTGCACTCCT TGGCGTCASC 660
 TCTCAGGTCC TCCATTCACA CGAGGTCTCT CTCGCTCTGG CCGCTCTTGC TGCTCCTGTC 720
 55 TGAAGAWATC AGACTGATTT CCTCTTAAGA CTCCTAGGGA TGTGGTGAAG AGCTGGGACT 780
 CAAGTGCACT CCACGGTGTG AAACATGAGG GARGTGAGGT GTCCGTCCAC TTCCCCATA 840
 AAGGTGTGCA TTTCAGTTAG GCTGCCCCGC CACAGAGCAG GCTTCATCTG CTCTGCCATC 900
 60

370

CAGCCCCATC TGGATGTGAG GTGGGGTGGG GACATCATGG GGTGATTGCA GAAAGGGGGA 960
 GTGGCGGCCC ACGCAGCTTC TGCTGAGGAG CTGACCGCTC TGAGCTGTTT TGTTCGTAT 1020
 5 TGCTGCTCTG TGTCTGCATG TATTGTGACC GTGCGGCTCC ACCTCTTCCA GCTGCTGCTA 1080
 CAGCTGAGGC CTGGATCCCG GCCTTTCCTT GTGACTTACG TGTCTGTCAC CGGCANGCAG 1140
 10 CCCTACAAAT CCTGGTGACC TGCTCTCCCA AGAACAGAGC CTGTCCCCAG ATGTCCCACT 1200
 AGCGATGAGT AACAGAGGTG GCTGTGGACT TCCTCTACTT CTCCTTGCTG GATCAGGGCC 1260
 TTCCTGCCTC CCGCTGGGCA GGTCTGGCCT TGCTCTCTTG GCAGGGCCCC AGCCCTCTG 1320
 15 ACCACTCTGC AGCTCACCAT GCAGCTGATG CCAAAGTTGT GGTGTCCAGT GTGCAGCAGC 1380
 CCTGGGAGCC ACTGCCACCT TCAGAGGGGT TCCTTGCTGA GACCCACATT GCTTCACCTG 1440
 GCCCCACCAT GGTGCTTGC CTGGCCCAAC CTAGCGTTCT GTGCCATGCT AGAGCTTGAG 1500
 20 CTGTTGCTCT TCTTCAGGG AGGAAATAGG GTGGAGAGCG GGAAGGTCT TGCTCCTAAG 1560
 TGTGCTGCT GTGGCTTTT TGCCTTCTCC AAAGACGCAC TGCCAGGTCC CAAGCTTCAG 1620
 25 ACTGCTGTGC TTAGTAAGCA AGTGAGAAGC CTGGGGTTTG GAGCCACCT ACTCTCTGGC 1680
 AGCATCAGCA TCCTACTCCT GGCACATCA GGCCAACGTC CACCCAGCC TCACATTGCC 1740
 AGATGTTGGC AGAAGGGCTA ATATTGACCG TCTTGACTGG CTGGAGCCTT CAAAGCCACT 1800
 30 GGGATGTCCT CCAGGCACCT GGTGCCATG ACCAGCTCCC CGTCTCCATA GGGGTAGGCA 1860
 TTCTACTGGT TTATGAAGCT CGAGTTTCAT TAAATATGTT AAGAATCAA GCTGTCTTTG 1920
 35 TTCAGGCTGC TATAACAAA ATATAATAGC CTGGGTGGCT TAAAC 1965

40 (2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

50 AGTGATCCCC TTGCCTCGGC CTCCTAAAAT GCTGGAATTG TAAGCGTGGG CCTCTGCACC 60
 CGGCCTGGTC CGCAATTTAA AAACGCACAG CCACCATTC CTYTCCAGAA AGCAGCCAGA 120
 TGCCTTTGGG AGAACCAGCC TCCTCCATGG AGGAAAGCTT GGGATCTGCC TTCCACCTG 180
 55 GGGAGGAGAG GGATCTGTGG AAAATCCTTC TGACGGACTT CCCCTCAGTG CCTGATCCAT 240
 ACTCAATAGT AGAAAAAGTA AGAAATATAC AAAGATAGCA GATACCGGA GACAGTTCCC 300
 60 CAAATAGCTG AGCGAWTAGC GCAGAAGCAA TATTGAAGAC CTAATAGCTG AGACATTTC 360

5 AGAACTGATA AAGTGCATCC AGCCACAGAT CAAGCAGCCC AGAAAATTCC AGGCAGCATC 420
AACAATAAAA TAGCCCCACA TGCACCCGTG AAAATGCAGA AGACCAAACA AAAAAGTCCG 480
GTCAACAGCC AGAGTTAAAG AGG 503

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(2) INFORMATION FOR SEQ ID NO: 118:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1133 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

GGCACAGCTT GGAATGAACC CCTGTGGATA AGGGGGACTA TTAGATAGAA TAAACATCAA 60
TAAATGCTTG ATGAATAAAC GCTAATCCTA CCTTCCCAGC CTGACACCTC CCAGTGGACA 120
25 CCACACTTCA CTTGAAGCCT TAGAAACCTT TCCCACCCAT GCTTCCAGCC CTGGCTTCAT 180
GTTGCCATTT CTCACCCCCA GAACAGGCCG CCCGCCTGAA GAAACTACAA GAGCAAGAGA 240
AACAACAGAA AGTGGAGTTT CGTAAAAGGA TGGAGAAGGA GGTGTCAGAT TTCATTCAAG 300
30 ACAGTGGGCA GATCAAGAAA AAGTTTCAGC CAATGAACAA GATCGAGAGG AGCATACTAC 360
ATGATGTGGT GGAAGTGGCT GGCCTGACAT CCTTCTCCTT TGGGGAAGAT GATGACTGTC 420
35 GCTATGTCAT GATCTTCAA AAGGAGTTTG CACCCTCAGA TGAAGAGCTA GACTCTTACC 480
GTCGTGGAGA GGAATGGGAC CCCCAGAAGG CTGAGGAGAA GCGGAACNTG AAGGAGCTGG 540
CCCAGAGGCA ANGAGGAGGA GGCAGCCCAG CAGGGGCCCTG TGGTGGTGAG CCCTGCCAGC 600
40 GACTACAAGG ACAAGTACAG CCACCTCATC GGCAAGGGAG CAGCCAAAGA CGCAGCCCAC 660
ATGCTACAGG CCAATAAGAC CTACGGCTGT KTGCCCGTGG CCAATAAGAG GGACACACGC 720
45 TCCATTGAAG AGGCTATGAA TGAGATCAGA GCCAAGAAGC GTCTGCGGCA GAGTGGGGAA 780
GAGTTGCCGC CAACCTCCTA GGCGCCCCGC CCAGCTCCCT TTGACCCCTG GGCAGGGCA 840
GGGGGCAGGG AGAGACAAGG CTGCTGCTAT TAGAGCCCAT CCTGGAGCCC CACCTCTGAA 900
50 CCACCTCCTA CCAGCTGTCC CTCAGGCTGG GGGAAAACAG GTGTTTGATT TGTACCGTT 960
GGAGCTTGA TATGTGCGTG GCATGTGTGT GTGTGTGTGA GAGTGTGAAT GCACAGGTGG 1020
55 GTATTTAATC TGTATTATTC CCCGTTCTTG GAATTTTCTT CCCATGGGGC TGGGGTACTT 1080
TACATTCAAT AAATACTGTT TAACCAAAA AAAAAAAAAA AAAAGAAAGA AGN 1133

60

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1101 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

GGGCACAGCT GAAGCTGCAG ACCTCCCCAG GGGATGGCTC CTCTCCCCCA GGAGCCCCGA 60
 GGCAGGGGAG GCAGAAAGCC TGGGCTCTGG GGGGTGGCCT GCGGACAGCT GTGCTGTGGG 120
 15 CCGGGGGCTG GGCCTGTCCC ACAGGNCGT GGAGCTCGTG GTTCTGAGCA GCCAGCTGGG 180
 TGGTGTCTGG GGATAGCTGG GAGGCACAGC GGCTGCCATG TGGGACTGGG ACTGGAGTGC 240
 20 TCCCTGGTCT TGGCCTCTGT GGCTCAGCCT TGCTCTGGTC TGCCTGAGTG CAGGGGCCAA 300
 GGGGCACAGG GCCAGTGAGG CCGGCCACGC TCGGGCCCTC ACCTGTGAGA TGGGGTCGGA 360
 ATTTKACACA GCCTANGGCT TGGTCTCTGG TKGINGAMCG TGGACTYCTK AGAACGGGAG 420
 25 TGCTGGTCCT GAAAGGCGTG GTTGGAGACC AGCTGCTTTT CTCGCTGTTT TTCTCTTAGG 480
 AGATTAAACA AAAACAGAAA GCACAAGACG AACTCAGTAG CAGACCCCAG ACTCTCCCCT 540
 30 TGCCAGACGT GGTTCAGAC GGGGAGACGC ACCTCGTCCA GAACGGGATT CAGCTGCTCA 600
 ACGGCATGC GCCGGGGGCC GTCCCAAACC TGCAGGGCT CCAGCAGGCC AACCGGCACC 660
 ACGGACTCCT GGGTGGCGCC CTGGCGAACT TGTTTGTGAT AGTTGGGTTT GCAGCCTTTG 720
 35 CTTACACGGT CAAGTACGTG CTGAGGAGCA TCGCGCAGGA GTGAGGCCCA GCGCCGAGA 780
 CCCAAGGCGC CACTGAGGGC ACCGCGCACC AGAGCGTGAC CTCGGCAGGC TGGACACACT 840
 40 GCCCAGCACA GGCAGACCCA CCAGGCTCCT AGGTTTAGCT TTTAAAAACC TGAAAGGGGA 900
 AGCAAAAACC AAAATGTGTG ACTGGCTTT GGAGGAGACT GGAGCCTCAG CCCTGTCTTG 960
 GCCACGGGCC GCTGGGGCTG GTGTGGGTGG GCCTTGTGTG CTGGATTGTG AGCTTATCTT 1020
 45 CCGTGTGTG TTTGGACCTG TTTAGTAAA CCCGTTTTTC ATTTAAAAA AAAAAAAAAA 1080
 AAACCTTGGG GGGGGGCCCC N 1101

50

(2) INFORMATION FOR SEQ ID NO: 120:

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 282 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

AGCTTCTCTG TCCAGTCTTG AACTCTGGGS TCTCTTGGAA CTTTCCTCAC CCCTCTCAGC 60
 5 CTGAATATTC CTTCCATGGA TTCCACTCAA CCAGACTTTG GATCTGTGCC TACTTAATCA 120
 ACCTTATCTT TGCAATATGT TGGGGCCAC CTCCACTCC TTGGTTCTTG TTCTCCTTG 180
 GCCTAACTTG TCCCTTCTCC ACTTCACATC CCCGGTGGGA CAGCATTCCT CCTTCCTCCC 240
 10 AACCTCCCTC CGTCTCARAA AAAAAAAAAA AAAAAAAAAA TT 282

15

(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 2635 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

25 TAAGGGGGTG TGTGCTCACC TCCTCCTGAC CCTTAACACT CCTGTCTGTC CCAGACCAAC 60
 AGAGAGAGCT GTCCCTGAGA CCCCAGAGAG AAGCAGCTGC CGAAAGCTGC AGCCTTTCCG 120
 30 CACTCTGAGA CATGATCTT CCTCTGCCA GGGGAGAGCC ACCCAGAGC CATGTCCAGC 180
 CCCACTTCCC TCAGCCCCCA GGGYTTCTTT CTGGCCCCCTC TGAGGATTCC CTAGGGCTGC 240
 CCCCAGAGG GGYTTCCCCA AGCTCTGTTT TGAAGCCTGC AATGTGAAA AGTGAGAAGT 300
 35 CAGAGGGAAC AGGACAGGTG CAGCCGGGCT CTGAGGCCAC ACCTCACACC TCGCTGTTCC 360
 CCAACATCCC CTGAGCAGTG TGAGCTCATC TCACCAGATG AGAAGAGGCC CTGTGCATTT 420
 40 YTTTGTGTTG TTTGTTGCTG TTTTCCCCCA CCCATCCAGT TCTCCTCAGC AAAGCAAATT 480
 CCTTAACACC TTTGGTGAG AATTCTTAC CCAGACTTGG GGCTGTGATG CCCTTCAGTG 540
 CGTGGTGAGT GCAGCGTGTG TCGTGTGCC TGTGTGTGAA CCTGGGGGCC ATCCTGGTGG 600
 45 CCTGGGAGCG TGAGGAGAGG CCCCTGTGT GCTGGGTGAG TGGTGGGTGT GGGGTCAATG 660
 CAGTGAGGCT CTCTGGGTGA GGCTCCCAAC CTGGCAGTCC CCAGCCTCCC AGCATCTGTG 720
 50 AGCGTCTGTT GGACTTTACA GAAGAGCCTC ATCCYGTCTG CCCCTCACTC TGCCCTGGAA 780
 TCAACATCTT CCGAGTCCTT CTTGGGGGAA ATAGCAGAGC CCCACTTAAC TCCATAAACT 840
 GCTTCCCATT CCGCAGCCCA GTTCTGATTG TTGAGGTGTC GCGTCGTTCC AGGTCCCCCA 900
 55 GTCCCCCTCT TCTCCTGTCC TCTCTCTGTC CTTACCTCC CCACTCCAGC CCCGGCTCAG 960
 TTCAGGGAAA TGCTGTTCCA YATCAGCCCT CTGCTCTCTG AGGCAGCCGC GCCTCTGACT 1020
 60 CGGAGCTACT TGAACTTCT GCTCTTGCTA GGATTGGAGT CTACCTATCT CTTCCATTG 1080

	TCCCAGCTGG AGTTCCTGGAA CTTTCCTCCT CGGGGTGGGG GTGGGGGTTG TTAGGATGC	1140
5	TGGGGGGCCT GGGGAAGGAA GGAGTTCAGA GGAGGGGTGT CCCCTGTCTT CTTGATGTC	1200
	CCCTCCGCTC CTGGGACACG TGCTCTCTCT GTCTCTGGGT CTTCTGGGTG TGCACGTTTG	1260
	TGTGTCCTTG TAAATATGTT TTAGGAAGAA AGCAAAAGGG ACTGAAGTAG CTTCTGGTAG	1320
10	GATTGCAGGG GTCCAGCCTT GCCTGTTTCC GAAGCCCCCA CACTGCCTTT CGCCCTACTG	1380
	AGACTGGTCC CCTCAAAAGG TAGACAAAAC AGCAGCTCCC TGTGGAGGTG AAGGGCGGCC	1440
15	TCAAAGTGGC TTTTGTGTAG ACAAGGTAA GGTTCCTCA TGACCAAGGT TGTAGATCGG	1500
	TCCTTCCTCA GCTCCTTGAT TTGTGACCTT GACCAAGGGG CCTGCCCTCC AGCCCTCCA	1560
	GTGCCCTCTC CTGATGCCT CGCTCCTTCC TGCCCCACT CCCCTGGTTT AGGAGGTAG	1620
20	GGGAATTAGG GCCATGCTGG AAGAAGCTTA ACCATGTGTT CAAAGAAAGG TTTCTTGCTT	1680
	GCTTGGTCTT GGAAGTCCCC TTGGCTGCCC CAGGCCTCCT TGGCCCAAGG GTGCTGGGG	1740
25	AGGTGGATGT CAGATCTGGT AGGTTCAGC AGAGAAATA AATGTGCTT GAGAGACCH	1800
	TCAGAGAGGG TCCAAGGGTG ATGGAGAAGG AAGCATGGCC TGGGAGCTTG GAAAGGARGG	1860
	GTGGTGGGTG GCGGCATCTT GACTGCCCCC TGTGTGCTCA CAGGTGGGGG GTGCTACCC	1920
30	CYCTTCACTC CAGCCCGCCT GCCTTCAGCC TTCCATGAGC TTCACCTGCT TCCAACTTCA	1980
	CTTTGGAGGG GGTGGGGTCC GTTGGCATCA ACACGGGGAC CCTGTGCTTC ACCAAGGCC	2040
35	GAGCCCTCAG CCCCTGGGGA GAACAAATGG CTGAGCTTTG ATACCTGGGG TCTTCAGAG	2100
	GCTGCGGGCT GCGGCAGTC CCAGGGGAGA GACACCAAG AAGGAGCTCC AGACATCCCG	2160
	AGGAAGTTC CAGCAGAGCA AACTGCTTTC CAGCCTGAG CCTGCTTAAA CTGTGTGATG	2220
40	TGCAATAACT GAGCTTAGAG TTAGGAATTG TGTTCAGTG CTTGGATTTC CTTCTGTAGA	2280
	TTTAAGTCTT GAAATGTAT CTCTCAGTAA TTTTAGATGT CTTTAAAAA ATCGAAAAAC	2340
45	AAAGTGTTAG ACTGTGTGCG TGTGCGTTGA TGGGCACTCA AGAGTCTCTT GAGTCATCCA	2400
	GCCCTGCCTT TCCCTGCGC CCCATCCTC TCAGTCCCG CCC/GCCTCC ACTTGGGGAC	2460
	CCTGCCTCGT GTGCTCTTAA TCTGCTATT ACTCAGCCTA AGGAAACAG TACACTCCAC	2520
50	ACATGCATAA AGGAAATCAA ATGTTATTTT TAAGAAAATG GAAAATAAAA ACTTTATAAA	2580
	CACCAAAAAA AAAAAAAAAA ACCCNGGGGG GGGGCCGGTA ACCCATTTGG CCTAA	2635

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(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 994 base pairs

375

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

	GAATTCGCCA GAGGTTCCGC GAAGATAGGG AATAAGGAAG CACAGGAGTA GGGGAGAAGG	60
	AAGCACAGGA GTAGGGGAGA TATACAGCGG TCAGGATAAG GGGGAAAGGG CGGTGGTTGC	120
10	SCAAGAGGTG AAACAAGATG TGAGAGACAA GGGGTAGGGA AGAAATGGGG CAGCGGTTAG	180
	G TTCAGAAGC GCATAGACCG TGGCGGACGG GCAATGCGAG GGGCACAGAA AGGAAC TGAG	240
15	GGGTGGGCTA TTTTAARGGA GATGGTCCTT CAGCCCTCTT YTTTCTGCG TAGTTCTCCT	300
	CCTCCAGGCC GCGCGCGGAT ATGTCGTCCG GAAACCAGCC CAGTCTAGGC TGGATGATGA	360
	CCCACCTCCT TCTACGCTGC TCAAAGACTA CCAGAATGTC CCTGGAATTG AGAAGGTTGA	420
20	TGATGTGCTG AAAAGACTCT TGTCTTTGGA AATGGCCAAC AAGAAGGAGA TGCTAAAAAT	480
	CAAGCAAGAA CAGTTTATGA AGAAGATTGT TGCAAACCCA GAGGACACCA GATCCCTGGA	540
25	GGCTCGAATT ATTGCCTTGT CTGTCAAGAT CCGCAGTTAT GAAGAACACT TGGAGAAACA	600
	TCGAAAGGAC AAAGCCCACA AACGCTATCT GCTAATGAGC ATTGACCAGA GGAAAAAGAT	660
	GCTCAAAAAC CTCGTAACA CCAACTATGA TGTCTTTGAG AAGATATGCT GGGGGCTGGG	720
30	AATTGAGTAC ACCTTCCCC CTCTGTATTA CCGAAGAGCC CACCGCCGAT TCGTGACCAA	780
	GAAGGCTCTG TGCATTCGGG TTTTCAGGA GACTCAAAAG CTGAAGAAGC GAAGAAGAGC	840
35	CTTAAAGGCT GCAGCAGCAG CCCAAAAACA AGCAAAGCGG AGGAACCCAG ACAGCCCTGC	900
	CAAAGCCATA CCAAAGACAC TCAAAGACAG CCAATAAATT CTGTTCAATC ATTTAAAAAA	960
40	AAAAAAAAA AAAAAAAAAA AAAAAGGGGA GGGG	994

45 (2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1542 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

	GGCASAGCCA CCTCGGCCCC GGGCTCCGAA GCGGCTCGGG GGCGCCCTTT CGGTCAACAT	60
55	CGTAGTCCAC CCCCTCCCCA TCCCAGCCC CCGGGGATTC AGGCTCGCCA GCGCCAGCC	120
	AGGGAGCCGG CCGGGAAGCG CGATGGGGC CCCAGCCGCC TCGCTCCTGC TCCTGCTCCT	180
60	GCTGTTCCGC TGCTGCTGGG CGCCCGGCGG GGCCAACCTC TCCCAGGACG ACAGCCAGCC	240

	CTGGACATCT GATGAAACAG TGGTGGCTGG TGGCACCGTG GTGCTCAAGT GCCAAGTGAA	300
5	AGATCACGAG GACTCATCCC TGCAATGGTC TTAACCCTGC TCAGCAGACT CTCTACTTTG	360
	GGGAGAAGAG AGCCCTTCGA GATAATCGAA TTCAGCTGGT TAMCTCTACG CCCCACGAGC	420
	TCAGCATCAG CATCAGCAAT GTGGCCCTGG CAGACGAGGG CGAGTACACC TGCTCAATCT	480
10	TCACTATGCC TGTGCGAACT GCCAAGTCCC TCGTCACTGT GCTAGGAATT CCACAGAAGC	540
	CCATCATCAC TGGTTATAAA TCTTCATTAC GGGAAAAAGA CACAGCCACC CTAAACTGTC	600
15	AGTCTTCTGG GAGCAAGCCT GCAGCCCGGC TCACCTGGAG AAAGGGTGAC CAAGAACTCC	660
	ACGGAGAACC AACCCGCATA CAGGAAGATC CCAATGGTAA AACCTTCACT GTCAGCAGCT	720
	CGGTGACATT CCAGGTTACC CGGGAGGATG ATGGGGCGAG CATCGTGTGC TCTGTGAACC	780
20	ATGAATCTCT AAAGGGAGCT GACAGATCCA CCTCTCAACG CATGAAGTT TTATACACAC	840
	CAACTGCGAT GATTAGGCCA GACCCCTCCCC ATCCTCGTGA GGGCCAGAAG CTGTTGCTAC	900
25	ACTGTGAGGG TCGCGGCAAT CCAGTCCCCC AGCAGTACCT ATGGGAGAAG GAGGGCAGTG	960
	TGCCACCCCT GAAGATGACC CAGGAGAGTG CCCTGATCTT CCCTTTCTC AACAAGAGTG	1020
	ACAGTGGCAC CTACGGCTGC ACAGCCACCA GCAACATGGG CAGCTACAAG GCCTACTACA	1080
30	CCCTCAATGT TAATGACCCC AGTCCGGTGC CCTCCTCCTC CAGCACCTAC CACGCCATCA	1140
	TCGGTGGGAT CGTGCTTTC ATTGTCTTCC TGCTGCTCAT CATGCTCATC TTCCTTGGCC	1200
35	ACTACTTGAT CCGGCACAAA GGAACCTACC TGACACATGA GGCAAAAGGC TCCGACGATG	1260
	CTCCAGACGC GGACACGGCC ATCATCAATG CAGAAGGCGG GCAGTCAGGA GGGGACGACA	1320
	AGAAGGAATA TTTCATCTAG AGGCGCCTGC CCACTTCCTG CGCCCCCAG GCCCTGTGG	1380
40	GGACTTGCTG GGGCCGTAC CAACCCGAC TTGTACAGAG CAACCGCAGG GGCCGSCCCT	1440
	CCCGNTGTT CCCCAGCCCA CCCACCCCT TGTACAGAA TGYTKGTTT GGGGTGCGGT	1500
45	TTGTWATTG GTTTNGGATN GGGAAGGGA GGGANGGCGG GG	1542

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(2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1390 base pairs

(B) TYPE: nucleic acid

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(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

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CAAGCTCTAA TACGACTCAC TATAGGGAAA GCTGGTACGC CTGCAGGTAC CGGTCCGAA

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	TTCCCGGGTC GACCCACGCG TCGGGCCTC AGGGTGGACG CATGGTCTG CACTGAGGCC	120
	CTCGTCATGG TGGCGCCTGT GTGGTACTTG GTAGCGGCGG CTCTGCTAGT CGGCTTTATC	180
5	CTCTTCCTGA CTCGCAGCCG GGGCCGGGCG GCATCAGCCG GCCAAGAGCC ACTGCACAAT	240
	GAGGAGCTGG CAGGAGCAGG CCGGGTGGCC CAGCCTGGGC CCCTGGAGCC TGACGAGCCG	300
10	AGAGCTGGAG GCAGGCCTCG GCGCCGAGG GACCTGGGCA GCCGCCTACA GGCCAGCGT	360
	CGAGCCAGC GGGTGGCCTG GGCAGAAGCA GATGAGAAGC AGGAGGAAGC TGTCATCCTA	420
	GCCCAGGAGG AGGAAGGTGT CGAGAAGCCA GCGGAAATC ACCTGTGGG GAAATTTGA	480
15	GCTAAGAAAC TGCGAANNT GGAGGAGAAA CAAGCGCGAA AGGCCAGCK TGAGGCAGAG	540
	GAGGCTGAAC GTGARGWCG GAAACGACTC GAGTCCCAGC GCGAATGAGT GGAAGAAGGA	600
20	GGAGGAGCGG CTTCGCCTGG AGGAGGAGCA GAAGGAGGAG GAGGAGAGGA AGGCCCGCGA	660
	GGAGCAGGCC CAGCGGAGC ATGAGGAGTA CCTGAACTG AAGGAGGCCT TTGTGGTGA	720
	GGAGGAAGGC GTAGGAGAGA CCATGACTGA GGAACAGTCC CAGAGCTTCC TGACAGAGTT	780
25	CATCAACTAC ATCAAGCAGT CCAAGGTTGT GCTCTTGGAA GACCTGGCTT CCCAGGTGGG	840
	CCTACGCACT CAGGACACCA TAAATCGCAT CCAGGACCTG CTGGCTGAGG GGACTATAAC	900
30	AGGTGTGATT GACGACCGGG GCAAGTTCAT CTACATAACC CCAGAGGAAC TGGCCGCCGT	960
	GGCCAACTTC ATCCGACAGC GGGGCCGGGT GTCCATCGCC GAGCTTGCCC AAGCCAGCAA	1020
	CTCCCTCATC GCCTGGGGCC GGGAGTCCCC TGCCCAAGCC CCAGCCTGAC CCCAGTCCTT	1080
35	CCCTCTTGA CTCAGAGTTG GTGTGGCCTA CCTGGCTATA CATCTTCATC CCTCCCCACC	1140
	ATCCTGGGGA AGTGATGGTG TGGQCAGGCA GTTATAGATT AAAGGCCTGT GAGTACTGCT	1200
40	GAGCTTGGTG TGGCTTGGTG TGGCAGAAGG CCTGGCCTAG GATCCTAGAT AAGCAGGTGA	1260
	AATTTAGGCT TCAGAAATATA TCCGAGAGGT GGGGAGGGTC CCTTGAAGC TGGTGAAGTC	1320
	CTGTCTTAT TATGAATCCA TTCATTCAAG AAAATAGCCT GTTGCAAAAA AAAAAAAAAA	1380
45	AAAAACTCGA	1390

50 (2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 1288 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

60 GGC GCGCGG TGAAAGGCGC ATTGATGCAG CCTGCGCGG CCTCGGAGCG CGGCGGASCA 60

GACGCTGACC ACGTTCCTCT CCTCGGTCTC CTCGCGCTCC AGCTCCGCGC TGCCCGGCAG 120
 CCGGGAGCCA TGCACCCCA GGGCCCCGCC GCCTCCCCGC AGCGGCTCCG CGGCCTCCTG 180
 5 CTGCTCCTGC TGCTGCAGCT GCGCGCGCCG TCGAGCGCCT CTGAGATCCC CAAGGGAAG 240
 CAAAAGGCGC ATCCGGCAGA GGGAGGTGGT GGACCTGTAT AATGGAATGT GCTTACAAGG 300
 10 GCCAGCAGGA GTGCCTGGTC GAGACGGGAG CCCTGGGGCC AATGGCATTC CGGTACACC 360
 TGGATCCCA GGTGGGATG GATTCAAAGG AGAAAAGGGG GAATGTCTGA GGGAAAGCTT 420
 TGAGGAGTCC TGGACACCCA ACTACAAGCA GTGTTCATGG AGTTCATGA ATTATGGCAT 480
 15 AGATCTTGGG AAAATTGCGG AGTGTACATT TACAAAGATG CGTCAAATA GTGCTCTAAG 540
 AGTTTTGTTC AGTGGCTCAC TTCGGCTAAA ATGCAGAAAT GCATGCTGTC AGCGTTGGTA 600
 20 TTTCACATTC AATGGAGCTG AATGTTCAAG ACCTCTTCCC ATTGAAGCTA TAATTTATTT 660
 GGACCAAGGA AGCCCTGAAA TGAATTCAAC AATTAATATT CATCGCACTT CTCTGTGGA 720
 AGGACTTTGT GAAGGAATTG GTGCTGGATT AGTGGATGTT GCTATCTGGG TTGGCACTTG 780
 25 TTCAGATTAC CCAAAGGAG ATGCTTCTAC TGGATGGAAT TCAGTTTCTC GCATCATTAT 840
 TGAAGAACTA CCAAATAAA TGCTTTAATT TTCATTTGCT ACCTCTTTTT TTATTATGCC 900
 30 TTGGAATGGT TCACTTAAAT GACATTTTAA ATAAGTTTAT GTATACATCT GAATGAAAAG 960
 CAAAGCTAAA TATGTTTACA GACCAAAGTG TGATTTTACA TGTTTTAAA TCTAGCATT 1020
 TTCATTTTGC TTCAATCAAA AGTGGTTTCA ATATTTTTTT TAGTTGGTGA GAATACTTTC 1080
 35 TTCATAGTCA CATCTCTCA ACCTATAATT TGGGAATATT GTTGTGGTCT TTTGTTTTTT 1140
 CTCTTAGTAT AGCATTTTTA AAAAAATATA AAAGCTACCA ATCTTTGTAC AATTGTAAA 1200
 40 TGTTAAGAA TTTTTTTATA TCTGTTAAAT AAAAATTATT TCCMACAACC TTAACAAAAA 1260
 AAAAAAAAAA AAAAAAAAAA AAAAAANA 1288

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(2) INFORMATION FOR SEQ ID NO: 126:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1517 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

AGTGGCTTAA AGGCATCGTT TTAGGGATTA CTGGGAAGTA TCTTCAAAGT AATACATGAG 60
 AAACATTCCT TCCTAAATCC TTTATTATAT TGAATATCGT ATTAATTGGT TTCAGAGGT 120
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TAAATTAACC ATGTATTCCT GCAATAAATG TCACTTGTNT CTGTATATA ATCTTTTSTA 180
 TATATTACCG GATTGATTCA TTAGTATTTT GTTGAGGATT TTTGTGTCTA TATTCATAAG 240
 5 AGATGCTGGT CTGCAGTTTT CTMTTTTGT GATAATCTGG TTTTGTATC AGTAATACAG 300
 GCCCCATGAA ACGAGTTGGG AAGTGTTTAC CTCTCTTGT TTTTTCAG AGTTTGTGAA 360
 GAATGCTAT TAATTCTTTA AATGTTTGGT AGAATCTACC ATTGAAATCA TGTGCTCTGG 420
 10 GCTMTTTT GAGGGAAGTG TTCTGATAAC TAATTCAGTA TCTACTTTT ATAGCTCTGT 480
 TCAGATTTTG CTCTTCCTG AGTTAGTTT GGTAATTTGT GTATCTCTAG GARTTTGTCC 540
 15 ATTCATTTA TCTATTGT TGGCATAAAT TAACTAAAT TTGGCCTGAG CCTACCTGTA 600
 TATCTTGAGT CCTCTGTAA GGAAGTGTAG CCTAAGTTGT ACATAAACAA ACTGAAATCC 660
 TAAATTAGGA ATGTAGTTT TGTAACAGCT CCTGAGTCTC AGGCAGTCAC AGCAGYCAAG 720
 20 TCTGTCAATT GCAGGCTGCT AACTAAGCAG CCCATGSTCA AATGAGGCAA AAACCTTTGC 780
 TTTTAACACA TAGTATAGCT TTGTAATCCT TTTCTTGCAC ACTCGGTAA TTTCTTCCTT 840
 25 TTTCATTCCC KGWATTTTCC AKGAATATGA RTCTYCCTTT TTTCCCTCC TGTAGTCTA 900
 GCTAATGGT TGTCATTTT GTTGATCTTT TGAARAACAA ACCTTTGGT CCACTTTCTT 960
 GTTGATATG CTGARTATTC TCATAATTGG AGTGGAAGC TGATCTTTGA TTAATTATTT 1020
 30 TACTTAGGGC TGAGGAGTTC ATGGACTTCG CAAAACCTCC TTGAATCTAA ATTGCATCTT 1080
 CTTCCTGGT TTCTGGGCTG AAACATGTTT TTTCCATCT WANAWACCCT TGGTCTTTTC 1140
 35 ATKGGCGATT AAGACTAGAG AAAGTTCTAG ATMCCTTGT CTTTATGCT GTCATTTGT 1200
 TTAAAGGCTT TCTATGTAGT AAACTATCT ATATAGACAA AATAGAGCCT TGAGTTGTGG 1260
 TCTGAATTT GATCAACATG ATTTACCACA TTCTGTACTG GATATTTCTT CACCTGCTGC 1320
 40 TACTGTAAAC CATTTTATTC TTGGATCTTC TGTAGATAT ATTATCACAG GTACTTTTTA 1380
 CAGGGGTGTC TAATCTTTTG GCTTCCCTGG GCACATTGAA AGAAGAAGAA TTGTCTTGGG 1440
 45 CCACACATCA AATACGCTAA CACTAATAAT AGTTGATGAG CTAAAAAAA AAAAAAAG 1500
 GCAAAAAAGN CCCAAA 1517

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(2) INFORMATION FOR SEQ ID NO: 127:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1073 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

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TGAATCTATT CTTTGAACAT TCTACAACAA GAATTACATT ATACTGTTAT ACCAGAGTAC 60
 TTCTGCAGTG TGAAATAGAT TGGTTTGGAA AATGAACCTG GCTTTGCTAT AAATTACATT 120
 5 CACAGGCCTT TTGCAAAATG TGTAACCTGC CTATCAAAGT AGTTTGTAGG GCAAATGCAG 180
 AATATATGTC TCCATCTGGT AAAGTACCTT WTAYTCATGT GGGAAATCAA GTAGTATCAG 240
 10 AACTTGGTCC AATAGTCCAA TTTGTTAAAG CCAAGGGCCA TTCTCTTAGT GATGGGCTGG 300
 AGGAAGTCCA AAAAGCAGAA ATGAAAGCTT ACATGGAATT AGTCAACAAT ATGCTGTTGA 360
 CTGCAGAGCT GTATCTTCAG TGGTGTGATG AAGCTACAGT AGGGRMGATC ACTCATGMTA 420
 15 GGTATGGWTC TCCTTACCCT TGGCCTCTGW WTCATATTTT GGCCTATCAA AAACAGTGGG 480
 AAGTCAAACG TAAGNTGAAA GCTATTGGAT GGGGAAAGAA GACTCTGGAC CAGGTCTTAG 540
 20 AGGATGTAGA CCAGTGCTGT CAAGCTCTCT CTCAAAGACT GGGAACACAA CCGTATTTCT 600
 TCAATAAGCA GCCTACTGAA CTTGACGCAC TGSTATTTGG CCATCTATAC ACCATTCTTA 660
 CCACACAATT GACAAATGAT GAACTTTCTG AGAAGGTGAA AACTATAGC AACCTCCTTG 720
 25 CTTTCTGTAG GAGAATTGAA CAGCACTATT TTGAAGATCG TGGTAAAGGC AGGCTGTCAT 780
 AGAGTTATGT GTTAGTCTCA GGAGTCTTAA CTTTGTAAAT ATGTTTACT TGAATGTTAC 840
 30 ATTAGATATT GGTGTCAGAA TTTTAAACC AAATTACTGC TTTTGAAC CTCAAATTAT 900
 ATAATGTATC TTATGTATGT GCTTTATATT GTTATTTGTG TATACATTAA AATAATCTG 960
 AATTATTTAA TCTGATATGT TGTATTCTGT ATCTTGAAAT TTTTGTTC TTGAAACATG 1020
 35 CATGCATTTA AAAATAAAGC TTAAACAAC GTAAAAAAA AAAAAAAAAA CTC 1073

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(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

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CAACCCCTGC CTTTTTTTGT TTTTCCATTT GCTTGGTAGA TCTTCCTCCA TCCCTTTATT 60
 TTGAGCCTAT GTGTGTCTCT GCCCGTGAGA TGAGTCTCCT GAATACAGCA CACTTACTGG 120
 TCTTGACTCT GTATCCAATT TGCCAGTCTG TGTCTTTCAT TTGGAGCATT TAGCCCATTT 180
 ACATTTAAGG TKAATATTGT TATGTGTGAA TTTRATCYTR TCATTATGWT GTTAGCTGGT 240
 TATTTTGCTT GTTAGTTGAT GCAGTTTCTT CCNGGCATCA ATGGTCTTTA CAANTTGGCA 300

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1275 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

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GGCAGAGCCT GTCCCTGCTG CCCCTGCAAA AAAAACCCCC TCTGGTGTGA GCAGGATGGT 60
TGGAGGTTAT GTGAGCTCCT TCTCCTTTCC TCCAGTTTCC TCTTCCCTTC TCCTCCCTGC 120
CTCTTTTGCT TTTCCCTTTC TTCTGGTAC CCCCTGCCCC TTCCTGTATT TTCTCCCATC 180
GCCATTCTCC CCTCTCCAC TGTCCCTAAC CCGTTCAAAC TCTTTCTCT TAAATGGTTG 240
AGATTTTCTC TCACCAAGCA CACCCAGTA TTAATTAAAC TAGCTGCAAA CAGGCAGCAA 300
GTGGTCTACC ATGACAGATG GGTTTTGTGT GTGTGTGTGT GTGTGTAATT GTAATAAAAC 360
ATATTGARTC ACTCAATAAA CACAGAGTGT CTAATACATG TATCARGCAC TATCATAGAT 420
GCTAATTAAC GAAACTGAAA TGGCCAGGCC CTCACAGTGG CTCATGCCTA TAATCCCAGC 480
ACTTTGGGAG GATGAGGCAG GAGGATCACT TGAGGCCGGG AGTTCAAGAC CAGCCTGGGC 540
AACATAGTAA GACTCCATCT CTACAAAAAA AAAATTTTTC TTATTATACT TTAAGTTTTC 600
GGTTACATGT GCAGAACGTG TAGTTTGTGT ACATAGGTAT ATACGTGCCC TGGTAGTTTG 660
CTGCACCCAT CAACCCATCA CCTACATTAG GTATTTCTCC TAATGTTACC CCTCTCCTAG 720
CCCCCACC CCCTGACAGG CCTGGTGTGT GATGTTCCCC TCCCTGTGTC CATGTGTTCT 780
CATTGGTCAA CTCTCACCTA TGGAGTGAGA ACATGTGGTA TTGGTMTTC TGATCTGTGT 840
ATAGCTTGCT GAGAATGTTG GTTTCCAGCT TTATCCACGT CCCTGCAAAG GGCATAAACT 900
CATCCCTTTT TATGGCTGCA TAGTGTCCA TGGGTATAC GTGCCACATT TTCTTAATCT 960
ATCATTGATG GACAAGTTT GCTATTGTGA ATAGTGCCAC AATAAACATA CGTGTGCGTG 1020
TGCTTTATA GCAGCATGAT TTATAATCCT TTGGGTATAT ACCCAGTAAT GGGATCACTG 1080
AGTCAAATGG TATTTCTCGT TCTAGATCCG TAAGGAATTG CCACACTGTC TTCCACAATG 1140
TTTGAATAA TATCACTCC CACCAACAGT GTAAAAGTGT TTCTATTTT CCACAACCTC 1200
TCCAACATCT GTTATTTCT GACTTTTAA TGAACGTCAT TCTAACTGGC GTGAGATGGT 1260
ATCTCATGTG GGTTT 1275

(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 472 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

10 CNGAAACCCC GTGAACCCCTC CCCGGGTAA AAAGCCCCC CTAAATGGGG GGAACGCTC 60
 ACACGTTATA AAAAAGCACT AGAATGTTTT GAAAGCGAGA AACACAGCT GTGTAGGGTA 120
 15 GCTAGCAGTT AGTGTGTAC AGAAGACAGA TATTTGTGCA TTTYTGCAIT TTCTAAGTTT 180
 GCTGCAATGA GCATGTATTA CTTTCATAGT TATAAACAC ATGCAAAATG CCCTTTTAAA 240
 ATGAAAAAA ATCCATGAGT GTAAGTGATA TATATGCTTT GGAAAGCCTG GGACGGTCAT 300
 20 TGTTTACTCT CAATAGTATG TGTTCGCTT TGTCTTTTG AGACATTTG TTTTAATCTG 360
 TTGATGACAA TAACCTGTTG ATAATATAAC TTGATAACAA ATAAATGAC TTATGATTGA 420
 25 AWMAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA NN 472

30 (2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 1950 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

40 ACCTCTCAGA ATCTTCTCTC AGCAACCTGA GTCTTCGCCG TTCCTCAGAG CGCCTCAGTG 60
 ACACCCCTGG ATCCTTCCAG TCACCTTCCC TGGAAATTCT GCTGTCCAGC TGCTCCCTGT 120
 GCCGTGCCTG TNATTGCTG GTGTATGATG AGGAAATCAT GGCTGGCTGG GCACCTGATG 180
 45 ACTCTAACCT CAACACAACC TGCCCTTCT GCGCCTGCCC CTTTNTGCCC CTGCTCAGTG 240
 TCCAGACCNT TGATTCCCGG CCCAGTGTC CCAGCCCCAA ATCTGCTGGT GCCAGTGGCA 300
 50 GCAAAGATGC TCCTGTCCCT GGTGGTCCTG GCCCTGTGCT CAGTGACCGA AGCTCTGCCT 360
 TGCTCTGGAT GAGCCCCAGC TCTGCAACGG GCACATGGGG GGAGCCTCCC GGCGGGTTGA 420
 GAGTGGGGCA TGGGCATACC TGAGCCCCCT GGTGCTGCGT AAGGAGCTGG AGTCGCTGGT 480
 55 AGAGAACGAG GGCAGTGAGG TGCTGGCGTT GCCTGAACTG CCCTCTGCCC ACCCATCAT 540
 CTTCTGGAAC CTTTGTGGT ATTTCCAACG GCTACGNTG CCCAGTATTC TACCAGGCT 600
 60 GGTGCTGGCC TCCTGTGATG GGCCTTCGMA CTCCAGGCC CCATCTCCTT GGCTAACCCC 660

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TGATCCAGCC TCTGTTT CAGG TACGGCTGCT GTGGGATGTA CTGACCCCTG ACCCCAATAG 720
CTGCCCCACCT CTCTATGTGC TCTGGAGGGT CCACAGCCAG ATCCCCCAGC GGGTGGTATG 780
GCCAGGCCCT GTACCTGCAT CCCTTAGTTT GGCAGTGTG GAGTCAGTGC TGCGCCATGT 840
TGGACTCAAT GAAGTGCACA AGGCTGTGGG GCTCCTGCTG GAAACTCTAG GGGCCCCACC 900
CACTGGCCTG CACCTGCAGA GGGGAATCTA CCGTGAGATA TTATTCCTGA CAATGGCTGC 960
TCTGGGCAAG GACCACGTGG ACATAGTGGC CTTGATAAG AAGTACAAGT CTGCCTTTAA 1020
CAAGCTGGCC AGCAGCATGG GCAAGGAGGA GCTGAGGCAC CGGCGGGCGC AGATGCCCCAC 1080
TCCAAGGCC ATTGACTGCC GAAAATGTTT TGGAGCACCT CCAGAATGCT AGAGACCTTA 1140
AGCTTCCCTC TCCAGCCTAG GGTGGGAAG TGAGGAAGAA GGGATTCTAG AGTTAACTG 1200
CTTCCCTGTT GCCTTCATGG AGTGGGAAC AGGCTGGGAA GGATGCCAG TCAAAGGCTC 1260
CAAGCGAGGA CAACAGGAAG AGGGATCCAC TGTTACCAA AGTCCTGATT CCCCCATCAC 1320
CAACCTACCC AGTTTGTTCG TGCTGATGTT GGGGGAGATC TGGGGGAGT TGGTACAGCT 1380
CTGTTCTTCC CTGTCTAT ACCGGGAACT CCCCTCCAGG GTACCCACAG ATCTGCATTG 1440
CCCTGGTCAT TTTAGAAGTT TTTGTTTAA AAAACAACTG GAAAGATGCA GAGCTACTGA 1500
GCCTTTGCCC TGAATGGAG GTAGGGATGT CATTCTCCAC CAATAATGGT CCCTCTTCCC 1560
TGACGTTGCT GAAGGAGCCC AAGGCTCTCC ATGCCTTCT ACCTAAGTGT TTGTATTTTA 1620
TTTTAAATTA TTTATCTGG AGCCACAGCC CCCTTGCTTA TGAGGTTCTT ATGGAGAGTG 1680
AGAAAGGGAA GGGAAATAGG GCACCATGGT CCGGTGGTTT GTAGTTCCTT CAAAGTCAGG 1740
CACTGGGAGC TAGAGGAGTC TCAAGCTCCC CTTAGGAAGA ACTGGTGCCC CCTCCAGTCC 1800
TAATTTTTCT TGCCTGCCCC GCCTTGGGA ATGCCCTACC CACCCAGGTC CTGACCTGTG 1860
CAATAAGGAT TGTTCCTGC GAAGTTTTGT TGGATGTAAA TATAGTAAAA GCTGCTTCTG 1920
TCTTTTCAA AANAAAAAA AAAAAAACT 1950

50 (2) INFORMATION FOR SEQ ID NO: 132:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 990 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

60 TGGAAGATTT AAAATAGGTT TCATATTTCT CTTGAATATG AATATATAAG CTTGAATAAG 60

384

CTGAGTCCCT TATTATTATG AATTTTCCT TATTATTTCT ACCAATGCTT CTTATATTAA 120
 AGCCTGATCT TTTCATATT ASTATATGTA CATTAGCTGC CTGTGGATTA ACATTTCCAT 180
 5 GAAATGCTAT TTTCATTTGT TGGATCTTAA ACTTTTGTG TCTTTATATA AGGTATGCTY 240
 CTTTAAAGCA TGATATTTTT AACACAATA GTTGAAAGAC AATCTYCACC TTTTACTTGT 300
 ATATTACAT GTATGTAT TTTCATGCA TATTACGTCT TATTATTTAA CCAACCTATT 360
 10 TTTTATTATC TAGGGCATTT TTCAGAAAGC CTTATTTTCT TGTATTAATC AAATATTTTT 420
 ATCATTTGAT TTTCCTCTAT TATTAGKAA TACGKTACYC YAAATATATA TTGTGGSTAT 480
 15 TTTCAGAAAT GCATATGCC TCCTTAATTT ATTAGAGGCT AACCTAAATT ATTACTTTTA 540
 CCACTTACTT GAAATCTCTG GAACTTTAGA ACATTTATTG TTTTATGCAT TTTAATTCTA 600
 CTTGTATTTT TACTACTCCT AAACATTATT ATTGTTTTAG ACAAGCCAAA ATATATNTTG 660
 20 TTATTACCTT ATCTCCATTT TCTTCTGTA TTTTATGCC ACTATGTATG CTCAATTTC 720
 TTCTATGTGA TGAACCTAAT TCAGTACTTT TGTMTTTTAA TCTGTGCAGG TAGCCTGGCC 780
 25 ATTAATTTT TATTTTGGT TTGCTGAAAA AATTGTGTTT ATTTCTATAT GCATACTTAT 840
 GCATATAGAA TCTAGTNG ACATATTTTT AGTATTTATA AATGTAAAGT CATWATTKG 900
 GCTCTATCA TTCTGKGA GAAATCAATT GTCAGCCCAA TAGTTTTCA TTTTAAATTA 960
 30 CNGAATTTTT TCATGTCTCT GTTTTAGGA 990

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(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1720 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

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GTCTGATAAG CGACTGTGGT TATTCCTCTA AAGTTTACTT CAGCACTAAC ACTAGTGCTT 60
 CCGCTGGAGT TTGCATTTT CCAGCTTTAT ACAGGATTTT CCTTTGACTG GAAGAGTCAA 120
 50 GGATATGAG ACTCAAGT GACATTTATT GTACAACATC AAGGGGAATA GGATACTCAT 180
 CAACTGGGA TTATTCTTAT CAAACATGG TCTTCTTTGA ATAAGAAAAA TACATAGTTG 240
 GTTATTATGG ACTTAAACT GTTTAAATG GATATTCTGA TAAATATTT GCTGCTCTGT 300
 55 AGAGTGTGGA AAATCTGAGA ATATTAGCTT TACTCATCTT GAGCTTTGAG GATGTTCTCT 360
 GTACGCCGAT GGTTCATAT TAACTAAAA AGCTGGGTAT TGTAAATCT CATTTATAAA 420
 60 AACTCAGATG AGAAGAAAT TTTCTTGAT GGTGAGACTG TTGTCTTAGT TCAGGAAATT 480

5 ATTTAATAAT CCTTTGTTAC CTGTGAATGA AGGAACTTTG TAATTCTGAT TTATCGTAAA 540
 ACATGAGCCT TTCCAGAGTC AGCTTAGACA CTGTTGTCGC AAATAGCCAT GCTTTGCCTT 600
 10 ATGCCAAGGA GGCCAGAGG GAGGGCCTAG TCTTCCTCTG TTGCTGTACA TATATTGAAA 660
 TGCTTTTTTT TTTTATTTTG CATTGTGTAT CTATAATGAG CTTTCTGAGC CCTGATATTA 720
 15 TGTGAGACAA ACAGGAGTTA TTGATGTTAT AACTCCCTT CCATTCAGGA TTTTCTGCTT 780
 GGAGGGAAAT ATGTTGACCT TAGAGAATTG TGAATATTGT TGCAATCTT GAATATATTA 840
 CCATGTGAAT AATAGAGACT GTGTTGCTCT CTAGTATAAG CTATATTTAT TTTTGATTCA 900
 20 TTTGAATTAC TAGTTATAAC TGGAGAAATT TTGTTACCTC TATCCTGGCT TGCCTGACTG 960
 GCTGTATAAT AGCAGCAGCC TCTTTTAGAG CATCTTAATG AAAACATGGA TGAAAGGAAT 1020
 TAATGATGAT ATCTGCAGAC TGCCTAGAAA ATGGCTTTTG TTCCAGCGT TAACATTTTC 1080
 TTCTCAATCA CATTTCAATG TTTGTGGAGA GTGGCAGATT CACACCAGAA AACTAGGTG 1140
 25 TTCATATCCA TAGCATGGAT GCAGAATAAG CAGTTGGGAG AGAAGCTTCT TCCTACCTGG 1200
 TACTCCTCCC ATTACCTCA GCCCAGCCCC AGACAGCGT TAGCATTCAG TGTGGGCCCT 1260
 CAGGCAGCCC TGAAGCCTGG CTGGGTCATC AGATGGGGG AGCCTGTGAC GGCACCAGC 1320
 30 GGCCTGATC CAGGGAAGAG TTCTGGAGG GTGTTGGCTG TTTTGTGTAG CTCAGTTTTT 1380
 TTCTGGGCTC CACCATTCCT AACTCCAGGT AGACAAGATA GATGTCACAC ACAACAATTT 1440
 TAAAGTATTT TGCTTAGTGC ATTTTGTTTA TGATTGCAGT GTTTGTTTCT TATTTAATAG 1500
 35 GCTTTTTACT TCATTCTATT AAATTTTAGT GTTTAGAAGA GGCGGGTACT GTCAGTGTG 1560
 AAAATATGTA ATATTTTATA TGTATACCA TGTCATATAT ACTTGCAATA TCAGACCTG 1620
 40 CATTCAATAT ACAATGCAAT TGACTCTTTG CAGACCTGCA TTTTTCAGTG AACAATAAAA 1680
 AGATTGTCTG GCACTCCAAA AAAAAAAAAA AAAAAAAAAA 1720

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(2) INFORMATION FOR SEQ ID NO: 134:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

GGCACGAGGC CATCTGGGCT CATTCAGCAG GAAATAATGG AAAAAGCTGC AATATCCAGG 60
 TGTTTACTAC AATCTGGAGG CAAGATCTTT CCTCAGTATG TGCTGATGTT TGGGTTGCTT 120
 60

386

GTGGAATCAC AGACACTCCT AGAGGAGAAT GCTGTTCAAG GAACAGAACG TACTCTTGGA 180
TTAAATATAG CACCTTTTAT TAACCAGTTT CAGGTACCTA TACGTGTATT TTTGGACCTA 240
5 TCCTCATTGC CCTGTATACC TTTAAGCAAG CCAGTGGAAC TCTTAAGACT AGATTTAATG 300
ACTCCGTATT TGAACACCTC TAACAGAGAA GTAAAGGTAT ACGTTTGTA AATCTGGGAA 360
GACTTGACTG CTATTCATT TTGGGTATCA TATGTACCTT GATGAAGANG ATTAGGTTGG 420
10 GATACTTCAA GTGAAGCCTC CCACTGGAAA CAAGCTGCAG TTGTTTATA TAATCCCATC 480
CAGGTTGAAA TGGGAGAGGA ACTTGACTC AGCATTGAGC ATCACAAAAG CAATGTCAGC 540
15 ATCAGAGTAA AGCAATGAAG AGCAGTTTTC CAATGAAAAC TGTGTAAATA GAGCATCAAC 600
AAGTACAAAA TTCTTGCTTT AATTAGTGGG GGTATATAAA AATTCCTTGT AATGGTCAAA 660
TATTTTTTAA AATTGACATT AATAAAGCAT ATTTTAAAAG TTTCT 705
20

(2) INFORMATION FOR SEQ ID NO: 135:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 323 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

AGCACACACC TCCTTTAGTT GCTCCTAAGG TCATGTTCAA CATTGCTGGA GTGCATTTTC 60
35 TGCTCAGGGA GCTTTCAGG ACCCGGAATG TTTGGTGCTC ACAGACYCTG GCAAGGATCG 120
GTATTGCTGT TCCTCAGTTT TGCCTGGGGA AATGAGGAGT CAGTGACGTT CAGTGACGTG 180
40 CCCAGAGTCA TGCCATTGGC GGGTGGCCCA GKGMTCCAGG TCTCCAGCAC CCCTCGGCCC 240
CCTCCTCACC AGGTCACATC ATCTCCTGGA TTAGAATCTG CTCACATAGT CTGTCCTGAA 300
AGGAAAAAAA AAAAAAAAAA AAC 323
45

(2) INFORMATION FOR SEQ ID NO: 136:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 582 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

55

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

GGACGGAATG GTGCAACCCT CCTWAMTTTT CTKGKGCTGT TGACAACAGA GGGAGGGAGG 60
60

GAAAACATTT TTYGTGGGAG AATCCTACYT CTGCAGSGGA GCCCTTAAGC GATKGATTTT 120
 GAATCTKGAC CCTTTACCAA CTAATTTTGA AGGAAGATAC CTTGGAAATA TTTGGCATTG 180
 5 AGTGGGTAC TGAAACAGCA TTAGTGAATT CATCTAGAGA ACTCTTTCAT TTATTCAGGC 240
 AACAACGTGA CAACTTGGAA ACCTTGTTAC AGTCCAGTTG TGATTTTGGG AARGTATCAA 300
 CTCTACACTG CAAAGCAGAC AATATTAGGC AGCAGTGTGT ACTATTTCTC CATTATGTTA 360
 10 AAGTTTTCAT CTTCAGGTAT CTGAAAGTAC AGAATGCTGA GAGTCATGTT CCTGTCCATC 420
 CTTATGAGGC TTTGGAGGCT CAGCTTCCCT CAGTGTGAT TGATGAGCTT CATGGATTAC 480
 15 TCTTGATAT TGGACACCTA TCTGAACTTC CCAGTGTAA TATAGGAGCA TTTGTAAATC 540
 AAAACCAGAT TAAGGTTTGA CTGGTTTCAT TTGATTTTGA AG 582

20

(2) INFORMATION FOR SEQ ID NO: 137:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1021 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

TTCGGCAGAG CCCTTGCGCG CTCTGAATA CCTGCKTTCT GTAGCGCTAG TTCTCTTCAA 60
 GATTTGCTTA GTGTCAATTC ATTTCGGTTT CTTTCTCGC CATGTTTTC TGTCGGAATT 120
 35 ACGGTTCTGT TTGGTTCTAT GTACTCTCTA AAATGTTATC GTTTTTCATT TGTCTACTAA 180
 TTTTCGTGCA TTGTPTACTA CTGAGTTTCT TAATATCTGA CTGGCCTCCG CCCACGGGCT 240
 40 CTGCAGANCA TAAATACTC AGGCTGATGG TAGTGCAGAG ACTCTCCCTC CTTGATCAGC 300
 GCAAACGTTG GTCTGAGGCT TGAGGGATGG AGCAACATTT TCTTGGCTGT GTGAAGCGGG 360
 CTTGGGATTC CGCAGAGGTG GCGCCAGAGC CCCAGCCTCC ACCTATTGTG AGTTCAGAAG 420
 45 ATCGTGGGCC GTGGCCTCTT CCTTTGTATC CAGTACTAGG AGAGTACTCA CTGGACAGCT 480
 GTGATTTGGG ACTGCTTTC AGCCCTTGCT GCGGGCTGCC CGGAGTCTAC TGGCAAAACG 540
 50 GACTCTCTCC TGGAGTCCAG AGCACCTTGG AACCAAGTAC AGCGAAGCCC ACTGAGTTCA 600
 GTTGGCCGGG GACACAGAAG CAGCAAGARG CACCCGTAGA AKARGTGGG CAGGCAGARG 660
 AACCCGACAG ACTCAGGCTC CRGCAGCTTC CCTGGAGCAG TCCTCTCCAT CCYTGGGACA 720
 55 GACAGCAGGA CACCGAGGTC TGTGACAGCG GGTGCCTTTT GGAACGCCGC CATCCTCCTG 780
 CCCTCCAGCC GTGGCGCCAC CTCCCGGTT TCTCAGACTG CCTGGAGTGG ATTCTTCGCG 840
 60 TTGGTTTTCG CGCGTTCTCT GTACTCTGGG CGTGCTGTTT ACGGATCTGT GGAGCTAAGC 900

AGCCTTAGAT AGCAGCAGAA GGCTTTTGG ATTCTCCTCC TTGAAAAGAT TCTCAGTTAC 960
CAAACGTCTC CACCTAGAAA ATAAAAATAC ATTAAGATGT TGAANAAAAA AANAAAAAA 1020
5 A 1021

10 (2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:
15 (A) LENGTH: 1777 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

20 CGGAAGATGA TGGCTTCAAC AGATCCATTC ATGAAGTGAT ACTAAAAAAT ATTACTTGGT 60
ATTCAGAACG AGTTTAACT GAAATCTCCT TGGGGAGTCT CCTGATCCTG GTGGTAATAA 120
25 GAACCATTCA ATACAACATG ACTAGGACAC GAGACAAGTA CCTTCACACA AATTGTTTGG 180
CAGCTTTAGC AAATATGTCG GCACAGTTTC GTTCTCTCCA TCAGTATGCT GCCCAGAGGA 240
TCATCAGTTT ATTTTCTTTG CTGTCTAAAA AACACAACAA AGTTCTGGAA CAAGCCACAC 300
30 AGTCCTTGAG AGGTTGCTG AGTTCTAATG ATGTTCTCTCT ACCAGATTAT GCACAAGACC 360
TAAATGTCAT TGAAGAAGTG ATTGGAATGA TGTTAGAGAT CATCAACTCC TGCCTGACAA 420
35 ATTCCCTTCA CCACAACCCA AACTTGGTAT ACGCCCTGCT TTACAAACGC GATCTCTTTG 480
AACAATTTG AACTCATCCT TCATTTCAGG ATATAATGCA AAATATTGAT CTGGTGATCT 540
CCTTCTTTAG CTCAAGGTTG CTGCAAGCTG GGAGCTGAGC TGTCAGTGGA ACGGTCCTG 600
40 GAAATCATTA AGCAAGGCGT CGTTGCGCTG CCCAAAGACA GACTGAAGAA ATTTCCAGAA 660
TTGAAATTCA AATATGTGGA AGAGGAGCAG CCCGAGGAGT TTTTATCCC CTATGTCTGG 720
45 TCTCTGTCT ACAACTCAGC AGTCGGCCTG TACTGGAATC CACAGGACAT CCAGCTGTTC 780
ACCATGGATT CCGACTGAGG GCAGGATGCT CTCCCACCG GACCCCTCCA GCCAAGCAGC 840
CCTTCAAGTT CTTTATTTTC TGGGTAACAG AAGTAGACAG ACAGGTTACT TGGTGATCT 900
50 TCTGTAAAG AGGATTGCAC GAGTGTGTTT TCCTCACACA CTTTGATTTG GAGAATTGGT 960
GCTAGTTGGC AATAGATAAC TCAGCGTAGA TAGTATTGCA AAAAGGGGAG GAAATACACA 1020
55 ACAATAATAA ATGTAAAAAC CTGCTATTCA ACATGCAGTT TTATTTGAG GCCAAAAATC 1080
TAGAGCTTTC CCAAGATCCT GTTGCCTTAG GCACATNCAC ACTTCAACAG TGCACACTAT 1140
CCAACAGTGC ACACTATTCA ACAGTGCACA CTATTCAAAA GCGTAGACTA TTTTTTTGCA 1200
60

389

TGTCAAGAT ATTTGTTTTG GTCTTATGTG TGTGTGAGAG AGAGAGATTG CTTTGACATT 1260
 AAGGAGCATC AATGAGAAAA GATGATGAGG CAGGAATTAA TAAAGAAATG AAGTCGTGTG 1320
 5 TGTGTGGTGT CCTGTCAGAG GGCACACAAT TTCATAAACA CCATGCCTGG ACAATTGTAT 1380
 ATTAATATTT AACACCTCTG CATCTTTTTC TTAAAAAAGA ATATGGGCCA GATACAGTGG 1440
 CTCACATTGT TAATCCCAGC ACTTTGGGGA GCCAAGTTAG CAGAATCCCT TGAGCACAGG 1500
 10 AATCTGAAAC CAGCTTGGGC AACATAGTGA GATCCCATCT NTACAAAAAA CTTAAAAATT 1560
 AGCCAGGCAT GATGGCACAT TCCTGTAGTC CTAGCTACTC AGGAGGCTAA GGTAGGAGGA 1620
 15 TTGCCTGAGC CCAGGAGTTC AAGGCTGCAG TGAGCTAAGN ACGTGCCAGT ACACTCCAGC 1680
 CTGAGCCACA AAGTGAGACC CTGTCTCGCA AAAAAAAN TTAAAAAGTC GGGGGGGGGC 1740
 CCGGTACCCA AATCGCCGGA TATGATCGTA AACAATC 1777
 20

(2) INFORMATION FOR SEQ ID NO: 139:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 643 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

TTTTTTTTTT TTTTITTTTT TTTTTTTTTT TTTTITTTGGG AATGAGAAAA TAACTTTATT 60
 35 TTCAATGTGTGG GGAGCGGGCC GATGTCCAGC CTCAGAACTT CTGGAACTGC TTCTTGGTGC 120
 CGGCAGCCTT GGTGACCTTG AGCACGTGA AGCGCACTGT CTTGCTCAGA GGCCGGCACT 180
 40 CGCCCACTGT GACGATGTCA CCGATCTGGA CGTCCCTGAA GCAGGGGGAC AGGTGTACAG 240
 ACATGTCTTT GTGGCGCTTC TCGAAGCGGT TGTACTTGGC GATGTAGTGC AGATAGTCTC 300
 GGCGGATGAC AATGGTCCCTC TGCATCTTCA TCTTGGGTCA CCACGCCAGA GAGGATCCGC 360
 45 CCTCGAATGG ACACATTACC AGTGAAGGGG CATTTCTTGT CAATGTAGGT GCCCCTCAAT 420
 AGCCTCCTTG GGGTGTCTTT GAAGCCGAGA CCGATGTTCT TGTTAGTAAC CCGCGGGAGC 480
 50 TTCTCCTTGC CAGTTTCTCC CAGCAGGACC CTCTTCTTGT TTTGAAAGAT GGTCCGCTGC 540
 TTTTGGTAGG CACGCTCAGT CTGAATGTCC GCCATCTTCT CGTGCCGMAY TCCTGCAGCC 600
 CGGGGGATCC ACTAGTTCTA GAGCGGCCGC ACCGCGGTGG AGC 643
 55

(2) INFORMATION FOR SEQ ID NO: 140:

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1220 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

GGCACGAGGA TGATAGACCT ACTGGAGGAA TACATGGTTT ACAGGAAGCA TACCTACATR 60
 10 AGGCTTGATG GCTCATCCAA GATCTCGGAG AGGCGAGACA TGGTTGCTGA TTTTCAGAAC 120
 AGGAATGACA TCTTTGTGTT CCTGTTAAGC ACACGAGCTG GAGGACTGGG TATCAATCTC 180
 15 ACTGCTGMAG ACACAGTGCA TTTTCTATGA TAGCGACTGG AACCCCACTG TGGACCAGCA 240
 GGCCATGGAC AGGGCCCACC GCTTAGGGCA GACAAAGCAG GTTACTGTGT ACCGGCTCAT 300
 CTGTAAAGGC ACCATTGAAG AACGATTCTT GCAAAGAGCC AAGGAGAAGA GTGAGATTCA 360
 20 GCGGATGGTG ATTTCAGGTG GGAACCTCAA ACCAGATACC TTGAAACCCA AAGAGGTGGT 420
 TAGTCTTCTT CTAGACGACG AAGAGTTGGA GAAGAAACGT ATGTACTCTA AACCTCTATA 480
 25 CACTCCCCCTC ACGTATCTGA GAATGGAAGA GGTACTTGGG TGTGTGCCAA GGGTTAGGCA 540
 AAGCCAGAGG CTGTATTTAG GGAAAGTATT TTTGTGCTCA TATTTTATAT AAAAACCCAA 600
 ACAAGAATGT GTTTGTAGGC CAGGCGTGGT GGCTCGCGCC TCTAGTCTCA GCATTTGCGG 660
 30 ARGCCAAAGT GGGCAGATCA CCTGARGTCA GGARTTTGAG TTTGARACCA GCCTGGCCMA 720
 CGTTGTGAAA CCCACCTCT ACTARGARTA CSGAAAATTG GTTGGGCATG GTGGCGGGCA 780
 35 CCTGTAATTC CAGCACTTTG GGAGGCTGGG GCAGAANAAT TGCTTGAGCC CAGGAGGTGG 840
 AGATTGCGGT GAGCCGAGAT YGTQCCATTG CAMTCCAGCC SGGGCAATAA GAGTGAAAYT 900
 CCATCTTTTA AAAACAAACA AAAACAAAAA ACACAAGACG GCTCACACCT GTAATCCCAG 960
 40 CACTTTGGGA RGCCGARGCA GGTGGATCAC GARGTCAGGA GTTCCAAGAC TAGCCTGGCC 1020
 AACCTGGTGA AGCCCCGTCT CTAATAAAAA TACMAATATT AGTCGGGCGT GGTGGTGGGC 1080
 45 ACGTGTAATC CCAGCTACTC GGGAGGCTGA GGCAGGAGAA TCCCTTGAAG CTAGGAGGCA 1140
 GAGGTTGCAG TGAGCCAGGA TCGTGCCATT GCACTCCAGC CTGGACAACA AGAGCAAGAT 1200
 TCCATCTCAA AAAAAAAAAA 1220
 50

55

(2) INFORMATION FOR SEQ ID NO: 141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 721 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

5 AATTCGGCAC GAGCCAGGTT AGCCGGAAGG GCAGCTCTCC AGGCCCTGCC CACCCACAG 60
 GGGGCTCCTT ATGCACAGCG GGGCGTCTCC TTGTGGCCAT AGAAACGGAA CTGGCTCTTT 120
 TCAACAGTGC TGCAAGAGGA TGGTTATTTA ACGCTGGCCC CCAAGGAGGA AAGGCACAGA 180
 10 CYTTCCTCCC TCCTGGAACA TCCAAGGGCA CTGGATCCTC TGTGTCCCTC TGAGATGGGG 240
 TGCCACTCCA GCAAGAGCAC CACGGTGGCA GCTGAGTCCC AGAAGCTTGA AGAAGAGYGC 300
 GAGGGAAGAG AGCCAGGTCT GGAGACCGGC ACCCAGGCAG CAGACTGCAA GGATGCCCCG 360
 15 CTGAAGGATG GAACCCCTGA GCCAAAGAGC TGAAATGCCT CTCTCCAGAG TCGGACCCTC 420
 ACCTCYTTCC TGGAAGTGGC TTTGGCCCCA GAACCATGAG ACAATCCCCA CCCTGAGAAG 480
 20 CTCCGATCAC TGGGAGGAGA GAGAAAGCCT CCAGCTTTGG GATTCAGGCT TCAGAAGTTT 540
 TTAGCAGCCT TTGCTCATTT GAGAGGTGGG GAAAGGATAA AGTTCCTATA AGGAAATCCC 600
 TAATTTCCCC CAGCTCTCC CCNCCNGAAG AAGGAACNAA AGAAAGTTCC TTCCACACGT 660
 25 TTTGTTGGAA ACTTTTCCCT TGCCAACTTT CCTTGGATTG CCAGAACAAA GCCCTCCAGA 720
 A 721
 30

(2) INFORMATION FOR SEQ ID NO: 142:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1468 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

ATGAATTAAT GTTTATAAAT GACTGTACTG AATTTAAAAC CGTACAGTTT CATTTGCATT 60
 45 TTGACATTAC TTTATTATAC ATTTTGCATT TAAAAGGCTG CACCAGTTGG CTTTCTTCT 120
 GTTTTATTCT CAAAATATAG AGATTCTGTG ATTTATTTGC CCTGTTATG GATTAAAAAG 180
 AAAATCTTAA TATAAGCAT TTCAATAGGA TGCATAGGTA TATTACGTTT TTAAATGCT 240
 50 TTAGATCTGT GATCTTGAC TTACTATTTA TTTTATCCCC TTAAAGTCAG GGATGCTTTA 300
 TTCTATTTTA AAGCACTTAT GAGTTACATG TTGTAATCAA GTTTGCACAA TATATTTATC 360
 55 TATATGAGGA ACCCATAAAT GAATAGCTAA TTTTAAAAAT GCCATTAAAA TGCATGAAAT 420
 KCTTATTAAT ACCTTACTAT ACTATTTCTT CAAGGCAAGT AAATTGACCA TGRGAAAGR 480
 ACACAGTTAT TAAACACTGT TGACAGGAAA ATTCTCCTTG ATAACATAGG ACAATTAATG 540
 60

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GAAAAAAAAA TTCTCATTAT TTGCAAAGAA TGAACAAGTT AATGAACAAA CAAACTAGAT 600
 TTGGTATGTT TTCAGCTTTT GTATCATGTT TAATTGTTTA ATTTGGTTGA AAAACTGCAG 660
 5 TTGAGAAATC AGATAGCAAT ATAGACATTC ACAGCAGCTC TGTGGATACC ATGTAATTGT 720
 CAGGTAATTT CAGAATGTTG AAAATTATTC AGTGCAGCCC TCATAGTATC ATACTTGAAG 780
 AAATTGATTA CAGTTCCACT AAATTGTTGA AGATAAATTA TTTTAAAGG TTATGAAAAC 840
 10 TAAGTTATAT TAATTCATAT GTTTGATTTT TAAATCCAC CTCCTCAAGC TATCCAATTT 900
 NCTGACTTTG AAAATAACCA TGAGAGATGC CACATTTCTC TCTGGGAAAC TACCACTCAA 960
 15 AGAATAATTG TTAATAATTA AGCTTTTAGG TATTAGAAGC TGTATATAAG TATAAATTA 1020
 AGATATAAGC AGATCACATG TAAATCATTC CTAAAGCACA AGAAAAGAAT GTGCCTTGAT 1080
 GTACATATAT TACTAAGTTG CCTCTCCCAG TTTACTTTAA AAATGGCTTT AAGGATAAAG 1140
 20 AATAAATGTG ATAGCTGTGC ATGCATTATA TATTTGCATT TGCAAAATTC CCATTGTTTT 1200
 AACAGCTGTG TGGCTGACTT TCAATTTTAA GACGTGAATT GACATACAGC CCATAACTTT 1260
 25 ATAATGGCTG CTCATTATC TTATCTTTCA GTTAGTGGAA AAACATTTCA ACCTGACTAA 1320
 AATTTGGAAT TGTGCTTTTT ATGTTCCATC CTCTGTGTT ACTAGATTTA GTTAAAAAT 1380
 TGTGTATGAC CATTAATGTA TGTCAATAAC ATGTAAATAA AAGATGTTGA ATCTTGTTGA 1440
 30 AAAGCAWRAA AAAAAAAAAA AAACCTGA 1468

35

(2) INFORMATION FOR SEQ ID NO: 143:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 300 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

45

TGAATTTTTT GCCAACTTA GTAAGTCTGT TAAATATTTG GAGGATTTAA AGAACATCCC 60
 AGTTTGAATT CATTTCAAAC TTTTAAATTT TTTTGTACT ATGTTTGGTT TTATTTTCCT 120
 50 TCTGTAATC TTTGTATTC RCTTATGCTC TCGTACATTG AGTACTTTTA TTCCAAACT 180
 AGTGGGTTTT CTCTACTGGA AATTTTCAAT AAACCTGTCA TTATTGCTTA CTTTGATTAA 240
 AAAAAAAAAA AAAAAAAAAA AAACCCNAG GGGGGGCGG GTNCCCAAT CCCCCCAAA 300
 55

60

(2) INFORMATION FOR SEQ ID NO: 144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2243 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

10 TGCTCCCTT CCTGCAGATT GTGGACAGTA GTTCTCAGC CTGCACCTG GATTCTTCT 60
 TCCCTTCCT AGCTCCATGG GACTCGCCCC AAGACTGTGG CTCAAGGAC CACCAGCCCC 120
 TTACTCTCA AGCCTGACT GTGGAGTGG TAGATGCCTC TGATCCTCAG TATTCTCTCT 180
 15 GGCAATGTT CACGGCTTCT CCTTCTGGG AGCTGGCTCC ATAACTTGAT TTTCCCCAAA 240
 CGTGTGCAA TCCCTGCTGC CCCTTAGCCA CCCAGGTCT TGTGTGGGTA TGAGTGTAGA 300
 GGATGGGGT ATGCCAGGCC TGGGCCGTCC CAGGCAGGCC CGCTGGACCC TGATGCTACT 360
 20 CCTATCCACT GCCATGTACG GTGCCCATGC CCCATTGCTG GCACTGTGCC ATGTGGACGG 420
 CCGAGTGCC TTYCGGCCCT CTCAGCCGT GCTGCTGACT GAGCTGACCA AGCTACTGTT 480
 25 ATGCGCCTT TCCCTTCTGG TAGGCTGGCA AGCATGGCCC CAGGGGCCCC CACCTGGCG 540
 CCAGGCTGCT CCCTTCGCAC TATCAGCCCT GCTCTATGGC GCTAACAACA ACCTGGTGAT 600
 CTATCTTCAG CGTTACATGG ACCCCAGCAC CTACCAGGTG CTGAGTAATC TCAAGATTGG 660
 30 AAGCACAGCT GTGCTCTACT GCCTCTGCCT CCGGCACCGC CTCTCTGTGC GTCAGGGGTT 720
 AGCGTGCTG CTGCTGATGG CTGCGGAGC CTGCTATGCA GCAGGGGGCC TTCAAGTTCC 780
 35 CGGGAACACC CTTCCAGTC CCCTCCAGC AGCTGCTGCC AGCCCCATGC CCCTGCATAT 840
 CACTCCGCTA GGCCTGCTGC TCCTCATTCT GTA CTGCTC ATCTCAGGCT TGTCGTCAGT 900
 GTACACAGAG CTGCTCATGA AGCGACAGNG GCTGCCCTG GCACTTCAGA ACCTCTTCTT 960
 40 CTACACTTTT GGTGTGCTTC TGAATCTAGG TCTGCATGCT GCGGCGGCT CTGGCCAGG 1020
 SCTCTGGAA GGTTCCTCAG GATGGGCAGC ACTCGTGGTG CTGAGCCAGG CACTAAATGG 1080
 45 ACTGCTCATG TCTGCTGTCA TGAAGCATGG CAGCAGCATC ACACGCCTCT TTGTGGTGTC 1140
 CTGCTCGCTG GTGGTCAACG CCGTGCTCTC AGCAGTCTG CTACGGCTGC AGCTCACAGC 1200
 CGCCTTCTTC CTGGCCACAT TGCTCATTGG COTGGCCATG CGCCTGTACT ATGGCAGCCG 1260
 50 CTAGTCCCTG ACAACTTCCA CCCTGATTCC GGACCTGTA GATTGGGCGC CACCACCAGA 1320
 TCCCCCTCCC AGGCCTTCCT CCCTCTCCA TCAGCAGCCC TGTAACAAGT GCCTTGTGAG 1380
 55 AAAAGCTGGA GAAGTGAGG CAGCCAGGTT ATTCTCTGGA GGTGGTGGTA TGAAGGGGTA 1440
 CCCCTAGGAG ATGTGAAGTG TGGGTTGGT TAAGGAAATG CTTACCATCC CCCACCCCA 1500
 60 ACCAAGTCTT TCCAGACTAA AGAATTAAGG TAACATCAAT ACCTAGGCCT GAGAAATAAC 1560

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CCCATCCTTG TTGGGCAGCT CCTGCTTTG TCCTGCATGA ACAGAGTTGA TGAAAGTGGG 1620
 GTGTGGGCAA CAAGTGGCTT TCCTTGCTTA CTTTAGTCAC CCAGCAGAGC CACTGGAGCT 1680
 5 GGCTAGTCCA GCCCAGCCAT GGTGCATGAC TCTTCCATAA GGGATCCTCA CCCTTCCACT 1740
 TTCATGCAAG AAGGCCCAGT TGCCACAGAT TATACAACCA TTACCCAAAC CACTCTGACA 1800
 GTCTCCTCCA GTTCCAGCAA TGCCTAGAGA CATGCTCCCT GCCCTCTCCA CAGTGCTGCT 1860
 10 CCCCACACCT AGCCTTTGTT CTGGAAACCC CAGAGAGGGC TGGGCTTGAC TCATCTCAGG 1920
 GAATGTAGCC CCTGGGCCCT GGCTTAAGCC GACACTCCTG ACCTCTCTGT TCACCCCTGAG 1980
 15 GGCTGTCTTG AAGCCCGCTA CCCACTCTGA GGCTCCTAGG AGGTACCATG CTTCCCACTC 2040
 TGGGGCCTGC CCTGCTTAG CAGTCTCCA GCTCCCAACA GCCTGGGGAA GCTCTGCACA 2100
 GAGTGACCTG AGACCAGGTA CAGGAAACCT GTAGCTCAAT CAGTGTCTCT WTAAGTCAT 2160
 20 AAGCAATAAG ATCTTAATAA AGTCTTCTAG GCTGTAGGGT GGTTCCTACA ACCACAGCCA 2220
 AAAAAAAAAA AAAAAAACTC GAG 2243

25

(2) INFORMATION FOR SEQ ID NO: 145:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1082 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

GCCAAGCTCT AATACGACTC ACTATAGGGA AAGCTGGTAC GCCTGCAGKT ACCGGTTCGG 60
 40 GGAATTCCTG GGTGACCCA CCGTCCGCT TCCGTGTGTC AAAATCCTCA CCTCCTTCAT 120
 AACCATCTCC CACAATTAAT TCTTGACTAT ATAAATTTAT GGTTCGATAA TATTATCAAT 180
 TTGTAATCAA TTGAGATTTC TTTAGTGCTT GCTTTTCTGT GACTCAACTG CCCAGACACC 240
 45 TCATTGTACT TGAAAACCTG AACANCTTGG GAATGCCATG GGGTTTGATA ATCTGCCAGG 300
 GACATGAAGA GGCTCAGCTT CCTGGGACCA TGACTTTGGC TCAGCTGATC CTGNACATGG 360
 50 GAGAACAACC ACATTTTCTT TTGTGTGTGC TTCTAGCAGC TGTTCGGGAG GACCKTGACC 420
 CAAYAGTGTT CCCATGCTGT TTCTTGTGAA ATGCTCTCGG CTATGTAGCA GCTTTTGATT 480
 CCCTGCATAC CCTAGGCTGC TGCCCTATC CTGTCCCTTG TTTATAACAT TGAGAGGTTT 540
 55 TCTAGGGCAC ATACTGAGTG AGAGCAGTGT TGAGAAGTCG GGGAAAATGG TGACTACTTT 600
 TAGAGCAAGG CTGGGCATCA GCACCTGTCC AGCTCTACTT GTGTGATGTT TCAGGAACTC 660
 60 AGCCCTTTT TCTGCCTAGG ATAAGGAGCT GAAAGATTAA CTTGGATCTY CTAATGGTCC 720

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AAATCTTTTG GTCACAATAA AGAGTCTCCA AATTAGAGAC TGCATGTTAG TTCTGGATGG 780
 ATTTGGTGGC CTGACATGAT ACCCTGCCAG CTGTGAGGGG ACCCGTTTTT TAAGATGCAT 840
 5 GGCCAAGCTC TCTGCAAATG GAAATGCTTA CACTGGGTGT TGGGGATGTT TGCTACCTCC 900
 TGCTATTTTT GTGGTTTTGG TTCTCCCACT ATGGTAGGAC CCCTGGCCAG CATGTGGGCT 960
 10 TGTCATGTCA GCCCCATTGA CTACCTTCTC ATGCTCTGAG GTACTACTGC CTCTGCAGCA 1020
 CAAATTCTTA TTTCTGTCAA TAAAAGGAGA TGAAATATAA AAANAAAAAA AAAAAACTCG 1080
 NG 1082
 15

(2) INFORMATION FOR SEQ ID NO: 146:
 20

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4313 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

CAAGCTGGTT TGAAACTAGG GGTGGGCTC GGCCGTCGTC GTTGTTTGTC GCCGCATCCC 50
 30 CGCTTCCGGG TTAGCCCGTT CCTGCCCCCC CCTCCTCTC CTCCCTTCGG ACCCATAGAT 120
 CTCAGGCTCG GCTCCCCGCC CGCCGCAGCC CACTGTTGAC CCGGCCCGTA CTGCGGCCCC 180
 35 GTGGCCACCA TGTCCCTGCA CGGCAAACGG AAGGAGATCT ACAAGTATGA AGCGCCCTGG 240
 ACAGTCTACG CGATGAAC TGAGTGTGCG CCCGATAAGC GCTTTCGCTT GGCGCTGGGC 300
 AGCTTCGTGG AGGAGTACAA CAACAAGGTT CAGCTTGTG GTTTAGATGA GGAGAGTTCA 360
 40 GAGTTTATTT GCAGAAACAC CTTTGACCAC CCATACCCCA CCACAAAGCT CATGTGGATC 420
 CCTGACACAA AAGGCGTCTA TCCAGACCTA CTGGCAACAA GCGGTGACTA TCTCCGTGTG 480
 45 TGGAGGGTGG GTGAAACAGA GACCAGGCTG GAGTGTGTC TAAACAATAA TAAGAACTCT 540
 GATTCTGTG CTCCCTGAC CTCCTTTGAC TGGAAATGAGG TGGATCCTTA TCTTTTAGGT 600
 ACCTCAAGCA TTGATACGAC ATGCACCATC TGGGGGCTGG AGACAGGGCA GGTGTTAGGG 660
 50 CGAGTGAATC TCGTGTCTGG CCACGTGAAG ACCCAGCTGA TCGCCCATGA CAAAGAGGTC 720
 TATGATATTG CATTTAGCCG GGCCGGGGGT GGCAGGGACA TGTTCCTC TGTTGGTGCT 780
 55 GATGGCTCGG TGCGGATGTT TGACCTCCGC CATCTAGAAC ACAGCACCAT CATTTACGAA 840
 GACCCACAGC ATCACCCT GCTTCGCCTC TGCTGGAACA AGCAGGACCC TAACTACCTG 900
 GCCACCATGG CCATGGATGG AATGGAGGTG GTGATTCTAG ATGTCCGGGT TCCTGCACAC 960
 60

	CTGTSGCCAG GTTAAACAAC CATCGAGCAT GTGTCAATGG CATTGCTTGG GCCCCACATT	1020
	CATCCTGCCA CATCTGCACT GCAGCGGATG ACCACCAGGC TCTCATCTGG GACATCCAGC	1080
5	AAATGCCCGG AGCCATTGAG GACCCTATCC TGGCCTACAC AGCTGNAAGG WGAGATCAAC	1140
	AATGTGCAGT GGGCATCAAC TCAGCCCGAA YTGTGCGCAT CTGCTACAAC AACTGCCTGG	1200
	AGATACTCAG AGTGTAGTGT TGGTGGCGCT GTGCCCACGA GGCAGGGGCT TTTGTATTTT	1260
10	CTGCCCTCTGC CCCACCCCCA AAGTAAGAAG AACATGTTT CCAGTGGCCA GTATGTCTTT	1320
	CATTGCTTTG CACCCACTGT TACCAGAAGC TGCTCTAGGA GTTCTGGCC AGTCACCCCA	1380
15	TCGCCCTCTG TGGCAGACTC AGTGCTGTGT GCGCCTCCT CAGCCCAGG CTGAGTTTAA	1440
	AGATTTTCTC TCCTTTCTCT TTCTCTTTG GTTCTCAAT TAAAAAATGT GTGTATATTT	1500
	GTTTGTCAAG CGTTGTGTG AGGAGCAGTT CACGCACTGG CTGTGTCTAT TCCTCTGCCC	1560
20	AGGTGTCTCT GTTTGCTGCC CAAKGWKKT TTTTCATGTCT CGTCCATGTC CATGTTCTGT	1620
	TTAGCACTWA CGTGGGAACA AATACCAATT TGTCTTTTCT CCTAGTATCA GTGTGTTTAA	1680
25	CAAAATTTAA CTTTGTATAT TTGTTATCTA TCAGGCTAAT TTTTATGA AAAGAATTTT	1740
	ACTCTCTGC TTCATTTCTT TGTCTTATAG TCCTCCCTCT TTGCACCTTC TTCTCTTCCC	1800
	TCAGTGCCCTG GAGCTGGTAC TGGGCCCTG GCCCATGAG CAGTTTGCTT TCTTGAGTCA	1860
30	CTGCCCTGTGT AGTACATACC TGACCGGAG TCCAAACCAC CTGGTGCTC TGAAGTCCAC	1920
	TGACTCATCA CACCTTTCTT AGCCTGGCTC CTCTCAAGG CATTCCTGGC TTGTAAACAG	1980
35	ACATAGGAAG CCTCTGTTTA CCCTGAAGCA CCACTGTCCA GCCCATGGT TCCCACTGGC	2040
	AGCATGGTAG AGCTGAGAGA AACAGGCTCT CAGGGTACCT GACTTGAGGG GAATCGTTTC	2100
	ATGAAGCTGA ACTTCAAGCA TATTTCCAGT ACATTCTTTC AGAGTCTGTT TTTCCATCCA	2160
40	AATATAAGCC CCAGGCCATT CCACTTAGTG TCTTTTCAAT GATAGGCAAG AATGATATCT	2220
	GAGTTGAACT TCGGTGCTTC TGTGTTTGA GTTTACTGTG CCTGGTGGTA TATTGGGCAT	2280
45	TCTTTGGATT GAGTGTCTG AGGTGAGAGA GTCTTCCGA GGCATCCTGT CTGTGCTTCC	2340
	AACCTGAAC AAGACCTTAC ATGAGAGATG GACTGATGGA CTGCGGCAAT CCTGGGCTGT	2400
	CAAGTGGATA GATAGTTAAA AAGCATTATA CTGTGGGTAA TGAAAAGGA GGAAGAAAAA	2460
50	AGAAGGAAAA GGAATTATAG ACCCCAGGG TCAGCCAGTT AAGAGCTCTA CCCACACCTG	2520
	TCAACCCCTC TCTCCCCAG TTTAGTTCT GAGCAGTATT GGAATTGTAG CCTGCAGTTG	2580
55	TCTTTTGAAT TGCAGGCCG AGTGCTTTT TGTATGTGA ATGAGTTCCA TGGAGGGGCA	2640
	TATGTGTGAT TCCACCGTTA GATGAGCCCT TGGGGCAGG AGTTTGGGAT GTGCTCTTGG	2700
60	GGGAAAGTTG GCTGTTTCTT TCGCTCTGC TCCTACCCGA AGTTTAAAG TCCCTCTGAA	2760

	TTGCTCATCT GAGATTAGTA GAGTAGCAGG CCTGAAGGAT GATGGTTTGG TCCTCTTTGG	2820
	TTCTCACCTG CTTGAGAAGT AAAACAGTAA CTTTGTCTCT CTGGGCCCTT AAGCTTTTTT	2880
5	GGTTAAGTCT TCCTTTTCAG AAGTAGATGT CATTATATGC CAAAAGTCTA GCTCTTTGCT	2940
	TTACCATACA GGGACCTGTC CCAAAGAAAA AGGCTCTTTT TTTAGCCAGC ATATTTCCCC	3000
	TTCTACCTT TTACTTTGTT GTTCTGATTT TAGGACTCTG GCTGGCCATG TGCTTGTTGGT	3060
10	TGCCTCTCCT GCATTTGCCA CTGGATTTGC ACTGCATCGT TTGGAGATAC AAAGCGAGCA	3120
	GTTCTTGTC AGAACCTCC TCTGCTTTTC ATTGTGTTTG ATAATGGTTA CTGGGTCCTT	3180
15	CTCTCAAGGG TAGCAAGGCC AAGCTGATGG CTGCTTGTTT AGGAGGCCAT CAGTTCCTTC	3240
	CTGTGAGAA GGGTCTGAAA TGGAAGTCAG TGGTAGAAGG GGCTGGTCTG CTGGGCAGGG	3300
	CTTACATCCA CTGAGTTCTA AGATTCCTTT CCTGATCTGC ACCTACGCCT GGTCTGTATG	3360
20	GTGGAATTTG TCAGCTGGAA CTCAGAAACA ACAACTTGAA AAAAAATAA TAATTAGAAC	3420
	ATATTGTCAT AAGATAGCTA TTTACTCTGG AAACCAACAA CTTTGTAGAT TTCCCTTGCC	3480
25	CTGTGGACGC CCAGCTCCTG TCATCCTTCC TTAGGTCCTG CAGTACAGTC TTCCCTGAA	3540
	TGCCACCGGG GACCCAGGGG GACTCCACCC CCCTAAGCAA GCACACACAT ACTCACAGTT	3600
	GATGAGTTGC TGGTCTTGA GTCCACGTC TCTTACCCTC CCTTTACTCC ACCAGCCCGA	3660
30	CGACCCATGA CTGAGGAGGG GATTTCTACA GTCTCAGGAT TTAGAAAGTC TGTAAGCCAT	3720
	CCATGCTCCA GAAAGCACCG ATCTGTTGTA GTTGCAAAAA CAACTCTGTA ATTTGTTGAG	3780
35	GTCTCAAAC TGACAGCCAG CGAGACTGGG TGGGAGGCCC TGGATCTGTT CTCCCTGACT	3840
	GCGGGAGGAG CAGCCACTAG GACTTTAGCA GGAAGCCCAC ATGGAGGCTC CGCCAGGCTG	3900
	TGGCCCAGCT GGTGATGGCC CTTTGTCTCC TGGCAGCCTG AGGCACAGCT GCCTGTATTG	3960
40	TCCTCATCTG TTCTGACTGA AGGATGGAGG TGCTGAATAA ATTAGGCCTC AGGCNTCTAC	4020
	CACCAGAGAG CTGGAGAATG GGTCCACGTC ATTCAAGGAC CTGAATTTT TATGCTCAGG	4080
45	AGCATTGGAA TCCTCTCTCT CCAGGGAGGA ATTAGCCTGC AAGGTTAGGA CTTGAAGAGG	4140
	GAAGGTATTT AATAACTGGG CGAGGATGGG TGTGGTGGCT CACACCTGTA ATCCAGCAT	4200
	TTTGGGAGGC TGAGGTGGCC AGATCCCAAG GTCAGAAGAT CGAGACCATC CTGGCTAACA	4260
50	TGGTGAAACC CCATCTCTAC TAAAAATACA AAATTAAATT GGCCGGGCGT GAA	4313

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(2) INFORMATION FOR SEQ ID NO: 147:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1183 base pairs

(B) TYPE: nucleic acid

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398

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

5 GGCAGAGCCT CAAGCTGACT TGGATTATGT GGTCCCTCAA ATCTACCGAC ACATGCAGGA 60
GGAGTTCCGG GGCCGGTTAG AGAGGACCAA ATCTCAGGGT CCCCTGACTG TGGCTGCTTA 120
10 TCAKWYGGGG AGTGTCTACT CAGCTGCTAT GGTACAGCC CTCACCTGT TGGCCTTCCC 180
ACTTCTGCTG TTGCATGCGG AGCGCATCAG CCTTGTGTTT CTGCTTCTGT TTCTGCAGAG 240
CTTCCTTCTC CTACATCTGC TTGCTGCTGG GATACCCGTC ACCACCCCTG GTCCTTTTAC 300
15 TGTGCCATGG CAGGCAGTCT CGGCTTGGGC CCTCATGGCC ACACAGACCT TCTACTCCAC 360
AGGCCACCAG CCTGTCTTTC CAGCCATCCA TTGGCATGCA GCCTTCGTGG GATTCCAGA 420
20 GGGTCATGGC TCCTGTACTT GGCTGCCTGC TTTGCTAGTG GGAGCCAACA CCTTTGCCTC 480
CCACCTCCTC TTTGCAGTAG GTTGCCCACT GCTCCTGCTC TGGCCTTTCC TGTGTGAGAG 540
TCAAGGGCTG CGGAAGAGAC AGCAGCCCC AGGGAATGAA GCTGATGCCA GAGTCAGACC 600
25 CGAGGAGGAA GAGGAGCCAC TGATGGAGAT GCGGCTCCGG GATGCGCCTC AGCACTTCTA 660
TGCAGCACTG CTGCAGCTGG GCCTCAAGTA CCTCTTTATC CTTGGTATTC AGATTCTGGC 720
30 CTGTGCCTTG GCAGCTCCA TCCTTCGCAG GCATCTCATG GTCTGGAAAG TGTTTGCCCC 780
TAAGTTCATA TTTGAGGCTG TGGGCTTCAT TGTGAGCAGC GTGGGACTTC TCCTGGGCAT 840
AGCTTTGGTG ATGAGAGTGG ATGGTGTCTGT GAGCTCCTGG TTCAGGCAGC TATTTCTGGC 900
35 CCAGCAGAGG TAGCCTAGTC TGTGATTACT GGCACCTGGC TACAGAGAGT GCTGGAGAAC 960
AGGTAGCCT GGCCTGTACA GGTACTGGAT GATCTGCAAG ACAGGCTCAG CCATACTCTT 1020
40 ACTATCATGC AGCCAGGGGC CGCTGACATC TANGACTTCA TTATTWATR ATTCAGGACC 1080
ACAGTGGAGT ATGATCCCTA ACTCCTGATT TGGATGCATC TGAGGGACAA GGGGGKCGGT 1140
STCCGAAGTG GAATAAAATA GCGGGCGGTG GTGACTTGCA CCT 1183
45

(2) INFORMATION FOR SEQ ID NO: 148:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 734 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

60

GAATTCGGCA GAGTGAAGCA TTAGAATGAT TCCAACACTG CTCTTCTGCA CCATGAGACC 60

399

AACCCAGGGC AAGATCCCAT CCCATCACAT CAGCCTACCT CCCTCCTGGC TGCTGGCCAK 120
 GATGTCGCCA GCATTACCTT CCACTGCCTT TCTCCCTGGG AAGCAGCACA GCTGAGACTG 180
 5 GGCACCAGGC CACCTCTGTT GGGACCCACA GGAAAGAGTG TGGCAGCAAC TGCMTGGCTG 240
 ACCTTTCTAT CTTCTCTAGG CTCAGGTACT GCTCCTCCAT GCCCATGGYT GGGCCGTGGG 300
 GAGAAGAAGC TCTCATACGC CTTCCCACTC CCTCTGGTTT ATAGGACTTC ACTCCCTAGC 360
 10 CAACAGGAGA GGAGGCCTCC TGGGGTTTCC CCRGGCAGT AGGTCAAACG ACCTCATCAC 420
 AGTCTTCCTT CCTCTCAAG CGTTTCATGT TGAACACAGC TCTCTCCRCT CCCTTGTGAT 480
 15 TTCTGAGGGT CACCACTGCC ARCCTCAGGC AACATAGAGA GCCTCCTGTT CTTTCTATGC 540
 TTGGTCTGAC TGAGCCTAAA GTTGAGAAAA TGGGTGCCAA GGCCAGTGCC AGTGTCTTGG 600
 GGCCCCTTTG GCTCTCCCTC ACTCTCTGAG GCTCCAGCTG GTCCTGGGAC ATGCAGCCAG 660
 20 GACTGTGAGT CTGGGCASGT CCAAGGCCTG CACCTTCAAG AAGTGAATA AATGTGCCT 720
 TTGCTTCTAT TTAA 734

25

(2) INFORMATION FOR SEQ ID NO: 149:

30

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1405 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

GGCACAGTGG ACCCCAGACT CCCTCTCCGC CTTTCTCTGC CTGGGAGAC CCACTGTGTG 60
 40 CATGGCATCA CTGACTCCCA TACCTCTGGC TATCAAAGT TTCTGCCATG GCCACCTGG 120
 AAGSAAACCA GAGGGAGGTA GACAGGGAGA TCAGGTCCCT TCTACTCTGG TTCCTGCTCT 180
 GTGAAATTGT CTCAGGCTGG CTGTGTCCAG ARGGTCCCTG GTTCTCTCAR GGATGCCAAA 240
 45 TCTACAAGAA TCTCTCTCT TCCAGTTCCT ATAACTCTC CTTCTTTTG TCTCTTTAGA 300
 CCTTGGAGTA GTAGCAGCCA GGTCTTTTCT ATCTCTGGGT TAGTGCATTA TCTCTGGTGG 360
 50 CTCCTTACC CAGGACTTTG GGAATGGTCT TTTTGAATA CATCTCTCTC AAATAATTCA 420
 ATTTTGAGTG TTCTGTATGT ATCCTGCTGG GAGGTTGTTA TATACAAATC ACTGTGCCCCG 480
 TTTAGCAGAG AAGGAGACTG AAGCTCAGG AGGTTAAGTG TCTTCTCTA GTCGTATTG 540
 55 TGGAGAAAGT GGCTGACTGG GGAATTGAAT GAGGTCCCTA GTTTCATGCT CGGAGGGCAA 600
 AGANGAATGT CCAATTGCC TGAGATAAGC CTCTGGTAAA ATGTACTGTA CATAATAGGT 660
 60 AATCAATAAA TGTGGCTGA TGACAAACAT GTTTCTTTG TTCATTAGTT ATAGTGATTA 720

	TGTTCTAAAT AACTCCMACA AGGAARTCAG CACATTTGGA ATATCAWTAT CTTTCCATGA	780
	TAATATCTTT CCMYGGAAAG AWAATGATAT TCCMAACTGG GAGTGTCCCW ASCARATCTG	840
5	ANTCTGTGTA TTGGCCCTGG GGTGGGCCAG CCCCTTAGAC TCTATGGTCT CATCTCTTT	900
	GTTTACAAAA TTGAGATAAG GCCTTATTCT CTCCCCACCC CACCCATCCA TATTGTTTTG	960
10	AGAATAAAAT GAGAGGATGT GTGTCAAGGG TGTATTTTGG CAATAGTCTC TGAGCCATTT	1020
	TCTGAGCACC TCCATACTGT TGACACTCAA GTAATATTTC ATCAGCATTC CATTCAGGNT	1080
	CCTCCCTTAA TGAGGTGTGC GATGTACAAG AGTYGTGAGG TGGCAAAGGA TGGGCTCCTG	1140
15	AGGAAACACT TAGGAACTG GGCTTTCTGC CATTAAGA GACAAACCTT TGTGGTGACC	1200
	TAATTAAAGT TTTTAAATT CAATTTGGAA AGTTAGCAAG CTAGCTCCTK TCCAGGWAAA	1260
20	ATAAGGAGTC AGTGCATGAC CTAACCGGTC CCGGGCTGCT TGCCATTCCA AACAACTGCA	1320
	GTAAGTTTAT CACNTCTTT CAGGGACTGA GGTTCACAG CACAGACTTG GATAAGGAAG	1380
	GATGTCCTAT GGGGTCACAT TGATG	1405
25		

- (2) INFORMATION FOR SEQ ID NO: 150:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2890 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

	TTATATGCTA CAGCTACAGT AATTCTTCT CCAAGCACAG AGGANTTTT CCAGGATCAG	60
40	GGGGATCGCG CGTCACTTGA TGCTGCTGAC AGTGGTCGTG GGAGCTGGAC GTCATGCTCA	120
	AGTGGCTCCC ATGATAATAT ACAGACGATC CAGCACCAGA GAAGCTGGGA GACTCTTCCA	180
45	TTCGGGCATA CTCACTTTGA TTATTCAGGG GATCCTGCAG GTTTATGGGC ATCAAGCAGC	240
	CATATGGACC AAATTATGTT TTCTGATCAT AGCACAAAGT ATAACAGGCA AAATCAAAGT	300
	AGAGAGAGCC TTGAACAAGC CCAGTCCCGA GCAAGCTGGG CGTCTTCCAC AGGTTACTGG	360
50	GGAGAAGACT CAGAAGGTGA CACAGGCACA ATAAAGCGGA GGGGTGAAA GGATGTTTCC	420
	ATTGAAGCCG AAAGCAGTAG CCTAACGTCT GTGACTACGG AAGAAACCAA GCCTGTCCCC	480
55	ATGCCTGCCC ACATAGCTGT GGCATCAAGT ACTACAAAGG GGCTCATTCG ACGAAAGGAG	540
	GGCAGGTATC GAGAGCCCC GCCCACCCCT CCCGGCTACA TTGGAATTCC CATTAAGTAC	600
60	TTTCCAGAAG GGCACCTCCA TCCAGCCAGG AAACCGCCCG ACTACAACGT GGCCCTTCAG	660

	AGATCGCGGA TGGTCGCACG ATCCTCCGAC ACAGCTGGGC CTTCATCCGT ACAGCAGCCA	720
	CATGGGCATC CCACCAGCAG CAGGCCGTGT AACAAACCTC AGTGGCATAA AYCGAACGAG	780
5	TCTGACCCGC GCCTCGCCCC YTATCAGTCC CAAGGGTTTT CCACCGAGGA GGATGAAGAT	840
	GAACAAGTTT CTGCTGTTTG AGGCACAGAC TTTTCTGGAA GCAGAGCGAG CCACCTGAAA	900
10	GGAGAGCACA AGAAGACGTC CTGAGCATTG GAGCCTTGA ACTCACATTC TGAGGACGGT	960
	GGACCAGTTT GCCTCCTTCC CTGCCTTAAA AGCAGCATGG GGSTTCTTCT CCCCTTCTTC	1020
	CTTTCCCTT TGCATGTGAA ATACTGTGAA GAAATGCCC TGGCACTTTT CAGACTTTGT	1080
15	TGCTTGAAAT GCACAGTGCA GCAATCTTCG AGCTCCCACT GTTGCTGCCT GCCACATCAC	1140
	ACAGTATCAT TCCAAATTCC AAGATCATCA CAACAAGATG ATTCACTCTG GCTGCACTTC	1200
20	TCAATGCCTG GAAGGATTTT TTTAATCTT CCTTTTAGAT TTCAATCCAG TCCTAGCACT	1260
	TGATCTCATT GGGATAATGA GAAAAGCTAG CCATTGAACT ACTTGGGGCC TTTAACCAC	1320
	CAAGGAAGAC AAAGAAAAAC AATGAAATCC TTTGAGTACA GTGCTTGTC ACTTGTTTAC	1380
25	AATGTCTCC TTTTAAAAA AAAAAATGA GTTTAAAGAT TTTGTTTACA GAGTAAATAT	1440
	ATATCCATTT AATGATTACA GTATTATTTT AAACCTTAAG TAGGGTTGCC AGCCTGGTTT	1500
30	CTGAAAAACC AAATATGCCG GACAGGGTGT GGCCACACCA AGAAGACGGG AAGACCTGGC	1560
	TTGTGACCTT GGCTTCCCAT GTCTTCTTG TCTACCCGC GAAGTGCCCT ATCCTGGAAG	1620
	TATGAAATGT TAGCCAATTA ATACCAAGAC ACCTCATCTG CTCCTTCCCC AGTGGATGGG	1680
35	GTTCTTCTGT AAAACTGTTT GCACATGGCC AGGGGAGGGA ACTAGGACCC TTGTGTCCTG	1740
	TCTGAGCCTT ATGGAGGCAG GACGCTGTCA TTGGCGGATG TGTCTGCTC CATTGAGATG	1800
40	GATGGCAAAC CCCATTTTAA AGTTATATTT CTTTGATTTT TGTTAATTTA GAGGTGTAGG	1860
	TTTTGTTTTT TGTTTTTTGG TTTTTTTTTA AGAGAAACAT TTATAACTGG ATAGCATTGC	1920
	AGTGAAAGCA GCTTGGGATG TTGGAGCTAA TGCCAGCTGT TTATACTGCT CTTTCAAGAC	1980
45	AGCCTCCCTT TATGGAATTG GCATTAGGGA ATAAACAAGC CTTTAAACGT GATAAAAGAT	2040
	CAAAACCTG GTTAGACATG CCAGCCTTTG CAAGGCAGGT TAGTCACCAA AGACTAACCT	2100
50	CCAAGTGGCT TTATGGACGC TGCATATAGA GAAGGCCTAA GTGTAGCAAC CATCTGCTCA	2160
	CAGCTGCTAT TAACCCTATA ATGACTGAAA TGACCCCTCC ACTCTATTTT TGTGTTGTTT	2220
	TGCACAGACT CCGGAAAAGT GAAGGCTGCC AATCTGAGTA GACTCAAAT GTGAGGAACT	2280
55	GCTGGTCTTG GATTTTTTTT CCATTAAATT CAGCTGATCA TATTGATCAG TAGATAAACG	2340
	TAAATAGCTT CAAATTTTAA AAGTGGAATT GCAGTGTTTT TPCACTGTAT CAAACAATGT	2400
60	CAGTGCTTTA TTTAATAATT CTCTTCTGTA TCATGGCATT TGTCTACTTG CTTATTACAT	2460

TGTC AATTAT GCATTTGTAA TTTTACATGT AATATGCATT ATTTGCCAGT TTTATTATAT 2520
 AGGCTATGGA CCTCATGTGC ATATAGAAAG ACAGAAATCT AGCTCTACCA CAAGTTGCAC 2580
 5 AAATGTTATC TAAGCATTAA GTAATTGTAG AACATAGGAC TGCTAATCTC AGTTCGCTCT 2640
 GTGATGTCAA GTGCAGAATG TACAATTAAC TGGTGATTTC CTCATACTTT TGATACTACT 2700
 TGTACCTGTA TGTCTTTTAG AAAGACATTG GTGGAGTCTG TATCCCTTTT GTATTTTTAA 2760
 10 TACAATAATT GTACATATTG GTTATATTTT TGTGAAGAT GGTAGAAATG TACTATGTTT 2820
 ATGCTTCTAC ATCCAGTTTG TACAAGCTGG AAAATAAATA AATATAACAT AAAAAAAAAA 2880
 15 AAAAAAAAAA 2890

20 (2) INFORMATION FOR SEQ ID NO: 151:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2399 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

30 GAAC TTTTCC ATCTGGCAAA CCGGAACTC CATCCCCATT AAACCAACTC CCCCTTTTGG 60
 TTTCCCCCCC AGNGGAATAG AATTGGACN CCCATATAAA TCCAGGAAAC CACCTAAATT 120
 CTTTAGTNGT TTGTGTTTGC AAGATCTAAG GTCATGGTAA ACATTAAGTT CTTAAAATTT 180
 35 TTGGGAGGGA CCAGTGCACC TCTCCCTCTG AATTGTTTNC CAATTTAAAA TTGGAGTAAG 240
 GTTTTAAAT GTCTNATTCC AITGGAAGGG TMTGTTATTT CATTTTGAGC CCAGAGGGGA 300
 40 GAGGCACATT TTAAATATCA GAATTAGATT AGCTTTGAGT TTGTACAATT GGGAACATAA 360
 TAGATTTTCA TAAATATGT GTGCCTTGTG GGAAGTGTCA ACTGTCTTTA TGTCTGCTTG 420
 TAAAAGTTTC AAAATATGTT TTCCCTCAAA AAGGCAACGT TACTTCATTT GCTTGAATAT 480
 45 TATGATAGGA ATGCTTACTG ATATTACTTG ATAGTCATAT ATAGCCTAGG AAATTTAACA 540
 TATATATAAC TATAGCAGTA TTAATAATGA TAGTTGTACT TCTTTAAAAC ATTAAATTTG 600
 50 AGGAAACTTT AATGCTGTCT CGTGACATT GCTTTACTAC AGTGAGGGG AATATCCTTT 660
 AGATTGAGCC TCAATTTACT GGTAGTAGT ATGTGAACTC TGGTATAAAA ACGTAAACTA 720
 GACAGTAGAG CCGATGAATT AAAATTGTAA ATTGCTACAT TGGCATTTTC TACCTCCTTT 780
 55 TCTGTCAGAG TATTACTTTT TCCAGCATTT ATTCTTATTT GTGAGTAAAG AGGAAATGGG 840
 AACCTGAGGT TAAAATTGAC ATTTTGTGTT CATTGAGAAT TTAAGCAGTA GGTACAGGAG 900
 60 AAGTGACTTG TCACATTAAT TTGGTGCCTA AATCTGTAAC TACAAGTTGT GATCGACATG 960

	TACAAAATGT CTAAGAAAGG TCATATGCTG AATATTTTAC TTTTCCTGTA TAGTCTGCAT	1020
	GATTGTGTTTC ATAAACCCAG CTTATTTTCCT CCAAAAAGCA AAATGGTCCT GTAATTTTAA	1080
5	AAGTAAATA AACGTGCCAT TTTGTCTGCA ATCTATAATT TCAGGAAGTT ATTGRAAGTT	1140
	CTGACTCAGG GCTTTTTAAC AGTTCAAGCA ATTGTCAGTT ATATTTTGGA AACTCCATCT	1200
10	GTGTAATTCT CCAGTGCCTT GAAAGAATTA TTAACCTGGC AACACTATTA AAACCTTATA	1260
	AAAGATGGTC TTTAGTGCAC GTGTATCATT ATATACACGT TTTAAAGTCA TATTGCTTAG	1320
	CTTGTAATA ATGATTCTGC ATGTGTGCTG GGTTTGGGTA ATTCTTTAAA GGAAGTTTTC	1380
15	TAGATTTGCA CTTGATGTTT GTTTTTTAAA AACTGATTAT TTATGGCCGT GACACTGTTA	1440
	CCAGAAAAGT AATTCTAATT AAGTTATTAT GCAAAGTCAT CTATAAGTAG CATCTGGGAA	1500
20	GAGGAGATSG AGGCCACAGT TTGCTATTTT AGTATGAAAG GAGGATCTGT TTGGGAAACA	1560
	TAGATTGTCT TCCCCTCAAA TGAGGGGAAA AAAAAAGACC CTTTGTTCAA ATGGATTCTG	1620
	TTGTAAAAAA TTATTTTAA AGGAAATCAC AAATTGTATG TCATTCTTAA TGCTAGTCTT	1680
25	ATAGAATAAA TCCATAAAAT TGTTTTTATG TTCAGTATGT TTATGTCATT CTAAATGCAG	1740
	CAAAATCAAT GATAGCAGTT CAATTGACTC ATAGCAGTGT TTTGTATTTT TTCTAATTCT	1800
30	TTAGCTTTCA ATATTGGATT AAAGTCTTGT TTGTGAATAT AGTTTCCGTA TGGCAAATGA	1860
	TTTCTTGCTT ATTAGCTTTT GTTAAAGAAT GCTTAGTAAG AGCTAAGCTT TTAAAAGTAA	1920
	TGCAAACATT TATCGTTAAT AAAACCTATG GTGTAATATC ATATAATGCT TTTCTTTGAT	1980
35	CTTTGGAGAA TTATCTTTT ATAGTAGTAT ACATGAATTT TGATTTTAA AGCATTTAAA	2040
	AACAAATCTC AATACATTAA AAAACCTGTT ATTGTTAAAA RGGAAATTAC CATGCCTTTA	2100
40	AGAAACAAGG ATGTACATCT TCAATTCAGC ATRAGTGTCC ACATCTAGAA GGCTCTCATT	2160
	GCAGTTGTTT ACAGTTAAGG TACCTCTATC TAAAGGGCCA AAGAAGCATT TCATAYTTTA	2220
	ACACCTCACA TTCTTTCAGG ATTAAGACAT ATGAAAATAG TCTGAATAGG ATAAATTTGG	2280
45	ATAGGAAGTA ACTTAACCAG TCTGGGAAGA TTCAGGCTTT TTCTATKAAA AAGCTTATTC	2340
	CTCTTCACAA CTCNGGTGGT AGGNMTTCAT TTTTCAAGAG GGTAGATATT TTAAAGCCA	2399
50		

(2) INFORMATION FOR SEQ ID NO: 152:

- 55 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 802 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- 60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

	CGTGCCTGTA GTAAGCTCAT CCCTGCCTTT GAGATGGTGA TGCCTGCCAA GGACAATGTT	60
5	TACCACCTGG ACTGCTTTGC ATGTCAGCTT TGTAATCAGA GATTTGTGTG TGGAGACAAA	120
	TTTTTCCTAA AGAATAACWT GAYCCTTTGC CARACGACT ACGAGGAAGG TTTAATGAAA	180
	GAAGGTTATG CACCCCMGGT TCGCTGATCT ATCAACATCA CCCCATTAAG AATACAAAGC	240
10	ACTACATTCT TTTATCTTTT TTGCTCCACA TGTACATAAG AATTGACACA GGAACCTACT	300
	GAATAGCGTA GATATAGGAA GGCAGGATGG TTATATGGAA TAAAAGGCGG ACTGCATCTG	360
15	TATGTAGTGA AATTGCCCA GTTCAGAGT GAATGTTTAT TATTAAAGAA AAAAGTAATG	420
	TACATATGGC TGGATTTTTT TGCTTGCTAT TCGTTTTTGT GTCCTTGGC ATGAGATGTT	480
	TATTTGGAC TATTGTATAT AATGTATTGT AATATTTGAA GCACAAATGT AATACAGTTT	540
20	TATTGTGTTA CCATTTGTGT TCCATTTGCT YCTTTGTATT GTTGCAATTA GTACAATCAG	600
	TGTTTAAACT TACTGTATAT TTATGCTTTC TGTATTTACC AGCTATTTTA AATGAGCTGT	660
25	AACTTCTAG TAAAGAATTG AAAAGCAAAT CCTCACTAAA GGATACACAG GATAGGATAA	720
	AGCCAAGTCN CATCAACATT AAAAAATACT AAAANANAAA ACACAAAAAA AAAAAANCCC	780
30	GGGGGGGGCC CGGAACCCAT TC	802

(2) INFORMATION FOR SEQ ID NO: 153:

35

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: -461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

45	CTAGGAGCAC CGAGCAGCTT GGCTAAAAGT AAGGGTGTG TGCTGATGGC CCTGTGCGCA	60
	CTGACCCGCG CTCTGCNCTC TCTGAACCTG GCGCCCCGA CCGTCGCCGC CCCTGCCCCG	120
	AGTCTGTTC CCGCCGCCCA GATGATGAAC AATGGCCTCC TCCAACAGCC CTCTGCCTTG	180
50	ATGTTGCTCC CTGCGCGCCC AGTTCTTACT TCTGTGCCCC TTAATGCCAA CTTTGTGTCC	240
	TGGAAGAGTC GTACCAAGTA CACCATTACA CAGTGAAGA TGAGGAAGTC TGGGGGCCGA	300
	GACCACACAG GTGGGAACAA GGACAGGGGG ATTTAAGCAG TCAAAAGGAA AAACATGTTA	360
55	AGACCCTAGA CTGTATATT GACACACTTG TACCTTGTA GGCAGAGGAA TGTAATTAAA	420
	AAGCACTTAT TTGGCWNAAA AAAAAAAAAA AAAAAAAAAA C	461

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(2) INFORMATION FOR SEQ ID NO: 154:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2388 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

5 G C C C A C G C G T C C G A A G C G G A G A C G C T G G T G G C C T G T T G T G G A G T A C G C T T T G G A C T G 60

15 A G A A G C A T C G A G G C T A T A G G A C G C A G C T G T T G C C A T G A C G G C C A G G G G G C T G G T G G C T 120

A A C C G A G G C C G G C G C T C A A G T G G C C A T T G A G C T A A G C G G C C T G G A G G A G G C A G C A G G 180

20 G G T C G A A G T G A C C G G G G C A G T G G C C A G G A G A C T C G C T C T A C C C A G T C G G T T A C T T G G A C 240

A A G C A A G T G C C T G A T A C C A G C G T G C A A G A G A C A G A C C G G A T C C T G G T G G A G A A G C G C T G C 300

T G G G A C A T C G C C T T G G G T C C C C T C A A C A G A T T C C C A T G A A T C T C T T C A T C A T G T A C A T G 360

25 G C A G G C A A T A C T A T C T C C A T C T T C C C T A C T A T G A T G G T G T G T A T G A T G G C C T G G C G A C C C 420

A T T C A G G C A C T T A T G G C C A T T T C A G C C A C T T T C A A G A T G T T A G A A A G T T C A A G C C A G A A G 480

30 T T T C T T C A G G G T T G G T C T A T C T C A T T G G G A A C C T G A T G G G T T T G G C A T T G G C T G T T T A C 540

A A G T G C C A G T C C A T G G G A C T G T T A C C T A C A C A T G C A T C G C A T C G G A T T G G T T A G C C T T C A T T G A G 600

C C C C C T G A G A G A A T G G A G T T C A G T G G T G G A G G A C T G C T T T T G T G A A C A T G A G A A A G C A G C 660

35 G C C T G G T C C C T A T G T A T T T G G T C T T A T T T A C A T C C T T C T T T A A G C C C A G T G G C T C C T C A 720

G C A T A C T C T T A A A C T A A T C A C T T A T G T T A A A A G A A C C A A A A G A C T C T T T T C T C C A T G G T 780

40 G G G G T G A C A G G T C C T A G A A G G A C A A T G T G C A T A T T A C G A C A A C A C A A A G A A A C T A T A C C 840

A T A A C C C A A G G C T G A A A A T A T G T A G A A A A C T T A T T T T T G T T C C A G T A C A G A C A A A A 900

C A A C A C A A A A A A C A T A A C T A T G T A A A C A G A G A A T A A C T G C T G C T A A A T C A A G A A C T G 960

45 T T G C A G C A T C T C C T T T C A A T A A A T T A A A T G G T T G A G A C A A T G C A T A A A A A A A G T T G C A C 1020

A A G T T C C T T A T T T C C T T A A T A T T T C A C T T C T A T T T A A T A C A A G C T G G G A C A T A A A A A T T 1080

50 C T G T T G G G G A T A C C T G G G G A A G A T G T G A G A A A C T A A T G C T G A A T T C A G C T T A T A C A T G A 1140

T G A A A A G A A A A A C C A G A C A A A A G G A G C A C A T A A A T A T G C A T A C A G T G T A A C T G T A T T A T 1200

T T T A A T A C C C A C G A T A A G G G A T T T T T G T T A G C A T G T T T A G G G G A A C C A G A T T G G T G G G 1260

55 A T C C T T G G G G C C A C A G G A A T C T G A G G C A A C G G A A G A T A T A T A G A T G A T C G T C C C C C T G C 1320

C G A A G G A A C C T G G C A Y C T G T C A A G C A G A T G C T G C A G T T C A A A C T T C A G C T T T T A A G A T A G 1380

60 A T A G C T A T T G A A G G C A G A G G T C A G C A G G A G G A T G T G T A T T T C T A A T C T A C C C T G G T A A A 1440

	GTCATAGGTA AGACTCAAAA GCGGGATCTT ATTCAAAAGG CAGGTATTTT CTTTGTTTTC	1500
	TGTCTTGAAA TAGCCCCCTC CCCTAAGGTG CATTCTCTCA AGTTTTTCAGT ATTGCTTTAT	1560
5	TTGCAGTGAT TAAAAGAGAT GAGAGACTTT GGAGACAGAC AACGTAAGCA ACACATACAC	1620
	ACATGAAATA CTCTAGACAG AGATGAATAT AAATCTGGCC TAATAACCAG TTTTCCATGT	1680
	AACAGTGATT TTGTGTTTCG GGCTGAAGCA GTGGTTATAT TAAAAGCCAC TAATTCCTTT	1740
10	ATCCCTTTAA AAGATTTTTA CAATTCTCCA ACCACAAACA GCACTTCTAA AACTAACTTT	1800
	ACTTCTGCC CATAATTGT TCTACATGGA AAAAAAAAT ATTACTTTGG CCAGGGGTGT	1860
15	GTGTAAATGT GGCAGAATTC CTAGGCAGGC TGACCTTTAC AGTATGGGCC TTAAAGATAC	1920
	TGGATCCTGG TTGGGCAACA AGTGTCACGC CTGAAGTTTC TGAAAACAAA TTAGAAGACT	1980
	GTTGGCTTGG CTAATCTCGT AGTTCAGGGC CAAGTTTCTG TAGTCAGAAT GAAGAATAAA	2040
20	ATTGAAAGAA AAAGGGGAA ATGCTTATAC TTGCCATTAA GTTGAATGCC TCAAGTCITA	2100
	ACTATGGCTT TGTAGATGAG GCAAAAGATT TCTTAGTGGT AAAATTTCTT CAACAGGTCA	2160
25	ATGCCAATCT GTATGCCATT TTAGTAAAGT AGGTAAGGAG AGTAGCCGCT CAGTAACTTT	2220
	GGCACTAAAG AAAGAGTGTG GCTCTAGAAC TTCCAATCCC ATTGCTAGAT GTGCCCTTTA	2280
	AAAGATGGTC CAGTGCTTTC AGGGAAGGAT GTTTAGCCAG TTTTCCTAGT ATTTGTTCTC	2340
30	TAAGATTTTT TGACCTGTGC TTAATAAGAC GGACGCGTGG GTCGACCC	2388

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(2) INFORMATION FOR SEQ ID NO: 155:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 642 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

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	AAAACAGACC ATTTAAAAAC TCAGACAAGA TTATATTTAA TATATTAATT ACTAAAAAGG	60
	CACAAGATTA CACTGAACAT ATTAGCTACT AAAAAGGCAC TGCTAAGACA TTCAAGCAAA	120
50	TAGCTATTAC ACACTACTGC AGATTTTACA GGTTTCTAAT TCTAACATAT GTTTGAAAAA	180
	TCCGTGAGTA TTCCAAAATA TATTTAATAA TGGAATATCT GCATTAATAT ACCATCCATG	240
	TGTTTTTACC ATTTGCCTTA ATATTGAATA TACTGTTTAC CTCACACTAA AAAGAAAACC	300
55	AGAAGCCTTA TTTGTGATTT TGGGAGTGGA AGCTTCCATT TTTGTGTCAA AAATGAATCC	360
	TGATTCTTAT GGAAATCTCT GTTATTAAGA TATTTCAAGA TGAGACAACA CTGAAGATCA	420
60	AATTGTGTTT AGTATCACTA TCTTCTCTCC TCGTTTCTCT CTACTCCTC ATCCTCCCAG	480

5 AATCTACCAG TTTATGGTAG AAAGATGGGA ACCTTATTG AATGTGTTTT TTTTTTCCA 540
TGATGTCCAA TTTGTGTG GGAAGGATT TGGATAAAAT TTTGTTTAA ATTTGGTAG 600
ATTTTATCT ATACAAATT AAATAAAATT ATGTTTGTA AG 642

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(2) INFORMATION FOR SEQ ID NO: 156:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

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GCCGCTGCCC CTCCACGGAG TTGCTGATCA TCTGGGCTGT GATCCACAAA CCCGGTCTTT 60
TGTCCTCCT AATATCAAAC AGTGATGTC CTGCTGCAG AGGGGAAACT GCACGTTTAA 120
AGAGAAAATA TCACGGGCCG CTTCCACAA TGCAGTGTCT GTAGTCATCT ACAATAATAA 180
ATCCAAAGAG GAGCCAGTTA CCATGACTCA TCCAGGCACT GAGCATATTA TTGCTGTCAT 240
GATAACAGAA TTGAGGGGTA AGGATATTTT GAGTTATCTG GAGAAAAACA TCTCTGTACA 300
AATGACAATA GCTGTGGAA CTCGAATGCC ACCGAAGAAC TTCAGCCGTG GCTCTCTAGT 360
CTTCGTGTCA ATATCCTTTA TTGTTTGAT GATTATTTCT TCAGCATGGC TCATATCTTA 420
CTTCATTGAG AAGATCAGGT ACACAAATGC ACGCGACAGG AACCAGCGTC GTCTCGGAGA 480
TGCAGCCAAG AAAGCCATCA GTAAATTGAC AACCAGGACA GTAAAGAAGG GTGACAAGGA 540
AACTGACCCA GACTTTGATC ATTGTGCAGT CTGCATAGAG AGCTATAAGC AGAATGATGT 600
CGTCCGAATT CTCCCTGCA AGCATGTTTT CCACAAATCC TGCCTGGATC CCTGGCTTAG 660
TGAACATTGT ACCTGTCCTA TGTGCAAACT TAATATATTG AAGGCCCTGG GAATTGTGCC 720
GAATTGCGCA TGTACTGATA ACGTAGCATT CGATATGGAA AGGCTCACCA GAACCCAAGC 780
TGTTAACCGA AGATCAGCCC TCGGCGACCT CGCCGGCGAC AACTCCCTTG GCCTTGAGCC 840
ACTTCGAACT TCGGGGATCT CACCTCTTCC TCAGGATGGG GAGCTCACTC CGAGAACAGG 900
AGAAATCAAC ATGTCAGTAA CAAAAGAATG GTTTATTATT GCCAGTTTG GCCTCCTCAG 960
TGCCCTCACA CTCTGCTACA TGATCATCAG AGCCACAGCT AGCTTGAATG CTAATGAGGT 1020
AGAATGGTTT TGAAGAAGAA AAAACCTGCT TTCTGACTGA TTTTGCCCTG AAGGAAAAAA 1080
GAACCTATTT TTGTGCATCA TTTACCAATC ATGCCACACA AGCATTTATT TTTAGTACAT 1140
TTTATTTTTT CATAAAATG CTAATGCCAA AGCTTTGTAT TAAAAGAAAT AAATAATAAA 1200

ATAAAAAAAAA AAAAACCCCG GGGGGGGCCC GGTCCCAAT TGGCCCTATG G

1251

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(2) INFORMATION FOR SEQ ID NO: 157:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 2127 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

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CCGCGGGGAG AGGGAAGCTG CAGCGAGAGG CGCGGATCTC AGCGCGGGAG CAGTGCTTCT 60

GCGGCAGGCC CCTGAGGGAG GGAGCTGTCA GCCAGGAAA ACCGAGAACA CCATCACCAT 120

20

GACAACCACT CACGACCTC AGGACAGATA CAAAGCTGTC TGGCTTATCT TCTTCATGCT 180

GGGTCTGGGA ACGCTGCTCC CGTGAATT TTTTCATGACG GCCACTCAGT ATTTCAAAA 240

25

CCGCCTGGAC ATGTCCAGA ATGTGTCCTT GGTCACTGCT GAACTGAGCA AGGACGCCA 300

GGCGTCAGCG CNCCCTGCAG CACCCTTGCC TGAGCGGAAC TCTCTCAGT CCATCTTCAA 360

CAATGTCATG ACCCTATGTG CCATGCTGCC CCGCTGTGTA TTCACCTACC TCAACTCCTT 420

30

CCTGCATCAG AGGATCCCC AGTCCGTACG GATCCTGGG AGCCTGGTGG CCATCCTGCT 480

GGTGTTCCTG ATCACTGCCA TCCTGGTGAA GGTGCAGCTG GATGCTCTGC CTTCTTTGT 540

35

CATCACCATG ATCAAGATCG TGCTCATTAA TTCATTTGGT GCCATCCTGC AGGGCAGCCT 600

GTTTGGTCTG GCTGGCCTTC TGCCTGCCAG CTRACACGGC CCCCATCATG AGTGGCCAGG 660

GCCTAGCAGG CTTCTTTGCC TCCGTGGCCA TGATCTGCGC TATTGCCAGT GGCTCGGAGC 720

40

TATCAGAAAG TGCCTTCGGC TACTTTATCA CAGCCTGTGC TGTATCATT TTGACCATCA 780

TCTGTTACCT GGGCCTGCCC CGCCTGGAAT TCTACCGCTA CTACCAGCAG CTCAAGCTTG 840

AAGGACCCGG GGAGCAGGAG ACCAAGTTGG ACCTCATTAG CAAAGGAGAG GAGCCAAGAG 900

45

CAGGCAAAGA GGAATCTGGA GTTTCAGTCT CCAACTCTCA GCCACCAAT GAAAGCCACT 960

CTATCAAAGC CATCCTGAAA AATATCTCAG TCCTGGCTTT CTCTGTCTGC TTCATCTTCA 1020

50

CTATCACCAT TGGGATGTTT CCAGCCGTGA CTGTTGAGGT CAAGTCCAGC ATCGCAGGCA 1080

GCAGCACCTG GGAACGTTAC TTCATTCTCTG TGTCTGTTT CTTGACTTTC AATATCTTTG 1140

55

ACTGGTTGGG CCGGAGCCTC ACAGCTGTAT TCATGTGGC TGGGAAGGAC AGCCGCTGGC 1200

TGCCAAGCTG GNTGCTGGCC CGGCTGGTGT TTGTGCCACT GCTGCTGCTG TGCAACATTA 1260

AGCCCCGCCG CTACCTGACT GTGGTCTTCG AGCAGCATGC CTGGTTCATC TTCTTCATGG 1320

60

CTGCCTTTGC CTTCTCCAAC GGCTACCTCG CCAGCCTCTG CATGTGCTTC GGGCCAAGA 1380

AAGTGAAGCC AGCTGAGGCA GAGACCGCAG AGCCATCATG GCCTTCTTCC TGTGTCTGGG 1440
 TCTGGCACTG GGGGCTGTTT TCTCCTTCCT GTCCCGGCA ATTGTGTGAC AAAGGATGGA 1500
 5 CAGAAGGACT GCCTGCCTCC CTCCTGTCT GCCTCCTGCC CCTCCTTCT GCCAGGGGTG 1560
 ATCCTGAGTG GTCTGGCGGT TTTTCTTCT AACTGACTTC TGCTTTCAC GCGGTGTGCT 1620
 10 GGGCCCGGAT CTCAGGCC TGGGAGGGA GCCTCTGGAC GGACAGTGGG GACATTGTGG 1680
 GTTTGGGGCT CAGAGTCGAG GGACGGGGTG TAGCCTCGGC ATTTGCTTGA GTTCTCCAC 1740
 TCTTGGCTCT GACTGATCCC TGCTTGTGCA GGCCAGTGA GGCTCTTGG CTGGAGAAC 1800
 15 ACGTGTGTCT CTGTGTATGT GTCTGTGTGT CTGCGTCCGT GTCTGTGAGA CTGTCTGCCT 1860
 GTCTGGGGT GGCTAGGAGC TGGGTCTGAC CGTTGTATGG TTTGACCTGA TATACTCCAT 1920
 20 TCTCCCTGC GCCTCCTCCT CTGTGTTCTC TCCATGTCCC CCTCCCACT CCCCATGCCC 1980
 AGTTCTTACC CATCATGCAC CCTGTACAGT TGCCACGTTA CTGCCTTTTT TAAAAATATA 2040
 TTTGACAGAA ACCAGGTGCC TTCAGAGGCT CTCTGATTTA AATAAACCTT TCTTGTTTTT 2100
 25 TTCTCCATGG AAAAAAAAAA AAAAAA 2127

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(2) INFORMATION FOR SEQ ID NO: 158:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1625 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

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CAAAAGATCT ATAATCAGGA CATGTGTTAT GTAAGTTGGA CAANAAAAAT TCTTCCCCTT 60
 TATGTCCACC CTTCTATGA TTGCAAGACA AAATTTCCCT CTTTACCTC ATCCCTATAA 120
 CATGGGAGGC TGAGAAAAAT GAGGGGAGAT GGAACCAGAT ACAAGGAGAT CCAATAAGAG 180
 AAGCTTATTT AAATATTGTG AAATAAAGGA AGAMCCAAAG CATTTTTTTA AGTGGGGAAT 240
 CCTTTTGAAC AGTTATTATT TATCCATATT ATTAAYAACA TCTTTCTGA CAAATCCAT 300
 CAGATGAAGT GTAAATGGAT AATCTTTTAA TGGATCTAAA CCTAGAAAGT TTCCTTACT 360
 GTTCATGCC GTGTCCAGA ATGTGAAAT GGTGTGTGGT TTTGCTTTC AAGTCTTCT 420
 CTGCTCCTC TTAATCTCT AATCCATGT CTTACAGAAG AATGAGAAAT TTCTTCTTA 480
 CTTGAGTATC ATGCTCTAAA AACTTGGCT TCAGTCACAG AAACGCTGGC TCTCCTGTGC 540
 TTATATTGAA GCCAACTGCC TTTAATCTT GGGCCCTCTT ATATTTTAA GGTGCAAAAT 600

	TTGAAGTCTC AGTCACCAGA CACAGGTTCT ATACAATTAA TGATGAGCTG GAGAAGTAAT	660
	ATGTAGCTAA TTTTCAAAA GCATTGAATA TACTTTCCGG AAAGAAAACA GAAATTAAAT	720
5	ATTGCCACAT CTGCCCAGAA TCCCATCTGA CACCTTAACT TTGTCAGGTT TCCTACAACT	780
	TGCTAATCAA GTTTTATACA TTCTAAATCT CCCAGTTTC TTTGGGGCTG GAAGATGCAA	840
10	CTTCCATTTA ATAGAACTT TGAAATCTTG GGGTAAGGA GCAGTGGGG GACTAGGGAG	900
	AAGGATAAGA AATAGAATTA TTGAAAAGCC CCCACCAGG ACCTTCCTGG CCAGAATATG	960
	CAGAGTAATT CCTGCTGGCT TCACCTTTGA AAGTCCCTCG AAATATGCA GATGAACTG	1020
15	AGTCTGTTTT TGATATTGTC AGATGTATTC TACCTTGGAA GTCCCNACAC CTAACTGGA	1080
	ATTCTGTAT TTACATCTCC TCCACTGTCC CCCACACCAC CCCTCAATTC CTGCTGCCCC	1140
20	TGCTAATGTT AAGCATTTTT CTCTTGTTAT CATCAGGTT ACATTAAAAM CAGRTACTTA	1200
	CAAAC TGACT TGAAGCACAG ATACTTTTAC GAATGTGATA AAATATTTTC TTAAGAAAAG	1260
	GAAAGAGGAT GTGGGTCAA TAAACACCG CATGGATGTT GATTGGTGAA TACTGGTGTA	1320
25	AGAAAAGGGA GCTCAGGAAT TTTTATTACT GTATTTGTAA ATGAGTTTGA AGGAATTTGT	1380
	AAATGCCACT GGTACATTTT TAAGGTGACA CATTTGCTCC TTATAAAGTT ATTAAAAATT	1440
30	ACAGGGTAAG CTTAAATGAC GTTTGCCAGT AGTTTACTT TATATAATCA ATATTGATAT	1500
	TGTTGCTGAA CTATGTAAT TTATGATGCA TTTTTCAGTC CCTTTTCAGA GCAAATGCTT	1560
	TTGCAATGGT AGTAATGTTT AGTTTAAATT GACTTAATAA ATTTTACCT GAGCAAAAAA	1620
35	AAAAA	1625

40 (2) INFORMATION FOR SEQ ID NO: 159:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1687 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

50	CGGGGTCACC AGTTATTAGA GGAAGTAACA CAAGGGGATA TGAGTGACG AGACACATTT	60
	CTGTCCGATC TGCCAAGGGA TGATATCTAT GTGTCAGATG TTGAGGACGA CGGTGATGAC	120
55	ACATCTCTGG ATAGTGACCT GGATCCAGAG GAGCTGGCAG GAGTCAGGGG ACATCAGGGT	180
	CTAAGGGACC AAAAGCGTAT GCGACTTACT GAAGTGCAAG ATGATAAAGA GGAGGAGGAG	240
	GAGGAGAATC CACTGCTGGT ACCACTGGAG GAAAAGGCAG TACTGCAGGA AGAACAAGCC	300
60	AACCTGTGGT TCTCAAAGGG CAGCTTTGCT GGNATCGAG GACGATGCCG ATGAAGGCCC	360

TGGAGATCAG TCAGGCCAG CTGTTATTG AGAACCGYG GAAGGGACGG CAGCAGCAGC 420
AGAAGCAGCA GCTGCCACAG ACACCCCTT CTTGTTTGAA GACTGAGATA ATGTCTCCCC 480
5 TGTACCAAGA TGAAGCCCT AAGGNAACAG AGGCTTCTTC GGGGACAGAA GCTGCCACTG 540
GCCTTGAAGG GGAAGAAAAG GATGGCATCT CAGACAGTGA TAGCAGTACT AGCAKTGAGG 500
10 AAGAAGAGAG CTGGGAACCC TCCGTGGTAA GAAGCGAASC GTGGGCCTAA AGTCAGATGA 560
TGACGGGTTT GAGATAGTGC CTATTGAGGA CCCAGCGAAA CATCGGATAC TGGACCCCGA 720
AGGCCTTGCT CTAGGTGCTG TTATTGCCTC TTCCAAAAAG GCCAAGAGAG ACCTCATAGA 780
15 TAACTCCTTC AACCGGTACA CATTTAATGA GGATGAGGGG GAGCTTCCGG AGTGGTTTGT 340
GCAAGAGGAA AAGCAGCACC GGATACGACA GTTGCTTGT GTTAAGAAGG AGGTGGAGCA 900
20 TTACCGGAAA CGCTGGCGGG AAATCAATGC ACGTCCCATC AAGAAGGTGG CTGAGGCTAA 960
GGCTAGAAAG AAAAGGAGGA TGCTGAAGAG GCTGGAGCAG ACCAGGAAGA AGGCAGAAGC 1020
CGTGGTGAAC ACAGTGGACA TCTNCAGAAC GAGAGAAAGT GGCACAGCTG CGAAGTCTCT 1080
25 ACAAGAAGGC TGGGCTTGGC AAGGAGAAAC GCCATGTCAC CTACGTGTGA GCCAAAAAAG 1140
GTGTGGGCG CAAAGTGCCG CGGCCAGCTG GAGTCAGAGG TCATTTCAAG GTGGTGGACT 1200
30 CAAGGATGAA GAAGGACCAA AGAGCACAGC AACGTAAGGA ACAAAGAAA AAACACAAAC 1260
GGAAGTAAGC AGAGCTGCCA GGCTCCCAGG AGAGCATGGG GACTAGGAGG AAGGGTGTGG 1320
CATGGCTCAG TCTGGCCCCC TTGATTACCG GCCTAGCCCC TGCTCACATC ACAGCTGTCT 1380
35 GAAGAACAGT GAGGTGGAGT GCCTAGAACT CCCGTGGTGG TCCTGAGCAG AGAGGAGGAT 1440
GTCCTCCTGC CTGCCTGAAG GTCTCCCATG AAAACACTGC TGAAGTGTGT TGACACTCAT 1500
40 GACCCTTTTT TTAACCGTT AAAGGGAAGT TCGGTGTTGG AGCGATACTC AATGTAGTCA 1560
GTCTACACCT GGACGTGTGG GCCACTTAAG CCCTCCCCAC CCCCATCCTA TTCCTRAATA 1620
AAACCAGGAT AATGGAARAA AAAAAAAAAA AAAAAAAG GGGGGGCCN TAAAGGNCC 1680
45 CANNTTT 1687

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(2) INFORMATION FOR SEQ ID NO: 160:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1842 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

	GGATGACAGA TTGCGACANA GATTTGTGAC CCTTCCTGCT GAACTTCAGA GGGAGCTGAA	60
	ANCAGCGTAT GATCAAAGAC AAAGGCAGGG CGAGAACAGC ACTCACCAGC AGTCAGCCAG	120
5	CGCATCTGTG CCCCAGAGAAT CCTTTACTTC ATCTAAAGGC AGCAGTGAAA GAAAAGAAAA	180
	GAAACAAGAA GAAAAAACC ATTGGTTCAC CAAAAAGGAT TCAGAGTCCT TTGAATAACA	240
10	AGCTGCTTAA CAGTCCTGCA AAAACTCTGC CAGGGGCCTG TGGCAGTCCC CAGAAGTTAA	300
	TTGATGGGTT TCTAAAACAT GAAGGACCTC CTGCAGAGAA ACCCTCGGAA GAACTCTCTG	360
	CTTCTACTTC AGGTGTGCCA GGCCTTCTTA GTTTCAGTC TGACCCAGCT GGCTGTGTGA	420
15	GACCTCCAGC ACCCAATCTA GCTGGAGCTG TTGAATTCAA TGATGTGAAG ACCTTGCTCA	480
	GAGAATGGAT AACTACAATT TCAGATCCAA TGGAAGAAGA CATTCTCCAA GTTGTGAAAT	540
20	ACTGTACTGA TCTAATAGAA GAAAAAGATT TGGAAAACT GGATCTAGTT ATAAAAATACA	600
	TGAAAAGGCT GATGCAGCAA TCGGTGGAAT CGGTTTGAA TATGGCATTT GACTTTATTC	660
	TTGACAATGT CCAGGTGGTT TTACAACAAA CTTATGGAAG CACATTAAAA GTTACATAAA	720
25	TATTACCAGA GAGCCTGATG CTCTCTGATA GCTGTGCCAT AAGTGCTTGT GAGGTATTTG	780
	CAAAGTGCAT GATAGTAATG CTCGGAGTTT TTATAATTTT AAATTTCTTT TAAAGCAAGT	840
30	GTTTTGTACA TTCTTTTCA AAAAGTGCCA AATTTGTCAG TATTGCATGT AAATAATGT	900
	GTTAATTATT TTAAGTATG ATAGATTCTA TTTACAAAAT GTTTGTTTAT AAAGTTTAT	960
	GGATTTTAC AGTGAAGTGT TTACAGTTGT TTAATAAAGA ACTGTATGTA TATTTGGTAC	1020
35	RGGCTCCTTT TKGTAAYCC TTAATAAATC AACTCTAGGA RGCAACTACT GTTTATTATA	1080
	CTAAARGGCT GAAAAMCCTC CAGGCAGAC TGCTAAGCTC TGAAATYCCT GAGAGGTCTC	1140
40	AGACCGGGAT TCTACTTGT CCAAGAAAGG GTAAAGCTTC TAAACCATCT TATCTTGTC	1200
	TCCAAGCATG AACACAGGAG CATGTYAAGA AAATCTTAC TACTTTCTYC CATGCGGAGA	1260
	AATCTACATA TTTTGAATTA GAAACACCCT CACACCCACT TGAAGATTTT TTTCTGGGA	1320
45	ACATTATGTC CCGTAGATCA GAGGTGGTGT TGTCTTTTGT CTCTACTGG CCATTGAGAA	1380
	ACTTTGATGA TAAAAAGAA CGGTATAGAT TTTTCAAACG TATATAAAAT ATTTTATGT	1440
50	TATATGTTAT GCCATAACTT TAAAAATAAA ATAGTTTAAA ATTCTATGCT AGTGGATATT	1500
	TGGAACCTTT TCCTCAAACA AACACCCAC ACTGACTTCA GCAAACCCCT AAAACTAGCT	1560
	ACAGATTACT ACTACGAATG AATCATYAAG TTTTGTGTCT GCAACAATTT AGAAGCACTA	1620
55	AGCCCAAATA TCAGGAAATG TGTGTATGAT GGAATTTTCT AGGACAAAAC AGATCAAGAT	1680
	TAAAACAGGA TCAAGGATTA ATGGTATAAA AATGGTCTAC TAAAACAGGA TCAAGGATTA	1740
60	AAACAGGATC AAGGATTAAT GGTATAAAAA TCTCTACTGG TTACCGGGTG GCNGGGCCAT	1800

ACAGGGTAGT GGTGGATGGA TAGTTTAGTT TGGNAAGGGT AA

1842

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(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 770 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

15

GGCAGGAGCC CTATGCTGTT CTTGTGATAA TGAGTGAGTC TCACAAGATC TGGTGGTGTT 60

ATAGGCATCT GGCATTTCCC CTGCTGACGC TCATTCTCTA TCCTGCCACC CTGGGAAGAA 120

20

GTGTCTTCTG TCATGATTGT AAGTTTCCTG AGGCCTCCCC AGCTATGTAG AACTGTGAGC 180

CAATTAAACC TCTTTTCTCT ATAAATTATC CAGTCTTATA TATTTCTTCA TAGCAGTGTG 240

25

AGAACAGATA ATACCGTAAA TGGTATCAC AGAGAGTGGG GTGTTGCTAT AAACACATCT 300

GAAATGTTA AAGCAAAATT GGAAGTGGT AACAGGCAAA GGCTGGAACA GTTKGAAGAA 360

CAGTTAAGAA GAAGACAGGA AAATATGAGA AATCTTGAAA CTCCTAGAG TCTTAAAGGT 420

30

CTCAGAAGAC ATGAAGATGT GGGAAGCTTT GGAAGTTCCT AGAGACTTGT TTGAATGGCT 480

TTGACCAAAA TGCTGATAGT GATATGGACA ATGAAGTCCA GGCTGAGCTT ATCCAGACAG 540

35

ACATAAGAAG CTCGCTGGGA ACTTGAGTAA AGATCACTCT TGCTAGGCAA AGAGACTGGT 600

GGCCTTTTTT CCTCTGCCCT AGAGATCTGT GGAATCTGA ACCTGAGAGA GATGATTTAG 660

GGTATCTGGC AGAAGAAATA TCTAAGCGGC AAAACCTTCM AGAGGAAGCA GAGCATAAAC 720

40

GTTTGAAAAA TTTCAGCCT GACNATGGGA GACCAAAGTT AAACCAATT 770

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(2) INFORMATION FOR SEQ ID NO: 162:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 519 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

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GAATTCGGCA CGAGCTGAGA GGCACAGGAG CAACAGCCAG TGCCCCCTGC AGAGGACCAC 60

TGGGGTCACA GACTTCARAC CTGATGACCT GGGCTCAGAT CCCAGCTCTG CACCTACCAG 120

60

CCGTGTGACA AGGTGTCCTC TCTGAGCCTC AGTCACACAC TGCCTTAACG GTTGGGCCTC 180

414

ATGGAGCTGT TTGTGAAGGT TAAATGGGAA GACATAAAGC ACTTAGCCCA GAGCCAAGGA 240
CATGCTGAAT AGGATAATGG TGGCCTCCTT TGGCGCTGTG CTGGTGCAGG TGTGCCGAGG 300
5 AAYTGGGCAG GGGTGACAGA TACCTCTTCT AACCTAGTTC CTTTCCAAGA ACCTAATTGG 360
TGTCTCTCCC TCCCCCAGGC AATTGGAAGG AGGAGGCTGG GCCCCAGCCC CAGAATACGG 420
GAGGTTTCTC ACCGTGGTAG GGAAATTGCT GGGTTGGGGG TGTGGGCAAC CACAGTGATC 480
10 GTCTCTCTGC AGGACGGATG AGGCTTTGCT GACAGAGGC 519

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(2) INFORMATION FOR SEQ ID NO: 163:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

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GGCAGGAGCG GCACGAGCAG CCAGTTGCTG ACTGGCACAT GGCCTCCAGC GTCCCGGCTG 60
GTGGGCACAC TAGAGCCGGA GGGATCTTCT TAATTGGTAA ATTGGATCTT GAAGCTTCAC 120
TGTMTAAATC TTTTCAGTGG CTTCCCTTTG TACTTAGAAA AAAATGCAAC TTCTTCTGCT 180
GGGACTCATC CGCTCACAGC CTTCCCTTCC ACCCTCTCTC TGCCTCATGC TCTGCCCTTG 240
CCTGCCATGC CTCCGATACT CACCTTTTGT ACCCCAGCAC CCGTGCCCTC TGCCCTCGA 300
TCTTTGCCTG GCTGGTTGCT CCTCACTCAG TGTTCAGGAC AAATGCTCCT GGCCCTACCC 360
CATCTAGCCA GTCTAGCCCG GTCTTCCCTG TCTTCCCTGT TTCATTATG GCTCTTATTG 420
TTTGTTWACT TGTGTGCTGT TGACTTTTAA CTCTCTCAGT CCCCACTGGA ATGCAAGCGA 480
TCTCCCAAGC TCCTAGAATT GTTCTGCCT CTTCACAGGC CCTTACGCTG TGTGTGCTCG 540
TGCCGAATTC GGCACGAGGG TATGTGCACT TGCTGGTATG TATGTAGGTG TTGCTAACA 600
CATACGTGCA CACGCAGAAT GCTTCCAGGG GACTGCACAG CCTCTAGTTC GCAGCCCCCA 660
CCCCCTCCCTT TGSCCTGCA CTCTCCCTC TCTGAGCTGC ATTGCATGA AAGGGTGCAN 720
GGTTCCTGAN CCGCNAGCG NCACCTCCTG GGA 753

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(2) INFORMATION FOR SEQ ID NO: 164:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

5 GGCACAGTTT ATTAATACCT ATTATGGGAA AGTCACTTTG GTTGGCATTG AAAATTACAT 60
 CATCTTTAAA GCAGTATTTG TCCCCAGATG GACTCATCAC TAGCAAAGAC TAGGTTTCATT 120
 GGAAGGCATA GGGTGAGAGA ATGGGAAGAT GRACTGGAGG CGGGTTGTTA AAGTGCTGTC 180
 10 AGTGAGTGAT TTTGTCTACT TGAATCAATGG TCCATGTTTG GGGGCATATT GTGTTTCATA 240
 AGAAGTGAAA GGTATTTGCA AAGTAAGCTA CAAATGACCC ATAAATCTGT TAACAACAGT 300
 15 CCTTAATATG CAAAGATGAA AAACAAGCAT TACTGCTACC CAAAGGGAAC TGGTGCTTGG 360
 TGATGTGCAG ATGGGGCTGT TGGTTAAGAG AGCTATTACA GGTTTCTCTT CTTAGGTTTC 420
 ATAGGAGGTA GTTACTGAGA TGAGATTGTT TTATCTTTTT GAATACAGAT CTCITGCTTT 480
 20 GAGTTAGTTC TGAGGATGGG AGTAATAAAG GAGTTTTTTG TTTTTTTGTT TGTITGTTTG 540
 TTTTGGCTCC TTAGTAATAC TCCTCTGACA TTTATTTCTA TTATTCITCA AAGAAAGGAA 600
 25 ACCAACTGAA ATGTTTGCTT TAACAAACAT TTTAATAAGT TCTCTGGGTT TTTTTTCCC 660
 CTTTTAAAAA AATTAGCATA TACCATAGCA ATAAAAGAAC TAATGTTAAC TATTGTATGC 720
 TACAACTTAA GTGATTTTTT TAAAGAAGCA CAATGTCATT GRAAGTATTA TTGAAAAGGA 780
 30 TCATAGTCAC ATTGAATTG TGAAGGCCAA AGAAATTGAA GGGAGTGATA TTTTCATTTT 840
 ATGATATTCA CATATTTAGT AAATTTTGTG TACAAGAATA CCAGGCAGAG TGTTTTACCC 900
 35 ATGGAAACAG GTTTCAGATT ACTTTGTTTT TACTGTTAGA GTCTCAAGTT TAGAAATGCT 960
 AACACTTAAA TCAGTTTTTT TCTCACTATA CTTGAAGATT GTTAATATTT TGATATCTTC 1020
 CTAGCTTGAT GGAATTTAAA CATATCTTCA GATCTGTGAC AGTGACAGCC AATAGGACTG 1080
 40 ATAATATTAG CTTCAAACCA ATAATATCCA GGGTTAAAAT AAAAATCATA GTGAAAGTAC 1140
 GATTGTAAAA TTATGCTATA TTAACITTTA AGTCTGTAAT AACTTGACAT CAAAATGTTA 1200
 45 TGTAATTACC ATAAATAATG GCTAGCGAGA ACATCTTTGG AAATTCCTCA ATTACCTTTC 1260
 TTACTACACT GTTTCAGAA TGAATGTAGA AATGATCCTG TTAGCTTTCT GAATGTTCTG 1320
 TGGTTGAATG TGTTTTTGCT TAAATAAAGC TTTTGGTATT TGTTTAAATW ACAAAAAAAA 1380
 50 AAAAAA AAAA ACTCGA 1400

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(2) INFORMATION FOR SEQ ID NO: 165:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2153 base pairs

(B) TYPE: nucleic acid

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(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

5	CAGGCCTCAG GGCCTCTGGT GGCTCTGGCC CAGACAGTAT TTGCAGTTCT TGTGCTATGG	60
	GTGGGAGTCT TCTTCCTCAA GTTCGGCAG CTGTGCTGTG NCTGGATGGG CTGCTCCTCC	120
10	CAGGGCTCAA GGGCTGTGGT CCGCTCAGGG TCTCATTTCC CCAGGCCAAG TTCAAGGCAG	180
	CAGCCCTTTG TGAGGCGCTC TTGGCCCTGG GCTGGAGGGA GAACTTTAAG CTTTTTGTCT	240
15	CACAGGGACG TGGTATGGGC CCTGGGTGCA GGTGCCACCA TTCTGCTAAT GAGAGCTTTG	300
	TCTGATCAGT CCTGGGTCCA TCAGTTTGTG CATGTGTCCG GCTGCCAGCC CGTCCCTTGG	360
	GATCCTTCCC CTGGGGTGTA GCCTTGTTC TTAGTATATA CTCATTCTCT CATGCTTTCC	420
20	TCAGCAGAAC ACTTCCACTT CTGAGGTGAG CTTTGTGCCC RTGCCCTTCC TCCACAGGTG	480
	TTGCCCTTTT ATAAAGACCT GATAGCAGAA TAAATTGGTG TTTCCCTGTT GACCCAGCAC	540
	CATTTCTGTG GGCCTAGAAT ATGGCCCTCA ACCCTTAGAG TGGGGCAGTG AGGGCTTGAG	600
25	GAGTGACCTC TCCTTTCTCA TGGTTTGTG CATTTTGGCT GCCAGCCCTT AATGGCACAG	660
	ATCTGCTGCT TCTAACAGAT GGCCAGGAGG TGACACCGAT TTCAGCCATT GCCAAGGTTA	720
30	GCACCTCTC CTTTGAGCCT AGGGCCACAC TGTTCATTGT CACTTTAGGC AAGTGCCTGT	780
	TTGGCTTTAA AGGTAAGCCT GCCAGCTGTG AGAAGCCTTG GTAAGTATG GACTCATTTT	840
35	CTGGTCTCTA AAGATGCAGC CTCTTAAGGG CTCCTTGATG GATGCCATCT CTCCTAGCCC	900
	CCAGCCCTGG TGCCACTGGT GGGCAGGTTT CCATTCTTTG GGGCTGGGAG GGACAGCTTG	960
	CCTGTTTCTG GTCACAAATT ACAGTCTTCT CTCCTGTACC ATTCTGTGGC TTCAGCATGG	1020
40	GGGCAGTAGC CTTTCATTAG TGTAGATAGT CATTCCCTGG TAGGGTGGAG GGTAAGACAT	1080
	AGGGTCTGGA ACTGTTTGGG ACCTTTTGGG GATGTCCTGT GCCTCCAGG TTCCTMGATT	1140
	CTGGGAGGAG AGGCTGCCGC ATTCTGTGTC TCCTCACAGC GAGCAAAGCT GCACCCACTT	1200
45	ACATTGAGTA TTTTCTTGGC ACTACAAAGA GTGGGAAGGC CTGGGATTG CTGCTGCTCC	1260
	CTTAGAGCAG GCGCCCTYTT TTCAGCACTT TGGACACCTG GAGACCCAGC CCTGTTATTT	1320
50	AATGGTAGTG GGCAAGTGTG TGTGCATACT GTCTGCCACT GCTTTCTCCC TGCCCCATGC	1380
	CAGAGAGCCC TGTCCCTGCC AGGCCAGCC TTCTTAGCCC CAACTTGGGA ACAAAGTGCA	1440
55	ACATGGGATC ATGGGTGGG GTGCTCAGGT GAGCCCTCTC TATAGTGCTT CCCTGGGCCA	1500
	AGCTGACACC AGCCCTGAG GGTGGGTGG GACGGGTGGT GCTTAAAAGA GGAAGGGAC	1560
	CAGTGTAGCA ACTTGCCAGG GACCCACCC CTCCCTCTCT GGGCTGTGC AGTGAGCATG	1620
60	GGGATTCCCA TCAAGGGGCC TGGCACCTGT GCTAGTTACG TAGCCGCTGN TCACGCGCTC	1680

5 ACTCCTGACC ACATGCACGT TCCCTAGATG CAGACTGCTT TGAAC TTAA AGCTGTACAA 1740
 TTTGGTTATG TTTGTGCTGA CTTAAAATAT ATTTTAATGA GGAAAAATA ATGGAGAACC 1800
 CTGGGAAGGA CCTGGTCTTT TIGCTTCTCG GGGAACTGTA AGCCCTCGCG TTCTGGGAAT 1860
 CGCTCTCTGC TGCTCTTTCC TGAAGCTAA GCCTGTCTCC ACCGCCGAG GCCTGCGCCG 1920
 10 GTGCTCCCGC CGCAGTTGCG TTTGCTTTGG ACCTTGCGTG CGGGGAGGG GGTGCTCGGT 1980
 CCGAGCCCGC TCCTTTCTGT ACACCTAGCG CTGCCCGCCC CGCTTGTCGTC TGAGGTCGTG 2040
 TATGTCAAAA ATAAAGCCGC TAGAAACGGA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2100
 15 AAACGAGG GGGGGCCGT ACCCAATTAA CCCNNTATGA TCTATAAAGC GTC 2153

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(2) INFORMATION FOR SEQ ID NO: 166:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1251 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

30 GCCCACGCGT CCGCCACGC GTCCGCGGT GCGGAGTATG GGGCGCTGAT GGCCATGGAG 60
 GGCTACTGGC GCTTCTGGC GCTGCTGGG TCGGCACTGC TCGTCGGCTT CCTGTCCGTG 120
 35 ATCTTCGCCC TCGTCTGGT CCTCCACTAC CGAGAGGGGC TTGGCTGGGA TGGAGCGCA 180
 CTAGAGTTTA ACTGGCACCC AGTGTCTCATG GTCACCGGCT TCGTCTTCAT CCAGGGCATC 240
 GCCATCATCG TCTACAGACT GCCGTGGACC TGGAAATGCA GCAAGCTCCT GATGAAATCC 300
 40 ATCCATGCAG GGTTAAATGC AGTTGCTGCC ATTCTTGCAA TTATCTCTGT GGTGGCCGTG 360
 TTTGAGAACC ACAATGTAA CAATATAGCC AATATGTACA GTCTGCACAG CTGGGTGGA 420
 45 CTGATAGCTG TCATATGCTA TTTGTTACAG CTTCTTTCAG GTTTTTCAGT CTTTCTGCTT 480
 CCATGGGCTC CGCTTTCTCT CCGAGCATTT CTCATGCCCA TACATGTTTA TTCTGGAATT 540
 GTCATCTTTG GAACAGTGAT TGCAACAGCA CTTATGGGAT TGACAGAGAA ACTGATTTT 600
 50 TCCCTGAGAG ATCCTGCATA CAGTACATTC CCGCCAGAAG GTGTTTTCGT AAATACGCTT 660
 GGCCCTCTGA TCCTGGTGTT CGGGGCCCTC ATTTTGTGGA TAGTCACCAG ACCGCAATGG 720
 55 AAACGTCCTA AGGAGCCAAA TTCTACCATT CTTATCCAA ATGGAGGCAC TGAACAGGGA 780
 GCAAGAGGTT CCATGCCAGC CTA CTCTGGC AACAAATGG ACAAATCAGA TTCAGAGTTA 840
 AACAGTGAAG TAGCAGCAAG GAAAGAAAC TTAGCTCTGG ATGAGGCTGG GCAGAGATCT 900

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ACCATGTAAA ATGTTGTAGA GATAGAGCCA TATAACGTCA CGTTTCAAAA CTAGCTCTAC 960
AGTTTTGCTT CTCCTATTAG CCATATGATA ATTGGGCTAT GTAGTATCAA TATTTACTTT 1020
5 AATCACAAAG GATGGTTTCT TGAAATAATT TGTATTGATT GAGGCCTATG AACTGACCTG 1080
AATTGGAAAG GATGTGATTA ATATAAATAA TAGCAGATAT AAATTGTGGT TATGTTACCT 1140
TTATCTTGTT GAGGACCACA ACATTAGCAC GGTGCCTTGT GCAKAATAGA TACTCAATAT 1200
10 GTGAATATGT GTCTACTAGT AGTTAATTGG ATAACTGGC AGCATCCCTG A 1251

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(2) INFORMATION FOR SEQ ID NO: 167:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 882 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

GACSMCTAG AACTATGGTC CCCCGGGACT GCAGGAATTC GGCACAGCGG CTGCGGGCGC 60
GAGGTGAGGG GCGCGAGGTT CCCAGCAGGA TGCCCCGGCT CTGCAGGAAG CTGAAGTGAG 120
30 AGGCCCGGAG AGGGCCAGC CCGCCCGGG CAGGATGACC AAGGCCCGGC TGTTCGGCT 180
GTGGCTGGTG CTGGGGTCGG TGTTCATGAT CCTGCTGATC ATCGTGTAAT GGGACAGCGC 240
AGGGCCCGCG CACTTCTACT TGCACACGTC CTTCTCTAGG CCGCACACGG GGCCCGCGCT 300
35 GCCACGCCCC GGGCCGGACA GGGACAGGGA GCTCACGGCC GAYTCCGATG TCGACGAKTT 360
TCTGGACAAK TTTCTCAGTG CTGGCGTGAA GCAGAGTGAC YTTCCAGAA AGGAGACGGA 420
40 GCAGCCGCCT GCGCCGGGA GCATGGAGGA GAGCGTGAGA RGCTACGACT GGTCCCCGCG 480
CGAMGCCCCG CGCACCAGA CCAGGGCCGG CAGCARGCGG ANCGGAGGAR CGTGCTGCGG 540
GGCTTCTGCG CCAAYTCCAG CCTGGCCTTC CCCACCAAGG AGCGCGCATT CRAAGACATC 600
45 CCCAACTCGG AGCTGAGCCA CCTGATCGTG GACGACCGGC ACGGGGCCAT CTACTGCTAC 660
GTGCCCAAGG TGGCCTGCAC CAACTGGAAG CGCGTRATGA TCGTGCTGAG CGGAAGCTGT 720
50 GCACCGCGTG CGCCTACCGC GACCCGYTGC GNTCCCGCGC GAGCACGTGC ACAACGCCAG 780
CGCGCACTGA CTTCAACAAT TCTGGCGCCG CTACGGGAAG TCTCCCCAC CTCATGAAGT 840
55 CAAGCTCAAG AATACACCAA TTCTTCTGCG GCGACCCCTC TG 882

60.

(2) INFORMATION FOR SEQ ID NO: 168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1208 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

GGGAAACTCA AAAGGATGAT GGAATGGTGTG ATGGAGCCAG AGCCTAGAAG TRAAGGGATA 60
 CAGAGTGAAG ATAGAGGTAT TTACGTATAT TTWAATATTA GCTTTGGAAT TACGTAGGGA 120
 TTCTTAAGAA AAGATCATGA CAGGACAGCC ACATTTGGTA AAATGTCAGG GCAGCCAGTG 180
 CATGGTCCTC CTGGGGCTCC TCAGTTGACG GGTTTAAATC ATTCCTGAT CCCCCTGCCC 240
 TGGTTTGAGG AATGCATACA GTACGTGAAA TGCCTGTGGT ATGAGTTGCA ATGGGCAATC 300
 AACCTGGGTA AATCCAAGAT TAATGATTAG TTCTAAAGAT CCAGTTGAAG TTCTAGAGTG 360
 GGAATTTTCC GTCAAGCARG TCAGCACAGC TTTATGCCTG TTCCTCTAAT AACGATAGGT 420
 AACAAATAGC TGTGKTWCA CAGCTAGGAR GATAACCAAA TCTAGAGTTC TTGARTCTCA 480
 TTTAATAAAT AAKTATTATG AGTACCAACT GCATATTTCA GGCCTGTCAT TTGACTCTGT 540
 TAAATACTGA TYCCTTAKGA CMSCCACWTC AGAWAACMTT AATCTGTCTG ATCAATAAAC 600
 AGCTTGACTT AGAGRGGTAA AATAGCTTGC CACAGGTWAC CCAATTAGTA GGTAACAGCG 660
 ACAGAATAAC AGTGCAGTTA AAATCTTAGA CTGGAGACTA ATTGCATAAG TTTGAATTTT 720
 AGTTCTGCTA TGTAAATTTG GGTGAGTACC TTAATTYACC TGAGTCTCGG TCTTTATATC 780
 TGTAGAATGG AGCTAATGAT ATTACTTAAT TTGCTTTATG TGAGATTAAA TGTACTAATA 840
 TATGTAAATC ACTTACAACA GCAATTGACA TATTTGACAT ACTTAATATA TTTGCTACTA 900
 ATACTATTAG CAACAGCATT CTGATTTTCC AAGTTGAAAT TCAGTGTTTT CTMTTTTACT 960
 TTGCCATAAT TTACAATGTT GTGCTCTGTA AACCATAAAT TTCCCTGAGG TGTGTGTCAGG 1020
 TTAAAAAATA ATCACTATGG CCCCARNMA CTTGGAAAAT AGAAATGAGA CCAGCTTCAT 1080
 CTATATTCTT TACTGCAAAT AACTTAGAAT TGTAATAGGC TAATATGTAC TGGGACTTCC 1140
 AATTTGGGAA TATGACAAAA ATAATACTAT TTAGCTAAAA CATATACAGA ACTTATTTTT 1200
 CCTCTGAA 1208

(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1307 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

5	GGCACGAGAG AAAAGAGGTT GAGAATGTTT TCTAGCAGGC AGAATGTGCA TACATGTTTT	60
	CATGARTGTC CTTTGGGTGC TGTTCCTTTT AAATCCTCTG TGCACAGGGC TCTGGCCTTT	120
	ARTAACTGT TTTTCTGTCT TACGTCATGC TGACTGGGTG CTAGGGGCTG ATTACAAAGG	180
10	GGAAGAGTTG AACAGACATC AGGGGCCGAT GAAACCAAAG GACTAGGAGT CAGGAGAACA	240
	AGTCAGGGAT TAGGAGACAG CGGTTTGGTT TATTGTTATC CAGCTGGAGG ACTCCTAGGG	300
15	GCAGCAGCAG GAGGAATACC AGGGCCACGG AGGGGCAGGA GTCTCACAGT GGAGGGCAGA	360
	CTCTAACAGA TGCCAGCTGA ACGCTCGCTG GCCCTGGATG TCATACGAGT TGGGGACCAG	420
	AAATCTGGGC TCAGAGAACC CGTCCAGGGA GATTTGAAGC CATGGGTTAT CTTCTAGAGT	480
20	TGATACTGAT AATATATTTT AATTTTATT GATGTTTAAT ACCTTCTGAA ACAGGAGGGT	540
	AAGATCAGAT GGAAGCCCY TCTGTTGAAG GATCTTGGGA ACCTTGGTGG TTTTTTTTTT	600
25	TTGGTTTTTT TTTTTTTGAT CGAGCTGTGG ACATCCTTCT TAATTCGATT NTGAGGATTT	660
	GTTTAACTAA AAAGTCCCA AACACAGAAA GGGCCTCCCC ACCTGCTTTG GGGAGCTGTC	720
	TGTSCTGGGA GTGCCAGGCA TCCSATGGGA CCCATCACTG CCAGTGTCTG TGCCTCCCAG	780
30	AGGTCAGCCC TGTGTCTGCC CTGGCTCTGT CTCCTCTGTG ACAGGGCAGA GCATTTCTGG	840
	TCAGTTTCTC CATGGTGCCT CCCACCCCTT TGTAAAGTGG ATGGACATGA TGAATTCAG	900
35	TTGTCTCACC CTGATAGCCT GGGTGTGAT ATTCACTTTA CCCGCACTCA GACACAGGCG	960
	ACCTTGAAGC AGTTCTCGGT GTGTAGAGTC CACGTGACAG TCCCCACAGC CTCCCCAGAT	1020
	AGCTGTGTGC CTGTGCGCTA CTGCTGTGCC ATTTTCCCAA CTINGGCGTT TCACTAAATG	1080
40	CAGCTGATCT CTCTCTCTGT GCACTCGTGA TCCATGTTGA ACAATACATG TAGGTTCTTT	1140
	TTCCACGCAA TGTAAGAACA TGATATACTG TACGTTGGAA AGCATTTACC TTATTTATAT	1200
45	ACCTGAATGT TCCTACTACA CAAATAACA TATATTAAAT WCTAAAAAA AAAAAAAAAA	1260
	CTGGAGGGGG GCGCCGGTAC CCAAATCGCC GGATAGTGAT CGTAAAC	1307

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(2) INFORMATION FOR SEQ ID NO: 170:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1624 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

	GGCACGAGGT CGCCGCCGCG GCCGCCTGGA ATTGTGGGAG TTGTGTCTGC CACTCGGCTG	60
	CCGGAGGCGA AGGTCCCTGA CTATGGCTCC CCAGAGCCTG CCTTCATCTA GGATGGCTCC	120
5	TCCTGGCATG CTGCTTGGGC TGCTGATGGC CGCCTGCTTC ACCTTCTGCC TCAGTCATCA	180
	GAACCTGAAG GAGTTTGCCC TGACCAACCC AGAGAAGAGC AGCACCAGAG AACRGAGAG	240
	AAAAGAAACC AAAGCCGAGG AGGAGCTGGA TGCCGAAGTC CTGGAGGTGT TCCACCCGAC	300
10	GCATGAGTGG CAGGCCCTTC AGCCAGGGCA GGCTGTCCCT GCAGGATCCC ACGTACGGCT	360
	GAATCTTCAG ACTGGGGAAA GAGAGGCAAA ACTCCAATAT GAGGACAAGT TCCGAAATAA	420
15	TTTGAAAGGC AAAAGGCTGG ATATCAACAC CAACACCTAC ACATCTCAGG ATCTCAAGAG	480
	TGCACTGGCA AAATTCAAGG AGGGGGCAGA GATGGAGAGT TCAAAGGAAG ACAAGGCAAG	540
	GCAGGCTGAG GTAAAGCGGC TCTTCCGCCC CATTGAGGAA CTGAAGAAAG ACTTTGATGA	600
20	GCTGAATGTT GTCATGAGA CTGACATGCA GATCATGGTA CGGCTGATCA ACAAGTTCAA	660
	TAGTTCCAGC TCCAGTTTGG AAGAGAAGAT TGCTGCGCTC TTTGATCTTG AATATTATGT	720
25	CCATCAGATG GACAATGCGC AGGACCTGCT TTCCTTTGGT GGTCTTCAAG TGGTGATCAA	780
	TGGGCTGAAC AGCACAGAGC CCCTCGTGAA GGAGTATGCT GCGTTTGTC TGGGCGCTGC	840
	CTTTTCCAGC AACCCCAAGG TCCAGGTGGA GGCCATCGAA GGGGGAGCCC TGCAGAAGCT	900
30	GCTGGTCATC CTGGCCACGG AGCAGCCGCT CACTGCAAAG AAGAAGGTCC TGTTTGCACT	960
	GTGCTCCCTG CTGCGCCACT TCCCCTATGC CCAGCGGCAG TTCCTGAAGC TCGGGGGGCT	1020
35	GCAGGTCCTG AGGACCTGG TGCAAGAGAA GGGCACGGAG GTGCTCGCCG TGCGCGTGGT	1080
	CACACTGCTC TACGACCTGG TCACGGAGAA GATGTTGCGC GAGGAGGAGG CTGAGCTGAC	1140
	CCAGGAGATG TCCCAGAGA AGCTGCAGCA GTATCGCCAG GTACACCTCC TGCCAGGCCT	1200
40	GTGGGAACAG GGCTGGTGCG AGATCACGGC CCACCTCCTG GCGCTGCCCG AGCATGATGC	1260
	CCGTGAGAAG GTGCTGCAGA CACTGGGCGT CCTCCTGACC ACCTGCCGGG ACCGCTACCG	1320
45	TCAGGACCCC CAGCTCGGCA GGACACTGGC CAGCCTGCAG GCTGAGTACC AGGTGCTGGC	1380
	CAGCCTGGAG CTGCAGGATG GTGAGGACGA GGGCTACTTC CAGGAGCTGC TGGGCTCTGT	1440
	CAACAGCTTG CTGAAGGAGC TGAGATGAGG CCCCACACCA GGAAGTGGACT GGGATGCCGC	1500
50	TAGTGAGGCT GAGGGGTGCC AGCGTGGGTG GGCTTCTCAG GCAGGAGGAC ATCTTGGCAG	1560
	TGCTGGCTTG GCCATTAAAT GGAAACCTGA AGGCCAAAAA AAAAAAAAAA AAAAAAAAAA	1620
55	AAAA	1624

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 2003 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

10 GGCACGAGCC AGCTTGACAG AGGAATCGGT GAGGTCTGT CCTGAGGCTG CTGTCCGGG 60
 CCGGTGGCTG CCCTCAAGGT CCCTCCCTA GCTGCTGCGG TTGCCATTGC TTCTTGCTG 120
 15 TTCTGGCATC AGGCACCTGG ATTGAGTTGC ACAGCTTTGC TTTATCCGGG CTGTGTGCA 180
 GGGCCCGGCT GGGCTCCCCA TCTGCACATC CTGAGGACAG AAAAAGCTGG GTCTTGCTGT 240
 GCCCTCCAG GCTTAGTGT CCCTCCCTCA AAGACTGACA GCCATCGTTC TGCACGGGGC 300
 20 TTTCTGCATG TGACCCAGC TAAGCATAGT AAGAAGTCCA GCCTAGGAAG GGAAGGATTT 360
 TGGAGGTAGG TGGCTTTGGT GACACACTCA CTTCTTTCTC AGCCTCCAGG AACTATGGC 420
 CTGTTTAAAG AGACATCTTA TTTTCTAAA GGTGAATTCT CAGATGATAG GTGAACCTGA 480
 25 GTTGACAGATA TACCAACTTC TGCTGTATT TCTTAAATGA CAAAGATTAC CTAGCTAAGA 540
 AACTTCCTAG GGAAGTAGG AACCTATGTG TTCCCTCAGT GTGGTTTCCT GAAGCCAGTG 600
 30 ATATGGGGT TAGGATAGGA AGAAGTTCT CGGTAATGAT AAGGAGAATC TCTGTCTCC 660
 TCCCACCTGT GTTGTAAGA TAACTGACG ATATACAGGC ACATTATGTA AACATACACA 720
 CGCAATGAAA CCGAAGCTTG GCGGCTGGG CGTGGTCTTG CAAAATGCTT CCAAAGCCAC 780
 35 CTTAGCCTGT TCTATTGAGC GGCAACCCCA AAGCACCTGT TAAGACTCCT GACCCCAAG 840
 TGGCATGCAG CCCCATGCC CACCGGGACC TGGTCAGCAC AGATCTTGAT GACTTCCCTT 900
 40 TCTAGGGCAG ACTGGGAGG TATCCAGGAA TCGGCCCTG CCCCACGGG GTTTTCATGC 960
 TGTACAGTGA CCTAAAGTGT GTAAGATGTC ATAATGGACC AGTCCATGTG ATTTCAATAT 1020
 ATACAACTCC ACCAGACCCC TCCAACCCAT ATAACACCCC ACCCTGTTC GCTTCCTGTA 1080
 45 TGGTGATATC ATATGTAACA TTTACTCCTG TTTCTGCTGA TTGTTTTTTT AATGTTTTGG 1140
 TTTGTTTTTG ACATCAGCTG TAATCATTC TGTGCTGTGT TTTTATTAC CCTGGTAGG 1200
 50 TATTAGACTT GCACTTTTTT AAAAAAGGT TTCTGCATCG TGGAAGCATT TGACCCAGAG 1260
 TGGAACGCGT GGCCTATGCA GGTGGATTCC TTCAGGTCTT TCCTTTGGTT CTTGAGCAT 1320
 CTTTGCTTTC ATTCGTCTCC CGTCTTGGT TCTCCAGTTC AAATTATTGC AAAGTAAAGG 1380
 55 ATCTTTGAGT AGGTTCGGTC TGAAAGGTGT GGCCTTTATA TTGATCCAC ACACGTTGGT 1440
 CTTTTAACCG TGCTGAGCAG AAAACAAAAC AGGTTAAGAA GAGCCGGGTG GCAGCTGACA 1500
 60 GAGGAAGCCG CTCAAATACC TTCACAATAA ATAGTGCAA TATATATATA GTTTAAGAAG 1560

5 GCTCTCCATT TGGCATCGTT TAATTATAT GTTATGTTCT AAGCACAGCT CTCTTCTCCT 1620
 ATTTTCATCC TGCAAGCAAC TCAAATATTT TAAATAAAG TTTACATTGT AGTTATTTTC 1680
 AAATCTTTGC TTGATAAGTA TTAAGAAATA TTGGACTTGC TGCCGTAATT TAAAGCTCTG 1740
 TTGATTTTGT TTCCGTTTGG ATTTTGGGG GAGGGGAGCA CTGTGTTTAT GCTGGAATAT 1800
 10 GAAGTCTGAG ACCTTCCGGT GCTGGGAACA CACAAGAGTT GTTGAAAGTT GACAAGCAGA 1860
 CTGCGCATGT CTCTGATGCT TTGTATCATT CTTGAGCAAT CGCTCGGTCC GTGGACAATA 1920
 AACAGTATTA TCAAAGAGAA AAAAAAAAAA AAAAACTCG NGGGGGGGCC CGGTACCCAA 1980
 15 TTCGCCCTAT AGTGAGCCNA TTC 2003

20

(2) INFORMATION FOR SEQ ID NO: 172:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 786 base pairs
 25 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

30 GGCACAGCGG CACGAGAAGA CTTTGGTGTT TAAGAGATTA ATGTGTTAGC CAGAACAAC 60
 CATTTCTCTA CCMGTGTGTA GTCCATTTAT CTTTAAAGAT TTTCTATTGG AATAATTTTG 120
 35 AAATTACTTT CTTAGTTTTC TTCATTAAAA ACTAAGAAA TGCTTTGTTT ATTATGAATT 180
 GCTATTCTC TTGATTATTA TTCTTGAGA AAGTCTATCA GACGTAATTC TTCTGATTG 240
 CTTCTAGGCT AGAGGAAAAT GTGAAAGATG ACAAATGAAA ATTTCAAAGG TTGTCAGTAG 300
 40 TATGACTTCT TTTATCGTTT GTCATTATCA CAAATATATC AACATAGGAC TTTTAAAAGA 360
 TATTTTGTA ATATTGGGCC TTAGTAGGAT TTTGCATGAA TTTTPTTTT CTTTATGCC 420
 45 CAGAGAGAAA GAGCAAAGAA ATAACCAAGG GTGATGTACT CGTATTGAAG GTTTACCAA 480
 TAAGGACTGC TTTTATTATG AACTATAGTC TATATTCTAA GTAAATCAAT TTTTCTATTA 540
 TGTGTTTTTT GTTCTGCAG GCAAGATCTC TGAACCTTAT GCAGAGGGTT CTTTAAAAA 600
 50 AACAAAGTTG AATTTTTTTA TTTCTTGAA TATTTTTTTT CATTGATTTC TCCAAGTAG 660
 AGCAGATTCA AATCTCCTTT GTACCCTATG TCTTTTTTGT TTGCTATTA GCTCAGTATT 720
 55 CCGTTTCTAC ATTTTCTTTT CCTAGAACCA GTCAATAAAT GACAAAAAAA AAAAAAAAAA 780
 ACTCGA 786

60

(2) INFORMATION FOR SEQ ID NO: 173:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1758 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

GGGACGAGCC CTGCCCACCT CCTGCAGCCT CCTGCGCCCC GCCGAGCTGG CGGATGGAGC 60
TGCGCACGGG GAGCGTGGGC AGCCAGGCGG TGGCGCGGAG GATGGATGGG GACAGCCGAG 120
15 ATGGCGGCGG CGGCAAGGAC GCCACCGGGT CGGAGGACTA CGAGAACCTG CCGACTAGCG 180
CCTCCGTGTC CACCCACATG ACAGCAGGAG CGATGGCCGG GATCCTGGAG CACTCGGTCA 240
20 TGTACCCGGT GGACTCGGTG AAGACACGAA TGCAGAGTTT GAGTCCAGAT CCCAAAGCCC 300
AGTACACAAG TATCTACGGA GCCCTCAAGA AAATCATGCG GACCGAAGCT TCTGGAGGCC 360
CTTGCGAGGC GTCAACGTCA TGATCATGGG TGCAGGGCCR GCCCATGCCA TGTATTTTGC 420
25 CTGCTATGAA AACATGAAAA GGACTTTAAA TGACGTTTTC CACCACCAAG GAAACAGCCA 480
CCTAGCCAAC GGTATTTTGA AAGCGTTTGT CTGGAGTTAG AAAGTTCTCT TCTTCAACAC 540
30 GTCCCTCCCC AGGGTGTTCC TCCTGTGAC CCAGCCGCTT CGACTTCGGC CCGCTTGCTC 600
ACGAATAAAG AACTCAGAGT TGTGTGTGCA ATGCACACCC AGACACACGC ACGCACACAC 660
ACGCGCGCGC ACACACATGC TTTTCTCTGT TCCCCTCCGC TTTCTGAAGC CTGGGGAGAA 720
35 ATCAGTGACA GAGGTGTTTT GGTTTTATG TTATGTGGGT TTTCTTTTGT ATTTTTTTTG 780
TTTGTTTTGT TTTTAAACAT TCAAAGCAA TTAATGATCA GACATAGGAG AAACCCTGAA 840
40 TAGAAACAAA ACTTTTGAAT GCTGGATTCA AAAAAAAAAA AAAGTTATCT GGACAGCTTC 900
TTTGAGACTA TTTAAAACT GGTACAACAG GTCTCTACAA CGCCAAGATC TAACTAAGCT 960
TTAAAAGGTC AAGAAGTTTT ATGGCTGACA AAGGACTCGC GCAACGCAGA AGGCCTTTCC 1020
45 CACCTTAAGC TTCCGGGGAT CTGGAATTT TACCCCATC CTCTCTGTT TGTCTGAGTC 1080
TCATCTCTCT GCAAGCAAGG GCTGAAATCA TTTGTTTTGG TTGTTTGTAG GGAGAGAGGC 1140
50 GGGGTGGGG GGTGCAAAATC TGCCAGCAGC TCTTACGTAA GGCATGTTTT ATGGGGAGG 1200
GCTGAGCTTT TATTTTCTCC TCTCCAGTGG GGTGGGCTTT TATTGTTTCT TGTMTGGGTT 1260
TGGAATGGAA ATATGGATAG CAGCATAAAG TACTTTTATT TTGACAAAAT TCATTTTTTT 1320
55 CAACAATGGA GACATAGATT TGACCCACAA TAACTTCTCC CCTCTCTTT TACTCTGCT 1380
CAAAAAGCAT CTCTCTCCC ATTACCCAAC CTTGGTCATA AGTGTGCCTG GCTGGTTTGC 1440
60 AGATATTTGT TCTGCTTTGT AAAAATTGGC CATTAGTGCA TTTATTGAGA TGATCTCTAA 1500

425

AGAGCTATGC CCTGACCTAC CCCTGATTCT ATGACATTGG GGCCCTTCTT TTGCTGAAAC 1560
TGCCCTTACGT AATGGTTTTA CTCCTTGAAA GAGATTTGAC GGAATCCATT TTATGCCAAG 1620
5 TGCTGCCCTG CACTGT'TTCT GCAATATGTG GTGTATGCTG TGGTGATCTT GCTGGGAATG 1680
ATTATAAGTG TGTGTGTGGT GGGGGAGTGG GTATTACATG CATTGCTGAA GAGTCAAAAA 1740
10 AAAAAAAAAA AAACTCGA 1758

15 (2) INFORMATION FOR SEQ ID NO: 174:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 888 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

25 CTGTTAGAAT GCCCAGTTTA CCTGGATGGC AACCCAACAG TGCTCCTGCC CACCTGCCCC 60
TCAATCCTCC TAGAATTGAG CCCCCAATTG CCCAGTTACC AATAAAAACT TGTACACCAG 120
CCCCAGGGAC AGTCTCAAAT GCAAATCCAC AGAGTGASMC ACCACCTCGG GTAGAATTG 180
30 ATGACAACAA TCCCTTTAGT GAAAGTTTTC AAGAACGGGA ACGTAAGGAA CGTTTACGAG 240
AACAGCAAGA GAGACAACGG ATCCAACCTCA TGCAGGAGGT AGATAGACAA AGAGCTTTGC 300
35 AGCAGAGGAT GGAAATGGAG CAGCATGGTA TGGTGGGCTC TGAGATAAGT AGTAGTAGGA 360
CATCTGTGTC CCAGATTCCC TTCTACAGTT CCGACTTACC TTGTGATTTT ATGCAACCTC 420
TAGGACCCCT TCAGCAGTCT CCACAACACC AACAGCAAAT GGGGCAGGTT TTACAGCAGC 480
40 AGAATATACA ACAAGGATCA ATTAATTCAC CCTCCACCCA AACTTTCATG CAGACTAATG 540
AGCGAGGCAG GTAGGCCCTC CTTCAATTTGT TCCTGATTCA CCATCAATCC CTGTTGGAAG 600
45 CCCAAATTTT TCTTCTGTGA AGCAGGGACA TGGAAATCTT TCTGGGACCA GCTTCCAGCA 660
GTCCCCAGTG AGGCCTTCTT TTACACCTGC TTTACCAGCA GCACCTCCAG TAGCTAATAG 720
CAGTCTCCCA TGTGGCCAAG ATTCTACTAT AACCCATGGA CACAGTTATC CGGGATCAAC 780
50 CCAATCGCTC ATTCAGTTGT ATTCTGATAT AATCCAGAG GAAAAAGGN AAAAAAARA 840
AMAAAAARA ARAAAGGAGA TGATGATGCA GAATTCACCC AAGGCTCC 888

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(2) INFORMATION FOR SEQ ID NO: 175:

60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2379 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

	GGCAGAGCTA GTGTGGACTC CATCCCCCTG GAGTGGGATC ACGNCTATGA CCTCAGTCGG	60
10	GACCTGGAGT CTGCAATGTC CAGAGCTCTG CCCTCTGAGG ATGAAGAAGG TCAGGATGAC	120
	AAAGATTCTT ACCTCCGGGG AGCTGTTGSC TTATCAGGGG ACCACAGTGC CCTAGAGTCA	180
15	CAGATCCGAC AACTGGGCAA AGCCTGGATG ATAGCCGCTT TCAGATACAG CAAACCGAAA	240
	ATATCATTCG CAGCAAAACT CCCACGGGGC CGGAGCTAGA CACCAGCTAC AAAGGCTACA	300
	TGAAACTGCT GGGCGAATGC AGTAGCAGTA TAGACTCCGT GAAGAGACTG GAGCACAAAC	360
20	TGAAGGAGGA AGAGGAGAGC CTTCTGGCTT TTGTTAACCT GCATAGTACC GAAACCCAAA	420
	CGGCTGGTGT GATTGACCGA TGGGAGCTTC TCCAGGCCCA GGCATTGAGC AAGGAGTTGA	480
	GGATGAAGCA GAACCTCCAG AAGTGGCAGC AGTTTAACTC AGACTTGAAC AGCATCTGGG	540
25	CCTGGCTGGG GGACACGGAG GAGGAGTTGG AACAGCTCCA GCGTCTGGAA CTCAGCACTG	600
	ACATCCAGAC CATCGAGCTC CAGATCAAAA AGCTCAAGGA GCTCCAGAAA GCTGTGGACC	660
30	ACCGCAAAGC CATCATCCTC TCCATCAATC TCTGCAGCCC TGAGTTCACC CAGGCTGACA	720
	GCAAGGAGAG CCGGGACCTG CAGGATCGCT TGTSGCAGAT GAATGGGCGC TGGGACCGAG	780
	TGTGCTCTCT GCTGGAGGAG TGGCGGGGCC TGCTGCAGGA TGCCCTGATG CAGTGCCAGG	840
35	GTTTCCATGA AATGAGCCAT GGTTCGCTTC TTATGCTGGA GAACATTGAC AGAAGGAAAA	900
	ATGAAATTGT CCCTATTGAT TCTAACCTTG ATGCAGAGAT ACTTCAGGAC CATCACAAC	960
40	AGCTTATGCA AATAAAGCAT GAGCTGPTGG AATCCCAACT CAGAGTAGCC TCTTTGCAAG	1020
	ACATGTCTTG CCAACTACTG GTGAATGCTG AAGGAACAGA CTGTTTAGAA GCCAAAGAAA	1080
	AAGTCCATGT TATTGGAAAT CGGCTCAAAC TTCTCTTGAA GGAGGTCAGT CGTCATATCA	1140
45	AGGAACTGGA GAAGTTATTA GACGTGTCAA GTAGTCAGCA GGATTTGTCT TCCTGGTCTT	1200
	CTGCTGATGA ACTGGACACC TCAGGGTCTG TGAGTCCCAY ATCAGGAAGG AGCACCCCAA	1260
50	ACAGACAGAA AACGCCACGA GGCAAGTGTA GTCTCTCACA GCCTGGACCC TCTGTCAGCA	1320
	GTCCACATAG CAGGTCCACA AAAGGTGGCT CCGATTCTC CTTTCTGAG CCARGGCCAG	1380
	GTGCGTCCGG CCGCGGCTTC CTGTTGAGAG TCCTCCGAGC AGCTCTTCCC CTTGAGCTTC	1440
55	TCCTGCTCCT CCTCATCGGG CTGCTGCTCC TTGTACCAAT GTCAGAGGAA GACTACAGCT	1500
	GTGCCCTCTC CAACAACCTT GCCCGGTCAT TCCACCCCAT GCTCAGATAC ACGAATGGCC	1560
60	CTCCTCCACT CTGAACTAAG CAGATGCCAT CTGCAGAAGT GCTGGTAGCA TAAGGAGGAT	1620

CGGGTCATAA GCAATCCCAA ACTACCAACA AGAGGACCTT GATCTTGGCG AAAGCCMTCG 1680
GTGTGGCAGC TTTAGCCTCC TCCAGATCAC ATGTGTGCAA ATTATGGCTT CAGAGGTGGA 1740
5 AGATAAACAG TGACGGGGGA ACAAACAGAC AACAAGAAGG TTTGGAAGAA ATCTGGTTTG 1800
AGACTCTGAA CCTTAGCACT AAGGAGATTG AGTAAGGACC TCCAAAGTTC CCCGGACTCA 1860
10 TGAATTCTGG GCCCTTGGCC NATTCTGTGC ACAGCCAAGG ACTTCAGTAG ACCATCTGGG 1920
CAGCTTTCCC ATGGTGCTGC TCCAACCATC AGATAAATGA CCTTCCAAG CACCATGTCA 1980
GTGTCGTACA ATCTACCAAC CAACCACTGC TGAAGAGATT TTAGAACCCTT GTAACATACA 2040
15 ATTTTAAAGA GCTTATATGG CAGCTTCCTT TTTACCTTGT TTTCTTTTGG GGCATGATGT 2100
TTTAACCTTT GCTTTAGAAG CACAAGCTGT AAATCTAAAA GGCACCTTTT TTTAGAGGTA 2160
20 TAAAGAAAAA CTAGATGTAA TAAATAAGAT CATGGAAGGC TTTATGTGAA AAAAGTTGAA 2220
TGTATAGTA AAAAAAAG ATATTTATGT ATGTACAGTT TGCTAAAGCC AAGTTTGTGT 2280
TGTATTGATT TCTTTGCATT TATTATAGAT ATTATAAAAT AAAAAAAAAA AAAAAAAAC 2340
25 TCGAGGGGGG GCCCGGTACC CAATTCGCCC TATAGTGAG 2379

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(2) INFORMATION FOR SEQ ID NO: 176:

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 1348 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

40

GCGCCTTCAC GATGCCGGCG GTCAGTGGTC CAGGTCCCTT ATTCTGCCTT CTCCTCCTGC 60
TCCTGGACCC CCACAGCCCT GAGACGGGGT GTCCTCCTCT ACGCAGGTTT GAGTACAAGC 120
45 TCAGCTTCAA AGGCCCAAGG CTGGCAITGC CTGGGGCTGG AATACCCTTC TGGAGCCATC 180
ATGGAGGTGA GGGGCAGGGG TGGGGACCGC TATGCCCAGG GTCCCTCAAA GTGCTGGAGG 240
GGCTGTRACT TGGTGGGGAG TGGGTCTGTC ACAGCCATCC TCTGTCCAGG GTGGGGCAAG 300
50 GCCTGGGACA GTGCCAGGCA CCCCAGGACC CCTTCCAGGC TTGTCTCCTG CTCCACCGCC 360
TCAACACCCC CCACCCTGC CCAAGCTGTT TCTCCTCTGC CTCTCTNNIT CCCTGCCCCA 420
55 GGACTTCTCT CTCTCCTCT GCCTCTCCTT GGACCCCTGC CCTTCTCTA CCTCTGACCT 480
GTGAACACAC AGACACATGC TCACACACTA AGTCCCARGC ACACMSAAAG GCAATGTGGA 540
CCAGCACAAA CCTCCACTCT CCCGGCTCCA TCCCACGGG CCTGTGGCTG GCCATGAAAA 600
60

CTGGGGGCTA CCTGGAGGGA AGCATCCTCA TCCCAGGTGA GTGGGCACCA GCCCTTCCCT 660
 GTATGTGTGT TGTGGGTGGA AGCAGGCATG AGAGCATCTT AGCCCATAGG TTTGTATTCA 720
 5 GGGACTTCCA AACCCAGACC TACAAAGAGT GTGTCTTCTA CCAGATCTTG TTCAAAAAAG 780
 GGTTTGTGAT GATGGAAC TA CACGATAGAG GGAGTGAGCA AGAACAAATGA GGATTAGAGT 840
 10 GGAGCGTGAA ATAGTCTAGG AGCATGGCTT CCAAAACATA TGCTGTGAGG TCTGTCCACC 900
 TGAGAGTTGG GCCATGGATT TAATTCTGAG CCTCTTAGCA GGCAAAGCAA AGACAGAAAG 960
 CAGATCGGCT GTGGATTCT GTCTATAAAA TGTGAGTTCT TGGCCGGGTG CGGTGGCTCA 1020
 15 CGCCTGTAAT CCCGGCGCTT TGGGAGGCCA GGGCGGATGG GTCGGGAGGT CAGGAGGTTG 1080
 GAAACCATCC TGGCCGGAAT GGTGAAGCCC TGACTCTACT AGAAGTGCAA AGATTGGCTG 1140
 20 GGTGTGGTGG CGTGCGCCTG TGGTCCCAGC TTCTCGGGAG GCTGAGGCGG GAGAGTTGCT 1200
 TGGGCCTGGG AGGCCGAGGT TGCGGTGAGC TGAGATCCTG CCAITGCACT TCAGCCTGGG 1260
 CACAGAGCCA GACTCTGGCT CAAAAA AAAA AAAA ACTCGAGGGG GGCCCGTACC 1320
 25 CAATTGCGCCG NATATGATCG TAAACAAT 1348

30 (2) INFORMATION FOR SEQ ID NO: 177:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1502 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

40 CTCAAAATAA ATAAATAAAT AAAAATTTGT ATTCCATTGA TTTGGGTAGA CACCAGGAAT 60
 GTGCATTTCT AACAAGCTTT CCAGGCGATC CTATAGTAAG TCATCTGTGG ACTACTTTAA 120
 45 GAAACTCTTC TATAGAGAAT GGAGTTGGAT TAATAATAGG TGATTTTTTA CACTGGACTG 180
 ATTCACAAGA ACCTAAACAG TAGTCCATGA AGCTGCTCAT CTGTGGTAAC TATTTGGCCC 240
 CGTCTCACTC TGAAAGCAGC AGGAGATGTT GTTTACTTTG TTTCTATCCC CTTTGTCTGG 300
 50 AGATTAATTT TGAATGAAA GTTTTCTCTCT CTATGCCATT CCTGGTTCTT TTCCAAAGCC 360
 TCATACAAGA GGATTAGGTC ACAATGCATG CATTACCTTT TAAAAGAATG CGATATTGAT 420
 55 ACCGATGCTT ACTTTTTTTT TTTTNACTA CTGTTTTAT TCCTTCCAGN AAAGTATAGC 480
 CCGCCTTTCT ATAGCATAGT TCTCTTAGG TGGAAATGATT CCTATAAGAT TTCTCATTAT 540
 TAAATCATGC ATTTTCAAG ATGGAATCAA TMTTGTATT AATCTAAGCT GATATTCTCA 600
 60 TTTGTTAGAA GAACAACCTA CATGCTAGAG AGAGAGGAGG AAATATACCC ACGACCACAC 660

AGCCAGTTAG TATCCAGTTG GTGCTGGACT CCAGCCAGGT GTCCTGCCTC ATGGTAGTTA 720
AATGATATAT AGAAAAGGTA AATTTTAA GAAATATTTA TTAATATATT CCTATAAAAC 780
5 ATTTTAAAGG TAACCACATA AAAATGGTTA ATTTTCCAT TCCAAAGTAA ATGCTAAGCA 840
TGTTTATTAA TGAAGCAGTA CTCTGATTA GTATATGACA TTCTGAAGTT AATTAAACTC 900
10 ATTGCACTAA ATGTGTCTTC CTGGTATAG TGGAGGATTT GAGGATGGA ATATAGAGTA 960
GAGTGCCTGC TTAAGCCTGG GAGCCCATCT TTATAGCTAT TTGATGTAAG AAAAGAGACA 1020
TGGNCCATTT CTAAACTATA TAAGTGAGT GTGTCTATTC CCAGCAGATA TAAAGGAAAA 1080
15 AGGAAACTTT TTTGATTCCC ACCTTCCCAG CCTCACCTAG CCATCTTCCA GCCTCAAATA 1140
TAGAGATGTT AGTGCAAGGT CCTGGGCTCT AGGTGATCAT TTCATAAGTC CTTTACAGAT 1200
20 AAAGAAAAAG TAGTGTGTTT ATGTTTGT TTAAGTAACC CCAAAACAAA TTTATATTGT 1260
ATTGAGCAAA ATTGGAATTC AGGTGTTTAA TTTTAGAACA TGAAGTGCCT GCTGTTTAA 1320
GCATTGACTT GTATAAAAAG AATGTCATGT CTCCAGTAAG CTTATGGGTT TTCTCATTTT 1380
25 TAGGTATATG GCTTTTAATC ATGTAAAGTG AACATTAGT TTTCTTGCAT TTTATTACAG 1440
GTTCCTTGTT GCAATAAAGA TGCTGCTGAA ATTAATTGAA AAAAAAAAAA AAAAAAACTC 1500
30 GA 1502

35 (2) INFORMATION FOR SEQ ID NO: 178:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 1637 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

45 ATTTTCTAGC CCACAAGGAC TGAAGTTCAG ATCCAAAAGT TCACTTGCTA ATTATCTTCA 60
CAAAAATGGA GAGACTTCTC TTAAGCCAGA AGATTTTGAT TTTACTGTAC TTTCTAAAAG 120
GGGTATCAAG TCAAGATATA AAGACTGCAG CATGGCAGCC CTGACATCCC ATCTACAAAA 180
50 CCAAAGTAAC AATTCAAACCT GGAACCTCAG GACCCGAAGC AAGTGCAAAA AGGATGTGTT 240
TATGCCGCCA AGTAGTAGTT CAGAGTTGCA GGAGAGCAGA GGA CTCTCTA ACTTTACTTC 300
CACTCATTTG CTTTGTAAAG AAGATGAGG TGTGATGAT GTTAACCTCA GAAAGGTTAG 360
AAAGCCCAA GGAAAGGTGA CTATTTTGAA AGGAATCCCA ATTAAGAAAA CTAAAAAGG 420
ATGTAGGAAG AGCTGPTCAG GTTTGTTCM AAGTGATAGC AAAAGAGAAT CTGTGTGTAA 480
60

430

	TAAAGCAGAT GCTGAAAGTG AACCTGTTGC ACAAAAAAGT CAGCTTGATA GAACTGTCTG	540
	CATTTCATGAT GCTGGAGCAT GTGGTGAGAC CCTCAGTGTG ACCAGTGAAG AAAACAGCCT	600
5	TGTAAAAAA AAAGAAAGAT CATTGAGTTC AGGATCAAAT TTTTGTCTG AACAAAAAC	660
	TTCTGGCATC ATAAACAAAT TTTGTTGAGC CAAAGACTCA GAACACAACG AGAAGTATGA	720
	GGATACCTTT TTAGAATCTG AAGAAATCGG AACAAAAGTA GAAGTTGTGG AAAGGAAAGA	780
10	ACATTTCAT ACTGACATTT TAAACGTGG CTCTGAAATG GACAACAAC GCTCACCAAC	840
	CAGGAAAGAC TTCCTGAAG ATACCATCCC ACGGAACACA GATAGAAAGA AGGAAAACAA	900
15	GCCTGTATTT TTCCAGCAAA TATAACAAAG AAGCTCTTAG CCCCCACGA CGTAAAGCCT	960
	TTAAGAAATG GACACCTCCT CGGTCACCTT TTAATCTCGT TCAAGAAACA CTTTTTCATG	1020
	ATCCATGGAA GCTTCTCATC GCTACTATAT TTCTCAATCG GACCTCAGGC AAAATGGCAA	1080
20	TACCTGTGCT TTGGAAGTTT CTGGAGAAGT ATCCTTCAGC TGAGGTAGCA AGAACCGCAG	1140
	ACTGGAGAGA TGTGTCAGAA CTCTTAAAC CTCTTGGTCT CTACGATCTT CGGGCAAAAA	1200
25	CCATTGTCAA GTTCTCAGAT GAATACCTGA CAAAGCAGTG GAAGTATCCA ATTGAGCTTC	1260
	ATGGGATTGG TGCACCCTGA AGACCACAAA TTAAATAAAT ATCATGACTG GCTTTGGGAA	1320
	AATCATGAAA AATTAAGTCT ATCTTAAACT CTGCAGCTTT CAAGCTCATC TGTATATGCAT	1380
30	AGCTTTGCAC TTCAAAAAAG CTTAATTAAG TACAACCAAC CACCTTTCCA GCCATAGAGA	1440
	TTTTAATTAG CCCAACTAGA AGCCTAGTGT GTGTGCTTTC TTAATGTGTG TGCCAATGGT	1500
35	GGATCTTTGC TACTGAATGT GTTTGAACAT GTTTTGAGAT TTTTTTAAAA TAAATTATTA	1560
	TTTGACAACA ATCCAAAAA AAAAAA AAAA AAAAAA AAAAAA AAAAAA	1620
40	AAAAA AAAAAA	1637

45 (2) INFORMATION FOR SEQ ID NO: 179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2911 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

55	GGTGGTTTTT GTTCTGCAAT AGGCGGCTTA GAGGGAGGGG CTTTTTCGCC TATACCTACT	60
	GTAGCTTCTC CACGTATGGA CCCTAAAGGC TACTGCTGCT ACTACGGGGC TAGACAGTTA	120
	CTGTCTCAGC TCTAGGATGT GCGTCTCTCC ACTAGAAGCT CTTCTGAGGG AGGTAATTAA	180
60	AAAACAGTGG AATGGAAAAA CAGTGCTGTA GTCATCCTGT AATATGCTCC TTGTCAACAA	240

	TGTATACATT CCTGCTAGGT GCCATATTCA TTGCTTTAAG CTCAAGTCGC ATCTTACTAG	300
	TGAAGTATTC TGCCAATGAA GAAAACAAGT ATGATTATCT TCCAAC TACT GTGAATGTGT	360
5	GCTCAGAACT GGTGAAGCTA GTTTTCTGTG TGCTTGTGTC ATTCTGTGTT ATAAAGAAAG	420
	ATCATCAAAG TAGAAATTG AAATATGCTT CCTGGAAGGA ATTCTCTGAT TTCATGAAGT	480
10	GGTCCATTCC TGCTTTCTT TATTTCTCTG ATAAC TIGAT TGTCTTCTAT GTCCTGTCCT	540
	ATCTTCAACC AGCCATGGCT GTTATCTTCT CAAATTTTAG CATTATAACA ACAGCTCTTC	600
	TATTCAGGAT AGTGCTGAAG ANGCGTCTAA ACTGGATCCA GTGGGCTTCC CTCCTGACTT	660
15	TATTTTGTG TATTGTGGCC TTGACTGCCG GGACTAAAAC TTTACAGCAC AACTTGCCAG	720
	GACGTGGATT TCATCAGAT GCCTTTTCA GCCCTTCCAA TTCCTGCCTT CTTTTCAGAA	780
20	ATGAGTGTCC CAGAAAAGAC AATTGTACAG CAAAGGAATG GACTTTTCCT GAAGCTAAAT	840
	GGAACACCAC AGCCAGAGTT TTCAGTCACA TCCGTCTTGG CATGGGCCAT GTTCTTATTA	900
	TAGTCCAGTG TTTTATTTCT TCAATGGCTA ATATCTATAA TGAAAAGATA CTGAAGGAAG	960
25	GGAACCAGCT CACTGAARGC ATCTTCATAC AGAACAGCAA ACTCTATTTC TTTGGCATT	1020
	TGTTTAATGG GCTGACTCTG GGCTTCAGA GGAGTAACCG TGATCAGATT AAGAACTGTG	1080
30	GATTTTTTTA TGGCCACAGT GCATTTTCAG TAGCCCTTAT TTTTGTAAC TGCATTCCAGG	1140
	GCCTTTCAGT GGCTTTCATT CTGAAGTCC TGGATAACAT GTTCCATGTC TTGATGGCCC	1200
	AGGTTACCAC TGTCATTATC ACAACAGTGT CTGTCTGGT CTTTGACTTC AGGCCCTCCC	1260
35	TGGAATTTTT CTGGAAGCC CCATCAGTCC TTCTCTCTAT ATTTATTTAT AATGCCAGCA	1320
	AGCCTCAAGT TCCGGAATAC GCACCTAGGC AAGAAAGGAT CCGAGATCTA AGTGGCAATC	1380
40	TTTGGGAGCG TTCCAGTGGG GATGGAGAAG AACTAGAAAG ACTTACCAA CCAAGAGTG	1440
	ATGAGTCAGA TGAAGATACT TTCTAACTGG TACCCACATA GTTTCAGCT CTCTGAACC	1500
	TTATTTTCAC ATTTTCAGTG TTTGTAATAT TTATCTTTTC ACTTTGATAA ACCAGAAATG	1560
45	TTTCTAAATC CTAATATTCT TTGCATATAT CTAGCTACTC CCTAAATGGT TCCATCCAAG	1620
	GCTTAGAGTA CCCAAAGGCT AAGAAATTCT AAAGAACTGA TACAGGAGTA ACAATATGAA	1680
50	GAATTCATTA ATATCTCAGT ACTTGATAAA TCAGAAAGTT ATATGTGCAG ATTATTTTCC	1740
	TTGGCCTTCA AGCTTCCAAA AACTTGTA TAATCATGTT AGCTATAGCT TGTATATACA	1800
	CATAGAGATC AATTGCCAA ATATTCACAA TCATGTAGTT CTAGTTTACA TGCCAAAGTC	1860
55	TTCCCTTTTT AACATTATAA AAGCTAGGTT GTCTCTTGAA TTTTGAGGCC CTAGAGATAG	1920
	TCATTTTGCA AGTAAAGAGC AACGGGACCC TTTCTAAAA CGTTGGTTGA AGGACCTAAA	1980
60	TACCTGGCCA TACCATAGAT TTGGGATGAT GTAGTCTGTG CTAAATATTT TGCTGAAGAA	2040

GCAGTTTCTC AGACACAACA TCTCAGAATT TTAATTTTAA GAAATTCATG GGAAATTGGA 2100
 TTTTGTGAAT AATCTTTTGA TGTTTAAAC ATTGGTTCCC TAGTCACCAT AGTTACCACT 2160
 5 TGTATTTTAA GTCATTTAAA CAAGCCACGG TGGGGCTTTT TTCTCCTCAG TTTGAGGAGA 2220
 AAAATCTTGA TGTCATTACT CCTGAATTAT TACATTTTGG AGAATAAGAG GGCATTTTAT 2280
 10 TTTATTAGTT ACTAATTCAA GCTGTGACTA TTGTATATCT TTCCAAGAGT TGAAATGCTG 2340
 GCTTCAGAAT CATACCAGAT TGTCAGTGAA GCTGATGCCT AGGAACTTTT AAAGGGATCC 2400
 TTTCAAAAGG ATCACTTAGC AAACACATGT TGACTTTTAA CTGATGTATG AATATTAATA 2460
 15 CTCTAAAAAT AGAAAGACCA GTAATATATA AGTCACTTTA CAGTGCTACT TCACACTTAA 2520
 AAGTGCATGG TATTTTTCAT GGTATTTTGC ATGCAGCCAG TTAACCTCTG TAGATAGAGA 2580
 20 AGTCAGGTGA TAGATGATAT TAAAAATTAG CAAACAAAAG TGACTTGCTC AGGGTCATGC 2640
 AGCTGGGTGA TGATAGAAGA GTGGGCTTTA ACTGGCAGGC CTGTATGTTT ACAGACTACC 2700
 ATACTGTAAA TATGAGCTTT ATGGTGTGAT TCTCAGAAAC TTATACATTT CTGCTCTCCT 2760
 25 TTCTCCTAAG TTTCATGCAG ATGAATATAA GGTAATATAC TATTATATAA TTCATTTGTG 2820
 ATATCCACAA TAATATGACT GGCAAGAATT GGTGGAAATT TGTAATTAAA ATAATTATTA 2880
 30 AACCTAAAAA AAAAAAAAAA AAAAAGCTCG G 2911

35 (2) INFORMATION FOR SEQ ID NO: 180:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 519 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

45 GGCACGAGCC CCAGGCCAGC CAGGCCAGG CCTACTTTGG CCACCTTAA ATTAGAATGT 60
 GGGGTCAGGG GTCACAGAAA AGCCATTTCT CTGACCTAGT GTTTGGCGTC CGGGAACCTT 120
 GTGCCCAACC TTCAGACCCT GGCAGTCTC ACTGAGGCCA TTGGCCAGA GCCCGCCATC 180
 50 CCCCAGARACC CCGGGAGGCC GCCTGTTGCC ACGTCCACAC CTGCCACACC CTCTGCCGGG 240
 CCCCAGCCCC TCCCAACCGG GACCGTGCTG GTCCTGCGG GTCCCTGCCCC ACCTTGCCCTT 300
 55 GGGGAGGCAT GGGCCCTCCT CCTCCACCC TGCCGGCCGT CACTCACCTC TTGCTTCTGG 360
 TCCCCAGGC CTAGCCCTTG GAAGGAGACA GGAGTCTAGG GAGGCTGAAG CCCACTCCCG 420
 GGGAGGCCCG TGCTCTCCA GCCCCAGGA CAGCAAGGAA AAGAGAAGAG AGCAGAGCAT 480
 60

TTCATGGCTC TAATAAAAAA AAAAAAAAAA AAAACTCGA

519

5

(2) INFORMATION FOR SEQ ID NO: 181:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 968 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

15 TCCCCCTGGG GCCGGA AAAA GCGGGGTTGG CCTGMCATT GGTNTCCAT GCCCCCCGCC 60
CATGCCCCAG TACTAGCCTG CAGTCCCAAT GTAGCCCCCTC CCTCYTCCMA GAGCCCYTCM 120
20 AACCGCCCCG STCANTTGTG ATTTTCAGGAG GATTTGATGA AGATGTTAAA GCGAAAGTGG 180
AGAACCTTCT CCGGATTTCC AGCCTGGAAA AAACGGACCC TGTTAGGCAA GCACCCTGCA 240
GCCCTCCCTG TCCCTTCTT CCCCTCCCCT TCYCCCGCCC GTGGAGACAG CTGTTYTCAG 300
25 CAGGGCTCTC CGCAGGGAGG GGGCCGGCTC CTTCCCTGGC AGCAACATCC TTGCCCTTGT 360
CACACAAGTC AGCCTCCATC TGCGCAGCTC TGTGGATGCG CTGCTGGAGG GCAACAGGTA 420
30 TGTCACCTGC TGGTTCAGCC CCTACCACCG CCAGCGGAAG CTCATCCACC CGGTCATGGT 480
TCAGCACATC CAGCCCGCAG CGCTCAGCCT CCTGGCACAG TGGAGCACCC TCGTGCAGGA 540
GCTGGAGGCT GCCCTGCAGC TGGCTTTCTA CCCGGATGCC GTGGAGGAGT GGCTGGAGGA 600
35 AAACGTGCAC CCCAGCCTGC AGCGGCTGCA ARCTCTGCTG CAGGACCTCA GCGAGGTGTC 660
TGCCCCCCCC CTGCCACCCA CCAGCCCTGG CAGGGACGTT GCTCAGGACC CCTGAGGGGA 720
40 GAGCTCATGC CAGGGGGCTC CTGCTGGAGG CTGGGGGGGC TCTGCWYTKY CWWWTGGCCT 780
GGGCAATACG GCCCAGTGG GCGTCGTGCC CTCTGGCCCA GCAGTGTCTT GCCCACACTC 840
AGTTCCTGAG GGCCCTGGGC AGCCCTGGG GGAGAGACTA GAAAACACAG AAGGAAGCAG 900
45 CACAGGGAGA CCCGCTTGT GATCTGCATG TGTGACACTG ATTCTTTGGA AATAAAGAGT 960
GGAAGCTG 968

50

(2) INFORMATION FOR SEQ ID NO: 182:

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1128 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

	TGTAAAAGTT ATCAGTAATC CTAATTCCTT TCCTGGGTTT TCCTTTTGTC ACTTATTAAT	60
5	CAGTTTTTGA AAGGACGAAT GAATTTAGAG ATGTACTCTG GAGCAGTATC ATGTTAAACC	120
	AGGGGTATAT TAGAAAAATC ATCCTCATAA TCATTCTGGG AAGTTTTTCC TCCCCAAAAA	180
	AAGCCATCCT GATGGGTTTT CAAAACCAGA AAAAAGCTCT TAATGAGGAA CAGACCACTG	240
10	GAGTACCCAT GAGCATCTCA GGAAACTGA GACCCCTGAG AAGCCTTGAT TTCGTGCAAC	300
	CCCCAAGGTT TCAGAGCCAG CAGCCCACTG CTGTGGTTGA CAGACGTGGT TTTKTGGRGA	360
15	AAGCAGCCAG AGGCCAGGAA TTTTCAGAGT CGTGAGTCAC GRTYTCCAC CCAAGATTAG	420
	AGCAMAGATT AGCCATACTG AGATTTGGTA AAATCAITCT GTCTAAGCAA TGGAGGTGTG	480
	TGCAMACGTG CAGTGCCTGT TCACAGGGGA TGCAGGCAGA TCSYGGGTTT AGGATGGGGR	540
20	AGGCCACCGC ACCCCCYTTC AYTGCTCTGC ACCTGCTCCC TCACGTGGAC ACTGTCCACA	600
	ACTGTGGCTC TCACAGGACA GTTGCCCAAG GAGCTCATAT CTTATTGGAG ATAGGGGGTC	660
25	GTACAGGTGA CATTCATGAG CAGTGTGAGC CGGGTGACAT GGGGGTGTC ACCCAGCATC	720
	TGTCCAGGAG CTCCTCCTGC AGCGGCTCTG GCAGGTGGCC TGAGGCTCCT TTTTGAGAGA	780
	GAACTGTTTG GCCCTCCTGT CTCCTCTCCT CTGATCTGTT CTTTCTTGGA ACACCACCCA	840
30	AGAACGTCAC CTCCTCCATC AGATTGTGAG CTCCTGGAGG GCAGGAGCTG TGTCTTCTA	900
	TTTATCTTCC TATCCCCAGA ACCTTGACACA GATCCTGGAA TGTGGTAGGT GCTCAGTAAA	960
35	TGTGTGTTGA ATAAATGAAT GAATGAATGA ACAAATGAAT GAATTTGCTT ACTTCAAGGC	1020
	AAAAGAACCA TGAAACTGTA TTTTGAGTTT CTATGTTATA GCAGTCAGCA AATCCTATTA	1080
40	AATACTTTGT GTTCCAAGC AAAAAAAAAA AAAAAAAAAA AAACTCGA	1128

(2) INFORMATION FOR SEQ ID NO: 183:

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

55	CCGCGGCGTC TGACCTCATG GCGTAGAGCC TAGCAACAGC GCAGGCTCCC AGCCGAGTCC	60
	GTTATGGCCG CTGCCGTCCC GAAGAGGATG AGGGGGCCAG CACAAGCGAA ACTGCTGCCC	120
	GGGTCGGCCA TCCAAGCCCT TGTGGGGTTG GCGCGGCCGC TGGTCTTGGC GCTCCTGCTT	180
60	GTGTCCGCGC CTCTATCCAG TGTGTATCA CGGACTGATT CACCGAGCCC AACCGTACTC	240

	AACTCACATA TTTCTACCCC AAATGTGAAT GCTTTAACAC ATGAAAACCA AACCAAACCT	300
	TCTATTTCCC AAATCAGCAC CACCCTCCCT OCCACGACGA GTACCAAGAA AAGTGGAGGA	360
5	GCATCTGTGG TCCCTCATCC CTCGCCTACT CCTCTGTC TC AAGAGGAAGC TGATAACAAT	420
	GAAGATCCTA GTATAGAGGA GGAGGATCTT CTCATGCTGA ACAGTTCTCC ATCCACAGCC	480
10	AAAGACACTC TAGACAATGG CGATTATGGA GAACCAGACT ATGACTGGAC CACGGGCCCC	540
	AGGGACGACG ACGAGTCTGA TGACACCTTG GAAGAAAACA GGGGTTACAT GGAAATTGAA	600
	CAGTCAGTGA AATCTTTTAA GATGCCATCC TCAAATATAG AAGAGGAAGA CAGCCATTTT	660
15	TTTTTTCATC TTATTATTTT TGCTTTTGC ATTGCTGTG TTTACATTAC ATATCACAAC	720
	AAAAGGAAGA TTTTCTTCT GGTCAAAGC AGGAAATGGC GTGATGGCCT TTGTTCCAAA	780
20	ACAGTGAAT ACCATCGCCT AGATCAGAAT GPTAATGAGG CAATGCCTTC TTTGAAGATT	840
	ACCAATGATT ATATTTTTTA AAGCACTGTG ATTTGAATTT GCTTATGTAA TTTTATTTGC	900
	TTGACTTTTT ATATGATATT GTGCAAATGT TTGCCATAGG CAATTGGTAC TTAAATGAGA	960
25	GGTGAGTCTC TCTTTGCCT TGGTGCTTTG GAAATTAAAT GTCACAAACG AGTATATAAT	1020
	TTTTTATCTG TACTTTTAGA GCTGAGTTA ATCAGGTGTC CAAAATGTGA GTTAAACATT	1080
30	ACCTTATATT TACTCTGTTA GTTTTATTG TTTTAGATTT ATTATGCTTC TTCTGGAAGT	1140
	ATTAGTGATG CTACTTTTAA AAGATCCCAA ACTTGTAAC TAAATCTGAC ATATCTGTTA	1200
	CTGCTGACTC ACATTCAATC TCCGCCATTC AAATACTATT TTTTATCCAC ATTTTTTTTT	1260
35	GTTCCTCAAC TGTAATGTAC AAGGATATGT GTGATAATGC TTGGATTG AGTAATATTT	1320
	TTTTTCTCTC CAAGAAACT GCTTTGGATA TTTTATAGATA ATTTAAACAT AATTAGGAT	1380
40	AATGATATTG CTCAATCTGA CCACAATTTT AGGTAAAACA TTAAATGTGT CAGAAATCTT	1440
	GGCAACAGAG ACTCTGCAGC TTGCAGTGA CATAGATAAA ATGTTACAGA GATACTATTT	1500
	TTTTGGTTGG AATTACTATA TTAAATTTAG AAGCAGAAAC TGGTAAAATG TTAAATACAT	1560
45	GTACAAATGC TTTTAGTTAG CAATTGATTG TAGCATGGGT TCCTCCAAGG TTTCAAGCAA	1620
	TGGGCAGACT TTAAATTTAT ATCAGATTG TTTACTTCGT TTATTATTTT ACAGTAAATT	1680
50	TGAATAAATC TTAGGGGTCA TTATCACTTA AATAATACTG TACCTAGGTC TTTCAAATTA	1740
	AAATTATACC TGAATGAAGT TGTTGTGATA CATAAAGGAT ATTTGTGTAC AATTACCTTT	1800
	TTTCCCCAC ACTTGTTTTT TTTGTTTTTG TTTTATATGG CAACTGGAAA GTATTTACTA	1860
55	TGGGATTCAT TTATGTCTGT CTTTCTATCA TAAAGAATTG ATCAATATGT AAATATGTGA	1920
	TTTGAACCAT GGTGACTTA CAAGTGTAC TACAGCTTTT TAGAAAACAT AGCCCTAATA	1980
60	TATGTTAAGC AGGACCCGGG TGAGCCAGTG GGCTTGCCT TTATGTAGAG CTGGAAGAAG	2040

5 GCCGTCCATC CTGTCTCTTG GCGGACAGT GTACTTTCCT AATAGGAAG GGAAGCACAA 2100
 TGGAAATACC CCTGAACCGT TTTATGTCAG TAATTTTTTT CATATCTGAA ACTATTATTT 2160
 AATATTTTGA ATAAGATTTT AAAAAATAAA TGGCAAAGAT ATAAATCTAA AAAAAAAAAA 2220
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA 2276
 10

(2) INFORMATION FOR SEQ ID NO: 184:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2500 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

TCCAAGCTAC GCCACTCGGG CTGGGGCGTT GGGAGCGGA GTGCAGAGCG TGGTCGTGGC 60
 25 GCGGCGGTG AGAAGAGCGA GCGKAGGAG GGGGTGCCAT GGCCGGGCAG CAGTTCCAGT 120
 ACGATGACAG TGGGAACACC TTCTTCTACT TCCTCACCTC CTTCGTGGGG CTCATCGTGA 180
 TCCCGGCGAC ATACTACCTC TGGCCCCGAG ATCAGAATGC CGAGCAAATT CGATTAAAGA 240
 30 ATATCAGAAA AGTATATGGA AGGTGTATGT GGTACGTTTA CGGTTATTAA AACCCAGCC 300
 AAATATTATT CCTACAGTAA AGAAATAGT TCTGCTTGCA GGATGGGCAT TGTCTTTATT 360
 35 CCTTGCATAT AAAGTTTCCA AACAGACCG AGAATACCAA GAATACAATC CTTATGAAGT 420
 ATTAAATTG GATCCTGGAG CCAQAGTAGC AGAAATTAAA AAACAATATC GTTTGCTGTC 480
 ACTTAAATAT CATCCAGATA AAGGAGTGA TGAGGTTATG TTCATGAGGA TAGCAAAAGC 540
 40 TTATGCTGCT TTAACGGATG AAGAGTCCCG GAAAAATTGG GAAGAATTG GAAATCCAGA 600
 TGGGCCTCAA GCCACAAGCT TTGGAATTGC CCTGCCAGCT TGGATAGTTG ACCAGAAAAA 660
 45 TTCAATTCTG GTTTTACTTG TATATGGATT GGCATTTATG GTTATCCTTC CAGTTGTTGT 720
 GGGCTCTTGG TGGTATCGCT CAATACGCTA TAGTGGAGAC CAGATTCTAA TACGSACAAC 780
 ACAGATTAT ACATACTTG TTTATAAAAC CCGAAATATG GATATGAAAC GTCTTATCAT 840
 50 GGTTTTGGST GGAGCTTCTG AATTGATCC TCAGTATAAT AAAGATGCCA CAAGCAGACC 900
 AACGGATAAT ATTCTAATAC CACAGCTAAT CAGAGAAATT GGCAGCATT AATTAAAGAA 960
 55 GAATGAGCCT CCACTTACCT GCCCATATAG CCTGAAGGCC AGAGTTCTTT TACTGTCTCA 1020
 TCTTGCTAGA ATGAAAATTC CTGAGACCCT TGAAGAAGAT CAGCAATTCA TGCTAAAAAA 1080
 GTGTCTGCC CTACTTCAAG AAATGGTTAA TGTAATCTGC CAACTAATAG TAATGGCCCG 1140
 60

GAACCGTGAA GAAAGGGAGT TTCGTGCTCC AACTTTGGCA TCCCTAGAAA ACTGCATGAA 1200
GCTTCTCAG ATGGCCGTTT AGGGACTTCA GCAATTAAAG TCTCCCCTTC TGCAGCTCCC 1260
5 TCATATTGAA GAGGACAATC TTAGACGGGT TTCTAATCAT AAGAAGTATA AAATTAAAAC 1320
TATCCAGGAT TTGGTGAGTT TAAAAGAATC AGATCGTCAC ACTCTACTGC ACTTCCTTGA 1380
10 AGATGAAAAA TATGAAGAGG TTATGGCTGT CCTTGGGAGT TTTCCATATG TGACCATGGA 1440
TATAAAATCA CAGGTGTTAG ATGATGAAGA TAGCAACAAC ATCACAGTAG GATCCTTAGT 1500
TACAGTGTG GTTAAGTTGA CAAGGCAAAC AATGGCTGAA GTATTTGAAA AGGAGCAGTC 1560
15 CATCTGTGCT GCAGAGGAAC AGCCAGCAGA AGATGGGCAG GGTGAACTA ACAAGAACAG 1620
GACAAAAGGA GGATGGCAAC AGAAGAGTAA AGGACCCAAG AAAACTGCTA AATCAAAAAA 1680
AAAGAAACCT TTAACAAAAA AACCTACACC TGTGCTATTA CCACAGTCAA AGCAACAGAA 1740
20 ACAAAGCAG GCAATGGAG TCGTTGGGAA TGAAGCTGCA GTAAAGGAAG ATGAAGAAGA 1800
AGTTTCAGAT AAGGGCAGTG ATTCTGAAGA AGAAGAAACC AATAGAGATT CCCAAAGTGA 1860
25 GAAAGATGAT GGTAGTGACA GAGACTCTGA TAGAGAGCAA GATGAAAAAC AAAACAAAGA 1920
TGATGAAGCA GAGTGGCAAG AATTACAACA AAGCATACAG CGAAAAGAGA GAGCTCTATT 1980
GGAAACCAA TCAAAATAA CACATCCTGT GTATAGCCTT TACTTTCCTG AGGAAAAACA 2040
30 AGAATGGTGG TGGCTTTACA TTGCAGATAG GAAGGAGCAG ACATTAATAT CCATGCCATA 2100
TCATGTGTGT ACGCTGAAAG ATACAGAGGA GGTAGAGCTG AAGTTTCCTG CACCAGGCAA 2160
35 GCCTGGAAAT TATCAGTATA CTGTGTTTCT GAGATCAGAC TCCTATATGG GTTTGGATCA 2220
GATTAAACCA TTGGAAGTTK GGAAGTTCAT GAGGCTGAAG CCTGTGCCAG AAAATCACCC 2280
ACAGTGGGAT ACAGCAATAG AGGGGGATGA AGACCAGGAG GACAGTGAGG GCTTTGAAGA 2340
40 TAGCTTTGAG GGAGGAAGAG GGAGGGAGGA AGGAAGGTGG TGGACTTAAG GCAGTTACTC 2400
TGGAATGGGA CCCACAGTGT TTTGCACCAT ATTTTGGCAA TTTTMTTTC CCGTTTMTNG 2460
45 GAAGTGTTTT CCMTNAANCC CAGGAACCAT TACAGAACCG 2500

50 (2) INFORMATION FOR SEQ ID NO: 185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1337 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

60 CTTCCGGTTC TCCGGGCAGC TGCCACTGCT GTAGCTTCTG CCACCTGCCA CGACCGGGCC 60

TCTCCCTGGC GTTTGGTCAC CTCTGCTTCA TTCTCCACCG CGCCTATGGT CCCTCTTGGA 120
 GCCAGCGTGG CGGGCCTGGC GGCTCCCGGG TGGTGAGAGA GCGGTCCGGG AACGATGAAG 180
 5 GCCTCGCAGT GCTGCTGCTG TCTCAGCCAC CTCTTGGCTT CCGTCCTCCT CCTGCTGTTG 240
 CTGCCTGAAC TAAGCGGGYC CCTGGMAGTC CTGCTGCAGG CAGCCGAGGC CGCGCCAGGT 300
 10 CTTGGGCCTC CTGACCCTAG ACCACGGACA TTACCGCCGC TGCCACCGGG CCCTACCCCT 360
 GCCCAGCAGC CGGGCCGTGG TCTGGCTGAA GCTGCGGGC CGCGGGGCTC CGAGGGAGGC 420
 AATGGCAGCA ACCCTGTGGC CGGGCTTGAG ACGGACGATC ACGGAGGGAA GGCCGGGGAA 480
 15 GGCTCGGTGG GTGGCGGCCT TGCTGTGAGC CCCAACCTG GCGACAAGCC CATGACCCAG 540
 CGGGCCCTGA CCGTGTGAT GGTGGTGAGC GGCGCGGTGC TGGTGTACTT CGTGGTCAGG 600
 20 ACGGTCAGGA TGAGAAGAAG AAACCGAAAG ACTAGGAGAT ATGGAGTTT GGACACTAAC 660
 ATAGAAAATA TGAATTGAC ACCTTTAGAA CAGGATGATG AGGATGATGA CAACACGTTG 720
 TTTGATGCCA ATCATCCTCG AAGATAAGAA TGTGCCTTTT GATGAAAGAA CTTTATCTTT 780
 25 CTACAATGAA GAGTGAATT TCTATGTTTA AGGAATAAGA AGCCACTATA TCAATGTTGG 840
 GGGGGTATTT AAGTTACATA TATTTTAACA ACCTTTAATT TGCTGTTGCA ATAAATACCG 900
 30 TATCCTTTTA TTATATCTTT ATATGTATAG AAGTACTCTR TTAATGGGCT CAGAGATGTT 960
 GGGGATAAAG TATACTGTAA TAATTTATCT GTTTGAAAAT TACTATAAAA CGGTGTTTTC 1020
 TGATCGGTTT TTGTTTCCTG CITACCATAT GATGTAAAT TGTTTTATGT ATTAATCAGT 1080
 35 TAATGCTAAT TATTTTGGCT GATGTCATAT GTTAAAGAGC TATAAATTCC AACAACCAAC 1140
 TGGTGTCTAA AAATAATTTA AAATTTCCCT TACTGAAAGG TATTTCCCAT TTTTGTGGG 1200
 40 AAAAGAAGCC AAATTTATTA CTTTGTGTTG GGGTTTTAA AATATTAAGA AATGTCTAAG 1260
 TTATTGTTTG CAAAACAATA AATATGATTT TAAATCTCT TAAAAAAA AAAAAAACC 1320
 CCGGGGGGGG GCCCGGN 1337
 45

(2) INFORMATION FOR SEQ ID NO: 186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 941 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

GGCAGGAGCC TGGACGCAGC AGCCACCGCC GCGTCCCTCT CTCCACGAGG CTGCCGGCTT 60

60

AGGACCCCCA GCTCCGACAT GTCGCCCTCT GGTCCGCTGT GTCTTCTCAC CATCGTTGGC 120
 CTGATTCTCC CCACCAGAGG ACAGACGTTG AAAGATACCA CGTCCAGTTC TTCAGCAGAC 180
 5 TCAACTATCA TGGACATTCA GTCCCCGACA CGAGCCCCAG ATGCAGTCTA CACAGAACTC 240
 CAGCCACCT CTCCAACCCC AACCTGGCCT GCTGATGAAA CACCACAACC CCAGACCCAG 300
 ACCCAGCAAC TGAAGGAAC GGATGGGCCT CTAGTGACAG ATCCAGAGAC ACACAAGAGC 360
 10 ACCAAAGCAG CTCATCCCAC TGATGACACC ACGACGCTCT CTGAGAGACC ATCCCAAGC 420
 ACAGACGTCC AGACAGACCC CCAGACCCCTC AAGCCATCTG GTTTTCATGA GGATGACCCC 480
 15 TTCTTCTATG ATGAACACAC CCTCCGAAA CGGGGGCTGT TGGTCGCAGC TGTGCTGTTC 540
 ATCAGAGCA TCATCATCCT CACCACTGGC AAGTGCAGGC AGCTGTCCCG GTTATGCCGG 600
 AATCATTGCA GGTGAGTCCA TCAGAAACAG GAGCTGACAA CCYGCTGGGC ACCCGAAGAC 660
 20 CAAGCCCCCT GCCAGCTCAC CGTGCCAGC CTCCTGCATC CCCTCGAAGA GCCTGGCCAG 720
 AGAGGAAGA CACAGATGAT GAAGCTGGAG CCAGGGCTGC CGGTCCGAGT CTCCTACCTC 780
 25 CCCCCACCT GCCCGCCCT GAAGGCTACC TGGCGCCTTG GGGGCTGTCC CTCAAGTTAT 840
 CTCCTCTGYT AAGACAAAA GTAAAGCACT GTGGTCTTTG CAAAAA AAAA AAAAAA 900
 AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA 941
 30 AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA

35 (2) INFORMATION FOR SEQ ID NO: 187:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 654 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

45 GAATTCGGCA CGAGGCAGCT TGTGCTTTAA AGGAGGTGTT CAAAGCATGT CTGAGCAGAG 60
 ACTTTTGGGC TCTGTTTTAA TTAATACTTT AAAATAATTC ATATTTAAAA TATCARATGT 120
 TTCCATAAAG AGGAGGATGT TTAAATGCCT CCAGACTACA TTCCTTTTTA TTSCITGATT 180
 50 TTACCTGGGA GTCCAAAGTT CAATCCCAT AAAGCAAGCG TTTTATTTGT CACTTTCAAT 240
 ATACATCCGA TTGCCATGCT TAAGATGCAA TATGGGCTGC GGAAATAGGT TAACCCACAG 300
 GCTCCAGGG CCCAGTGTAG AAGGTGAGAG ATTCTGTAA AATGATTCAA ATAAAAGGAA 360
 55 GACCCTGGCC GGGTGCCGTA RCTCACGCT GTAATCCCAG CACTTTGGGA GGCCGAAGCG 420
 AGTGGATGAC GAGGTTAGGA GTTGAGACC AGCCTGGCCA ACATCGTGAA ACCCGTCTC 480
 60 TACTAAAAAT AAAAAATTA GCCGGCATG GTGCAGGCA CCTGTAATCC TAGCTAGTTG 540

	GGAGGCTGAG GCAGGAGAAT CGTTTGAATC TGGGAGTTGG AGGTTGTCAG TGAGCTGAGA	600
5	TCGCGCCACA GCACTCCAGC CTGGGTGACA GGGTGAGACT CTGTCTCAAA NAGA	654
10	(2) INFORMATION FOR SEQ ID NO: 188:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 1848 base pairs	
	(B) TYPE: nucleic acid	
15	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:	
20	GAAACTGGAC CGGAGAACCG GAGCGAAGCG AAGCGGAAGC CCGGAATGAG GCCGGACTGG	60
	AAAGCCGGAG CGGGGCCAGG CGGGCCTCCC CAAAAGCCTG CCCCTTCATC CCAGCGGAAA	120
	CCGCCGGCCC GGCCGAGCGC GCGGCCGCT GCGATTGCAG TCGCGGCGGC GGAGGAAGAG	180
25	AGACGGCTCC GGCAGCGGAA CCGCCTGAGG CTGGAGGAGG ACAAACCGGC CGTGGAGCGG	240
	TGCTTGGAGG AGCTGGTCTT CGGCGACGTC GAGAACGACG AGGACGCGTT GCTCGGCGCT	300
30	CTGCGAGGCC CGAGGGTTCA AGAACATGAA GACTCGGGTG ACTCAGAAGT GGAGAATGAA	360
	GCAAAGGTA ATTTTCCACC TCAAAGAAG CCAGTTTGGG TGGATGAAGA AGATGAAGAT	420
	GAGGAAATGG TTGACATGAT GAACAATCGG TTTCGGAAGG ATATGATGAA AAATGCTAGT	480
35	GAAAGTAAAC TTTCGAAAGA CAACCTTAAA AAGAGACTTA AAGAAGAATT CCAACATGCC	540
	ATGGGAGGAG TACCTGCCTG GGCAGAGACT ACTAAGCGGA AAACATCTTC AGATGATGAA	600
40	AGTGAAGAGG ATGAAGATGA TTTGTTGCAA AGGACTGGGA ATTTCATATC CACATCAACT	660
	TCTCTTCCAA GAGGCATCTT GAAGATGAAG AACTGCCAGC ATGCGAATGC TGAACGTCCT	720
	ACTGTTGCTC GGATCTCCAT CTGTGCAGTT CCATCCCGGT GCACAGATTG TGATGGTTGC	780
45	TGGGATTAGA TAATGCTGTA TCACTATTTC AGGTTGATGG GAAAACAAAT CCTAAAATTC	840
	AGAGCATCTA TTGGAAGG TTTCCAATCT TTAAGGCTTG TTTTAGTGCT AATGGGGAAG	900
50	AAGTTTtagc CACGAGTACC CACAGCAAGG TTCTTTATGT CTATGACATG CTGGCTGGAA	960
	AGTTAATTCC TGTGCATCAA GTGAGAGGTT TGAAAGAGAA GATAGTGAGG AGCTTTGAAG	1020
	TCTCCCCAGA TGGGTCCTTC TTGCTCATAA ATGGCATTGC TGGATATTTG CATTTGCTAG	1080
55	CAATGAAGAC CAAAGAACTG ATTGGAAGCA TGAAAATTAA TGGAAGGGTT GCAGCATCCA	1140
	CATTCTCTTC AGATAGTAAG AAAGTATACG CCTCTTCGGG GGATGGAGAA GTTTATGTTT	1200
60	GGGATGTGAA CTCAAGGAAG TGCCTTAACA GATTTGTGA TGAAGGCAGT TTATATGGAT	1260

TAAGCATTGC CACATCTAGG AATGGACAGT ATGTTGCTTG TGGTTCTAAT TGTGGAGTGG 1320
TAAATATATA CAATCAAGAT TCTTGTCTCC AAGAAACAAA CCCAAAGCCA ATAAAAGCTA 1380
5 TAATGAACTT GGTACAGGT GTTACTTCTC TGACCTTCAA TCCTACTACA GAAATCTTGG 1440
CAATTGCTTC AGAAAAATG AAAGAAGCAG TCAGATTGGT TCATCTTCCT TCCTGTACAG 1500
TATTTTCAAA CTTCACAGTC ATTAAAAATA AGAATATTC TCATGTTTAT ACCATGGATT 1560
10 TTTCTCCGAG AAGTGGATAC TTTGCCTTGG GGAATGAAA GGGCAAGGCC CTGATGTATA 1620
GGTTGCACCA TTAATCAGAC TTCTAAAGAG ACTATTTGAA GTCCAGTTGA GTCACAAGAG 1680
15 AAGCCTGTCT TGATATATCA TCTCAGAAAC TTTCTTGAAT ATGTGATAAT ATATGGAAAA 1740
TGATTATAG ATCCAGCTGT GCTTAAGAGC CAGTAATGTC TTAATAACA TGTGGCAGCT 1800
TTTGTTTGAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAATCTGA 1848
20

(2) INFORMATION FOR SEQ ID NO: 189:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1146 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

AAAAAAAAACC CAGGGGAACN TTGGGGGCGG CTTTNNNTTC CCCCTCCAGG CCATTGGGGA 60
35 ATTCTTCAAG TTAATCCTGC TTTGCTCTTG GCCAACAGGG CTTGTAGGGG GGAGAGACCC 120
AGGATCATCA AGGGGPTCGA GTGCAAGCCT CACTCCCAGC CTTGGCAGGC AGCCCTGTTC 180
40 GAGAAGACGC GGCTACTCTG TGGGGCGACG CTCATCGCCC CCAGATGGCT CTTGACAGCA 240
GCCCCACTGCC TCAAGCCCCG CTACATAGTT CACCTGGGGC AGCACAACCT CCAGAAGGAG 300
GAGGGCTGTG AGCAGACCCG GACAGCCACT GAGTCCTTCC CCCACCCCGG CTTCAACAAC 360
45 AGCCTCCCCA ACAAGACCA CCGCAATGAC ATCATGCTGG TGAAGATGGC ATCGCCAGTC 420
TCCATCACCT GGGCTGTGCG ACCCCTCACC CTCTCCTCAC GCTGTGTAC TGCTGGCACC 480
50 AGCTGYCTCA TTTCCGGCTG GGGCAGMACG TCCAGCCCCC AGTTACGCCT GCCTCACACC 540
TTGSGATGCG CCAACATCAC CATCATTGAG CACCAGAAGT GTGAGAACGC CTACCCCGGC 600
AACATCAGAG ACACCATGGT GTGTGCCAGC GTGCAGGAAG GGGGCAAGGA CTCCTGCCAG 660
55 GGTGACTCCG GGGGCCCTCT GGTCTGTAAC CAGTCTCTTC AAGGCATTAT CTCCTGGGGC 720
CAGGATCCGT GTGCGATCAC CCGAAAGCCT GGTGTCTACA CGAAAGTCTG CAAATATGTG 780
60 GACTGGATCC AGGAGACGAT GAAGAACAAT TAGACTGGAC CCACCCACCA CAGCCCATCA 840

CCCTCCATT CCACCTGGTG TTTGGTTCCT GTTCACTCTG TTAATAAGAA ACCCTAAGCC 900
AAGACCCTCT ACGAACATTC TTTGGGCCTC CTGGACTACA GGAGATGCTG TCACTTAATA 960
5 ATCAACCTGG GGTTCGAAAT CAGTGAGACC TGGATTCAAA TTCTGCCTTG AAATATTGTG 1020
ACTCTGGGAA TGACAACACC TGGTTTGTTC TCTGTTGTAT CCCCAGCCCC AAAGACAGCT 1080
10 CCTGGCCATA TATCAAGGTT TCAATAAATA TTTGCTAAAT GAAAAAARAA AAAAAAAAAA 1140
ACTCGA 1146

15

(2) INFORMATION FOR SEQ ID NO: 190:

(i) SEQUENCE CHARACTERISTICS:
20 (A) LENGTH: 906 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

ACTCCCTCAC CCAGGTCCCA GCCCTGGGAA CCACCTACCG TGAGCCCTTT TGCAGATATA 60
GACTCATTTC ATCCTCAGAT GGTCTTCAA GGTAGTACT TTAGTCCCAT TTAGAGATG 120
30 AGACGATGA GCCAGAGGG GTGNGTAAC TTGCCTGGGG GCTCACGAGC ACAAAGGAG 180
CCGAGGCAGG ATCTGACCCT TGTCTCTGG CCTCACTGCC CTCACTTTGC CATGACCCGA 240
35 AGTTATGTCC CTACAAAGCA ATGCATGGTC CAAGGYTCTT TTTATTGTAT TTTATTTTT 300
AAGGGTCCTG TTCAAACTG GTGTGAGCTC TGAGGAGTCC TGAACCTGG GTGCAGCATC 360
CTAGCATCCT GGGAGTCTT TTCGCCCCAC ACTGAGCTGG GCTCCTCGAG GGTGGGGCT 420
40 GCTGTCCCTG GAAGCCTGGC AGCAGCACTG TATCGGGTTG GCTGAAGCTG ARCGCCGTGG 480
GGTGACGGGC TCCMGAATC CCCGTTGGC TGAAGGGGTT CCCTGTAGCC MGGGATGTTT 540
45 ATGAGGTCTC TCTGATGCCC CAGGCGCAGG ACATGTGTGC GGGTGGAGAA AAGCAGGCCC 600
TTTCAGTGCC AGCTCCACTC AATTTCTATG TGGACCAAGA ACGATAAACT TAAAAAATT 660
TTTTTCCTAA GGTATCTTCA GAATATGGTG TATTTTTATG TGGAAAAGAA AAGTTATGAA 720
50 GGCAGCTGTT ACTTTAAGAG AAAATTCATT AAAAGTCCTC GAGGTATGAA GATGACGGCG 780
TGCTTCTCAA TCATTTTGGC ATAACCTGAT TGTGGCTGTA ATTTTTTTTT TTTTTTTTGT 840
55 CAAGCATGTC AGACAATAAA GTCTTTGTAA AAAGRGAAAA AAAAAAAAAA AAAAAAAAAA 900
ACTCGA 906

60

(2) INFORMATION FOR SEQ ID NO: 191:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1941 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

CTTCAGCTGA AGCCAGGGA CCCCTTTTCC ACCCTGGGCC CCAATGCCGT CCTTTCCCG 60
CAGAGACTGG TCTTGAAAC CCTCAGAAA CTCAGCATCC AGGACAACAA TGTGGACCTG 120
15 ATCTTGCCA CACCCCCCTT CAGCCGCTG GAGAAGTTGT ATAGCACTAT GGTGCGCTTC 180
CTCAGTGACC GAAAGAACCC GGTGTGCCG AGATGGCTGT GGTACTGCTG GCCAACCTGG 240
20 CTCAGGGGA CAGCTGGCA GCTCGTGCCA TTGCAGTGCA GAAGGGCAGT ATCGGCAACC 300
TCCTGGGCTT CCTAGAGGAC AGCCTTGCCG CCACACAGTT CCAGCAGAGC CAGGCCAGCC 360
TCCTCCACAT GCAGAACCA CCCTTTGAGC CAAYTAGTGT GGACATGATG CGGCGGGCTG 420
25 CCGCGCGCT GCTTGCTTG GCCAAGGTGG ACGAGAACCA CTCAGAGTTT ACTCTGTACG 480
AATCAGGCT GTTGACATC TCGGTATCAC CGTTGATGAA CTCAKTGGTT TCACAAGTCA 540
30 TTTGTGATGT ACTGTTTTTG NATTGGCCAG TCATGACAGC CGTGGGACAC CTCCCCCCCC 600
CGTGTGTGTG TGC GTGTGTG GAGAACTTAG AAACAGCTG TTGCCCTTTA TTTATGAAA 660
ACCACCTCAG AATCCAGTTT ACCCTGTGCT GTCCAGCTTC TCCCTTGGGA AAAAGTCTCT 720
35 CCTGTTTCTC TCTCTCTT CCACCTCCCC TCCCTCCATC ACCTCAGGC TTTCTGTTC 780
TTGTCTCAC CTTACTCCCC TCAGGACCCT ACCCCACCCT CTTTGAAAAG ACAAAGTCT 840
40 GCCTACATAG AAGACTTTTT TTATTTTAA CAAAGTTACT GTTGTTTACA GTGAGTTTGG 900
GGAAAAAAA TAAATAAAA ATGGCTTTCC CAGTCCTTGC ATCAACGGGA TGCCACATTT 960
CATACTGTT TTTAATGGTA AAAAAAAAAA AAAAAAATAC AAAAAAAAT TCTGAAGGAC 1020
45 AAAAAAGGTG ACTGCTGAAC TGTGTGTGGT TTATTGTTGT ACATTCACAA TCTTGCAGGA 1080
GCCAAGAAGT TCGCAGTTGT GAACAGACCC TGTTCAGTGG AGAGGCCTGT GCAGTAGAGT 1140
50 GTAGACCTT TCATGTACTG TACTGTACAC CTGATACTGT AAACATACTG TAATAATAAT 1200
GTCTCACATG GAAACAGAAA ACGCTGGGTC AGCAGCAAGC TGTAGTTTTT AAAAATGTTT 1260
TTAGTTAAAC GTTGAGGAGA AAAAAAAAAA AGGCTTTTCC CCCAAAGTAT CATGTGTGAA 1320
55 CCTACAACAC CCTGACCTCT TTCTCTCTC CTTGATTGTA TGAATAACCC TGAGATCACC 1380
TCTTAGAACT GGTTTTAACC TTTAGCTGCA GCGNCTACGT CNAWCGNIGT GTATATATAT 1440
60 GACGKTGTAC ATTGCACATA CCCTTGGATC CCCACAGTK GGTCTCTCTC CCAGCTACCC 1500

CTTTATAGTA TGACGAGTTA ACAAGTTGGT GACCTGCACA AAGCGAGACA CAGCTATTTA 1560
ATCTCTTGCC CAGATATCGC CCCTCTTGGT GCGATGCTGT ACAGGTCTCT GTAAAAAGTC 1620
5 CTGCTGTCT CAGCAGCCAA TCAACTTATA GTTTATTTT TTCTGGGTTT TTGTTTGT
TTGTTTCTT TCTAATCGAG GTGTGAAAAA GTTCTAGGTT CAGTTGAAGT TCTGATGAAG 1740
10 AAACACAATT GAGATTTTTT CAGTGATAAA ATCTGCATAT TTGTATTTCA ACAATGTAGC 1800
TAAAACTTGA TGTAATTC TCCTTTTTT CCTTTTTTGG CTTAATGAAT ATCATTATT 1860
CAGTATGAAA TCTTTATACT ATATGTTCCA CGTGTTAAGA ATAAATGTAC ATTAAATCTT 1920
15 GGTAAGACTT TAAAAAAA A 1941

20

(2) INFORMATION FOR SEQ ID NO: 192:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 2118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

30

AAATAATAAT AANAATAAAT AAAAATWAAG TGCTTAKTGT AACTCAGCGG ACAGGGCTCC 60

CAGCTGCTCT GGCACGTGGG ACACCTCCA CCCTGCACAC AACAGGCATG CAAAGAGGAC 120

35 TGGATATGGT GGGGTAGAGT GCTTCTGGTG GTTCTACTTT AAGAAAACAT CTGCCAAGAG 180

AGAAGAGTGC CCAGGAAAGA CCAGGAAAT ACAAGTACAT GGCTGCTTCA TACCATATAC 240

40 CCCAATTCTT TAAAGCAGCA AAAGGCACCT TTTTTCAG GCCAGAGTGA ATCTAAAAACA 300

AACCTGGCTT TGCTTACAGG GAAGCTGTCC CAGAAGGACT GAGTGATGCC TCTGTTCCTC 360

TAAGTCTGG AGAGTCTTTG CAAGTTTCCA ACGACATTC CAACCAGGTG GGAGAGACCA 420

45 GCAGTTGACG AGACAAGTCA GACCCAAAAA ACGACGCCAA GGATGTGAGT GGGTGCCTAT 480

TTGGGAGTAG GATGATTGGA GGAAACAGG AAGAAAAACC GGTGAGAAAG TGGCACTTTG 540

50 GAAGTGAAA GCTGTTTGCA AATAGCAACT CTGGCTAAAG CGAAAATGTT AATCAAGTAG 600

AAAGTAAAT TCAGGATCTT AGAAGCTCAT CCTTCTGATG AGAACTATTT TTTTTCCTG 660

GAAGGAATA TTATTACTTT AAAAGTGAGG GTAATTTACA TATGGGGTGT ATATATTCTA 720

55 AAAATAGTAA TAAAGTACC TTTTATAAGC AATGTGTGTG GGCTTGTAGA AGAAAGCAGG 780

GAGGAAAAA AGGCAGGCAA AACTAGTCTA GGTCTAGGCC CTAAAAATGA GCTTCCTTCC 840

60 CACTTGACTG GAAACGCCCA TGTGATTCT AGGCTGAAA TAGGTAGGAT TTAACGAGTA 900

ACCTAGTTCC CTTCGTCTC TGATTTCTGA TCAGCTGATG GAGCTGCTAG TAAGAGGGGC 960
CGATCATGCT CCCAGACGAG TCCTTTGGCC TCTTGCTCTC CATCCCAAGC CTGACTCCTT 1020
5 CAGCAGCAGC CCCCTCCTTC TGTGTCCATC TGATGCAGGC AAGCAGGAGC AGTAAGAGGG 1080
CATCCCATGT TCCAGTTCAC CTTCTATGGG GTGACTARGA GGTTCCTGGT AACTAGGGCA 1140
GCCCARGCCC AGCAGGTTCG AAAAGCAGCT GCAAGCTTCA GAAACCCACT TCCTCCAACA 1200
10 CCAGGGAGGT GGCAGAGAGC CCATCCAAAA GCCCACTGGG AGAGGCATAA GATTCTGTGC 1260
CAGGCCCCCA GGTCCTCTCT GTGTCAAGTA GGCTCTGCTA CTGGCCTCTG AAGTAAAGGC 1320
15 AAANACAAAC GGCAGGGCA GGTGGCAGG AATAAAAAAC TCTGGACAGA AACCTTTTA 1380
ATAAAGGAAA TTCCACCCCT CCCAATCCTT CCATGGAAGG GTGAGACCTT AATGTGATGT 1440
AAGAGGAAGG TCTTCTCTGG CTTTCAGGGA AACAGCTGCA GCTGAAACTT AGGGGCCCAT 1500
20 TCCAGGGCAC TTTTCACCAC AGCCAGTGCA GCCGCTCCA GTGCCACTGT CAGCCCCATC 1560
ACTGCCAATT TCACAAAGCG GTTGGTCTT GGCTTGGTCA GGACATCTTT TGTTCGATCT 1620
25 TCAGGCCGCA GAAGTCCCCG AANACCGCTG CCGCAGCACC ATATCAGGCC TCTGTGGGC 1680
TGATGCCAGC TCAAAGTCTT TGAAAGTAGA GGCTGCCGTC CTCTCAGCTT GCTGTGGGC 1740
AGCGGCCTCC CGAGCAAGTT CGGATGGGGG AACTGAACA AAAAGGTCTC CTSTCTGCTG 1800
30 ATCAGTGTCT CATAGGGCAA GTCCTGAGGG ATCTGGGACA ACAGGTGGTG GACCGAGGCC 1860
ATGTCACAGT CACAGTCCAG GACTTCCTGC TCGCGATACA ACACAATCAC GGCTGCAAAG 1920
35 TAAATCGGCA TCAGTGGGTG GCAGGCCAGG AAGAAGTCAT ATAACCGCAC GACGTGCCTG 1980
AAGTCAGACA GGACATGCCC AAACCAGGTG ATGAGCCAGC TGAGGGCAAA GATGGTCCCT 2040
ACCTCAGCAC TCTGCATGAA GTCATGGAGC TCTGATTCA CCTGGTCAAT GATGGGCATC 2100
40 AGATAGTTTA ATATATGC 2118

45

(2) INFORMATION FOR SEQ ID NO: 193:

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 1538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

55

CCGGGTTCGG CTCTGTGTCA GCAGCCGGGC GGCGCTCGGG CGGGACATGG CAGCCTGTAC 60
AGCCCCGGCG CCTGGCCGTG GGCAGCCGCT GGTGGTCCCG GTCGCTGACT GNGGCCCGGT 120
60 GGCCAAGGCC GCTCTGTGCG CGGCCGNAGC TGGAGCCTTC TCGCCAGCGT CGACCACGAC 180

5 GACGCGGAGG CACCTCTCGT CCCGAAACCG ACCAGAGGGC AAAGTGTGG AGACAGTTGG 240
TGTGTTTGAG GTGCCAAAAC AGAATGGAAA ATATGAGACC GGGCAGCTTT TCCTTCATAG 300
CATTTTGGC TACCGAGGTG TCGTCTGTGT TCCCTGGCAG GCCAGACTGT RTGACCGGGA 360
TGTGGCTTCT GCAGCTCCAG AAAAAGCAGA GAACCTGCT GGCCATGGCT CCAAGGAGGT 420
10 GAAAGGCAAA ACTCACACTT ACTATCAGGT GCTGATTGAT GCTCGTGACT GCCACATAT 480
ATCTCAGAGA TCTCAGACAG AAGCTGTGAC CTTCTTGGCT AACCATGATG ACAGTCGGGC 540
CCTCTATGCC ATCCCAGGCT TGGACTATGT CAGCCATGAA GACATCCTCC CCTACACCTC 600
15 CACTGATCAG GTTCCCATCC AACATGAACT CTTTGAAAGA TTTCTTCTGT ATGACCAGAC 660
AAAAGCACCT CCTTTTGTGG CTCGGGAGAC GCTAAGGGCC TGGCAAGAGA AGAATCACCC 720
20 CTGGCTGGAG CTCTCCGATG TTCATCGGGA ACAAAGTGGT AACATACGTG TCACTGTCAT 780
CCCTTCTAC ATGGGCATGA GGAAGCCCA GAATTCACAC GTGTACTGGT GGCCTACTG 840
TATCCGTTTG GAGAACCTTG ACAGTGATGT GGTACAGCTC CGGAGCGGC ACTGGAGGAT 900
25 ATTCAGTCTC TCTGGCACCT TGGAGACAGT GCGAGGCCGA GGGGTAGTGG GCAGGGAACC 960
AGTGTATCC AAGGAGCAGC CTGCGTTCCA GTATAGCAGC CACGTCTCGC TGCAGGCTTC 1020
30 CAGTGGGCAC ATGTGGGGCA CGTTCCGCTT TGAAAGACCT GATGGCTCCC ACTTTGATGT 1080
TCGGATTCCT CCCTTCTCCC TGGAAAGCAA TAAAGATGAG AAGACACCAC CCTCAGGCCT 1140
TCACTGGTAG GCCAGCTGAG GCCCCAAGTG CCCAGGCTTG GTCACCGGA AGAACAACCTC 1200
35 TCATCCACA ATTGCTGCAG AACTCTTCTC TCCCCATCAT GGGCCACAGT GGGTCTCTTA 1260
ATTTGATGT GGGGTCTTT TTGTGGGAG GGGTGTATA ACTTTCTTC AGAAGACCCA 1320
40 TGTGGGACAC CTCCAAGGCT GGCTCTCTCA TAAGCCCTGC CTACACCATG TTCCAGTAAA 1380
CCTCTCCACC AAGGAAGTGT GTTCAGCTGC CACAGGCTG GAGGAGTTTC CTGGCCTGTC 1440
ACGTGAGGTT TGATCAGTAA ACCAGTGCAS GYTTGGCCAA AAAAAAAAAA AAAAAAAAAA 1500
45 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AACTCGA 1538

50

(2) INFORMATION FOR SEQ ID NO: 194:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 1098 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

60

	AGACCCTGTC TCAAATAATA ATAATAATAA TAATCTTATT TTGGAGAATA AAGAGACCTS	60
	TGGATTGAG GTGCCATTG GGTAGAAAGA AAAGACGTTT ACACCGAGAA ATAGTCTGTG	120
5	TTGCCCTGAA GGAGCAGAGG GATGCATCGC TGGAGGTGAC CTACAGTTGA AGAAGACTCA	180
	TTATGACAGA CCTTGTCCTT CTCCTTGTG GAAAGTGTTC CCTCTGCTGC TACTGCTCAT	240
	GAGACTCTTC CCCCTCCCTG TCCCAGGGAA CCAAAGGCTT TTNCTACCAC ACCCTTTCCT	300
10	NGCCCCCGC CTCCTATGTC TGCTGTGCCT TTGTACTCAG CAATTCCTNG TTGCTCCCA	360
	TTATCTTCCA GCCGGATACA GAGTGAATAG TTAACCACAC TTAGGTCAA TAGGATCTAA	420
15	ATTTTGTGTC CTGCTCCNGT GTAAAGAGGC CAGTGTTTGT GTGTTGCAAG CAGCCTTGGA	480
	ATAGTAACTC TTCTCATTTG TTTGGGATCT GGCCAMCAAG TTCCAGAATG ATACACGGAT	540
	CAGTGCAGAA GTTCATCAGG CTCTCGGACC TTAGGGCTGT TGGAGAAGGC TTCAGCAGCA	600
20	GAACTGATGG TKAWKGYTCG TGTTCCTCCAT CCTCAACTTT CTTTGCTTCG ATCATAACA	660
	AGAATACATT TGGAAAGGCA AAAAATGAAC ACTGTTGTTC ATTGCAGCCG TGTTTTGTA	720
25	CACAGATGCA CAGTCTGCTG TGAAGACCTT CTCTCAAGTG GSATYTGGGA GTCCATGCCA	780
	GATCATGGTG CTTTCATGAGA GACTGACAGC TATCAGGGGT TGTGGCACTT AGTGAGGACT	840
	CTCCTCCCCC AGTGTGTGCT GATGACACAT ACACACCTGA CAATAGCTTG AGTCTTCTCT	900
30	GTTCCTTTTA CTCTGTAGCC AACATACACA TGATTTAAAA CCCTTTCTAA ATATCTATCA	960
	TGGTTCATCC TTGTCCAAAT GCAGAGTCAG AGCTATTTGT ACTTCATTAT TATTTCCAAG	1020
35	GCGAATAGTT GCGTTTCTTT TTGCAAAAAA AATTAAAGTT TTTGTATGTT GCAAAAAAAA	1080
	AAAAAAAAAA CTACGTAG	1098

40

(2) INFORMATION FOR SEQ ID NO: 195:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1001 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

	GAATTCGGCA CGAGATAGCT TGCATCTCAT CCCAGTAAAA CCACTTATTT ATAACATATC	60
	AACGTATTGA CAAGGTGAA GAGCAAGATT GTTCTGAGGT GAGATGCAA TTTCAAAGGG	120
55	GTGAGCACTA ATTGTTCCAG TGATTGTTTA TTTATTGGCT AGGACATAAT TACTCTCTTT	180
	GAGGTTACAC ATCTGCCTCC AGGTTCTGT GTGCTTGTGC CCTTGGGATC AGGCCAGGGC	240
60	AGACTGTGAT CACTGAGATT CAAACTCCCA GARTAAATCAG CAAGAGCTTT CTAGAGACCA	300

AGGCCAGGCC TGATCCCTGA GGGATGCATG AGAAGGCTTG GAATCTCATT CTGCTATGGT 360
GGCTCTCTCT TGATCTTCTT GGAGTAGCAA AAACAGCAAT GTGGGCCCAA TGGTGTGGCC 420
5 TAAATGATCA CAAAGGTAAA TGAGTAAAGG GCTCAGCAGA TGAGTAAGGA GCCTTGTCTT 480
GAGAAATTAG CACTGGGCTC TGCATTGAGA AACATGTGAT AAGCATTGCC CATTGCACAT 540
10 TGCCTTTATT GTGTAAGGAC ATGAAATTC AGTTTTCAT AGCTAGTGAT GAATACCTGA 600
AGGGAATTGC AGACATATTT TATTTTATTT TTAATTGACA GATGGAATTG TATATATTTA 660
TCATGTACAT AATCATGCTT TAAAATATGT ACATTATGGA ATGGCTAAAT CAACTAACC 720
15 TAGGCATTAT CTCATATAAT TGTCAATTTT GTGGCGAGAA GACTAAAAAT CTACCCTTTC 780
AGCATTTTAA AAGAATACAA TGTGTTTAT TAACAACAGT CACCATTGG TACTAGAT 840
20 CTCTTGAAGT TCTTCCTCTT ATCTAACTGA GATCTTGTA CCTTGATAA CAGCTCCCAA 900
GCCCTTCCCC AACCCTGCT CCACCCGTGG TAACCACCAT TCTATTCTCA ACTTCCTGGT 960
AATCACCATT CTAGACACAG GGAAGACTCT CTACCCTCTG A 1001
25

30 (2) INFORMATION FOR SEQ ID NO: 196:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1443 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

ATAAACTGAA ATAGGTCATG CAAATATAAA ATATTATTTT TAAATTATTT GTCATAAGAA 60
40 ACGATGGTGG CCATATTTTG CTTTAATAAT GGAAAAATG TGGTTAGCAT TCTKTGGAAG 120
GTGGTCATCA GATAGTAGAC ATTTTCTAGG ATTTATTTCT ACCTGCATAT GTGGAAATGT 180
45 GTACTACTTT AGATTTATWT AATGGCAGCT AACTCAGAGG CATCAAAATG TGCTAATGGT 240
GTAATATGGC CTTTGTCTTG CTGTCTGTT TTGTARGCCT TCAATCAAGC ARGGGCAGGG 300
CCGTACAGTG AACTTGTCTT TTGSCAGACG CCAGCGTCTG CCCCTGACCC CGTCTCCACT 360
50 CTCTGTGTCC TGGAGGAGGA GCCCCTTGAT GCYTACCCTG ATTCACCTTC TCGGTGCCTT 420
GTACTGAACT GGGAAGAGCC GTGCAATAAC GGATCTGAAA TCCTTGCTTA CACCATTGAT 480
55 CTAGGAGACA CTAGCATTAC CGTGGGCAAC ACCACCATGC ATGTTATGAA AGATCTCCTT 540
CCAGAAACCA CCTACCGGTG AGTGCAAGGG AGTAGAAATC TGCATCAGCA CATCAGCACT 600
TGGGGATCTA AGTAAACCTC TCGGGGAAAA TGACCAAGTG GATGTCATCT CCCAGCTGTT 660
60

TCTAAGAGCC CAGATGTCCA GAGTATGTGTC TCACCTTGAT CCCTCAGGCC AGAAGACCTG 720
 TGAAAAAGCC AACTGGTTC AGGGACTCAC TGGACGGTTT TGTGTCCACT TTAACATGCA 780
 5 CCGTCTCTAC CCCAGAGTGG ACTCARATCC TCAAGTCATC CTCTGAACAT TGGTCTGCA 840
 AATTATAAAA GGGCTTTGGC AATATGTIAG CCCAAGAAAT TGGCTTCTTC CAAAAATTGT 900
 GCCGACNITA ACAGTGGCTT AAATGATGGT AAAACTTTTA AGATTTCCTAA AAGGTGGCA 960
 10 TTGGAGATAC GTTGACTTTT ATTAAACMAC CTATAGTTGT TTAATGAATT CTAAAAAAT 1020
 ATCTGGAGCT CAGGGGTICA ACTGAGGGAA CACATGTGA GRATCATGT TTAATTAATTA 1080
 15 AATGCCAGGT AACCCGTGA AATTATCAAA AACATCTTCC ACGTACCAGA AAGACCTCA 1140
 GAGGATAGTT CTGTTATGGA GAAGATGAAA TGGTTTASTA GTGTAGGAC CATGGAAAGG 1200
 TGAGCTTAGA TTTGGATAGT AAAACCTCAA GACCTATTT AAAAGTATT TTATGAATGC 1260
 20 AGCATAAATA ATTTAATTCA GTGTTAANAT GCCAAGCTA GTATATTGAG CTGAATGTGA 1320
 AAAGAAACTC ACATTGGGAG AATGCCACCT TTTCCTTATA AGATAGCTTT GAAATACCA 1380
 25 TTTTAGACAG ATGGAATTG AATAGCTTTA GAAAGGCCAA ATGTTTGATC TTGGGGAAA 1440
 AAA 1443

30

(2) INFORMATION FOR SEQ ID NO: 197:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1282 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

GAAAAAAGAA AGTATGACCC AGTAGCTAGG CACCTGGGC CCCGCCAGT TGACACATAA 60
 AATTAAGTGT CACAGTATCA TCTTAGAAGT GAAGAGGCC CTTTATCTT GCAATGCCCC 120
 45 TCTACCACCA CCTACTGACA AAGAACATGG TGCTATCTGG CATGGGAGAA ATTTTCAGTT 180
 TGCTATGGCT TGTATGTGTC CCCTCAAATT CAGTGTGTC CAATGTGACA GCATCAAGAG 240
 50 GTGGGTCTT TAAGAGATCA CTAGGCCATG AGGGATTCTC TTAGGACTGG GATGAAGGCC 300
 CATAATAAAA GAGGTTTCAG GGAGCATCCT GCTAGCTTGC CTTCTGTATG TGAAACACA 360
 GCAAGAAAGC CCTAGTCAAC AAGTGCCAGC TCCTGATCT TAGACTTCC AATCTCCAGA 420
 55 ACTGTGAGAA ATACATTTCT GTTCCTTACA AATTACCCAG TCTCCTGTAT TCTTTTATAG 480
 CAGCACAAA TGAAGATACC ATACCTGAAC ACCTGACAT TCTTCACAG GAAATAAATG 540
 60 CACTGCTTTA TTCTGGTCTC AGTATTGTGT CCTTAATAAG GAAATGAGAA AGGTGGATC 600

5 AGGGCATAGG ATGAACAAGT TACTGCTAGA CCTCTCAGAA TGCCACTAAT GGTAAAGATT 660
 GTATTTTCAT CATTNCTTGT CTCTTCGGAA GCTAACGCCA TGCTATTAATA GGCATTAAAT 720
 AGATGTCTAA AAACACCTTA AGTATTTGTC TAGAAATCTG GTGCATTGTC CAGAAAGAAC 780
 CAAAATTCMA AATAATTTCA AAGGGCCTAA AGCACTATTT AATCGAATT CATTASTTTT 840
 10 TAATGGTACT ACCACTCTCA AATTTAAAAT GTCATCTTAC GTTCCCTCTC CTGGCATGG 900
 ATTTATTGCT AAAACCTGGT AAACACTTTA ATCCVTTTCA ATCCATTAC CACTGCTCTT 960
 GTCCAGAATT ACTCGCAGAC TAATAGTCAC CTGACTTCTC CCCTGCTATC CCGATTGCT 1020
 15 GTCTAATTCT GGTTACAAAT AAGTAACTGC CAACTATTC TTTCTAAAA GAAACTGA 1080
 TCTCGTCACT CCTTTGCTCA ACAATGTAAA AGCTCCCATT GTCTCCAAA TAAACCAGC 1140
 20 TTTCCACTGT GTATACAATA CATCCATGAT CTGTATCCAG CATCATTTG TATTGCTCA 1200
 CTTTATACAC CACCCCCCAT GCCACATCAA ATTAAATTAT CCTGATAAT GCAATGCAA 1260
 25 AAAAAAAAAA AAAAAAATC GA 1282

30 (2) INFORMATION FOR SEQ ID NO: 198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 951 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

40 ATTTCCGAAC GAGGACTGAA GTGGGAGCGG CGGCAGGGTA GAAGACGAA GGGGATCTA 60
 TGTGGTAACT AAAGAATGTT TCTGTTTGT TAATTATTGT GTGTGTGGG TTTTATTGTT 120
 TGCTTAAGAG AATCAAAAAC TGAAAAAAT GGAATACAG GAATGGCTC TTGTTTATTT 180
 45 TTTTGCTGTG TTTACAGCTT GTTAATGCTC TACTGTCTTT GTTCAGAG AGATTGTTC 240
 ACTGCCCAGC TCGTTTGTG TCCTGAGCCC TATGCCCAGC CCACCTTATA AATCATGCCT 300
 GTTTAGATGT TTGATTTTGT TCTGTTTGT ATTGTTATCT TAAAGGTGA TAACTCTGAC 360
 50 ATGCCAGACA TCAAATTAAG CTCAAATTAA GCTCTGTTT AATGTTTAA ACACCTAATT 420
 TATATTCTAA TTGATCCAG CCACTGATGC ATGTACTTGA CTACTTTTG CTAAATAAGC 480
 55 ATATTAATTT TCCACATCAG GCCATCAGAT CTGAGAACC AACAGTTAC TAGAATCCG 540
 TGTCTACTAA TGTTCACCT GCATGCAGCC TTCATTAAAT TTGTAGCAA ATATAAGTG 600
 ATCATTATGT AGTTTCTGGA TTAAAAAAT TTGTGTGTA AGTTGCTTG TAAAGTCAT 660

GTGGAATTAA TGGGACAGTG TGCCCTTTGT GTTAGATGTT AGAGCAAAAG AAAGGGCTTA 720
 TAGTGTTAGT ATTGGAGCAC TTTGAAGATA GATATTTTCA GAAAAGATGT AGGATTTAAA 780
 5 AGTTAAATTT TAAATTTTAG AAAAAGATAT GATGGCAATT GGAAATAGTC ACAATGAAGT 840
 TCTTCATCCA GTAGGTGTTT AACAGTGTTA TTTTGCCACT GGTAATGTGT AAAGTGTGAG 900
 TGATTTACAA TAAATGATTA TGAATTCAAA AAAAAAAAAA AAAAAACTCG A 951
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15 (2) INFORMATION FOR SEQ ID NO: 199:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1740 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

TTATTATAAT AATGATGATG ATTCCAAGGA AAAACCTAC AGCGAATGTT CCATTCTAC 60
 25 CCCGCACGCA GACACTCTCC CTAACACTGA TAACCTGAGC CCCAGCACT GGACGGAAGA 120
 ATGCTGGCGT CTCCGTGTGT ACTGGTTCAG GGTTCCTGGCC CCAGCCTTGT CAGGACCCCC 180
 30 TGGTGTCCAG AGCCCCACC CCTCCGCAA CAAGCAGCTG ATGCCCCAGT GATTCTCTAT 240
 ACATTTTTC A C T C G G C C A A T A T G T C C A G A A A A A C T G C T T A C T T C T C T T T C T T G C C T G G 300
 AGCCTTCATT GTTACCCTT A C G T T G C A A T A T A G G A A T T A A T G C T A C A A A T A A A A G T A A 360
 35 AGCTTACCTG AAAAGTGCAT AGTTGGGGC AATGGTATCT ACATCTCCA CTGTGGGAAA 420
 ACCAGCAAAG CATCAAACT CTCAATTCTC CTGTTACCRA ATGCAGATCT GAATTATAAG 480
 40 ATGTTTATGT TTGACCATTG TTTCAACAAT GGGATTTTGT TACGAATTAT CCCTTTAACT 540
 GAAACCCCTCA GTTTACTGT TTACATTATT AGGAAAACAG GGATATCTTT TGAATCTAAA 600
 AATTTGATGT ACAGCATGTG ATTTTGAAG TTTACATGTA AAGTCACAGT ATAGGTGAAA 660
 45 TAACGTTTGT CATATTTTGA GACGTATCCT GCAGCCATGT TTTTACGTGA GTGTTTGTAGT 720
 CAAAGTACAT GGTAGACAGT CTTTCACAAT AAAAGGAAAA GGATTTTTTT TCCTCCAAAT 780
 50 GTACATTTAT CAACCTAATG ATTGATTTTT TTA AAAAGAG ATTTGCCCC AGTCTGGTTT 840
 ATGAAAGTTC ATTGCCCTAA ACTGTGCTGA TTGTTTTTAA TCAAGTTATA AATTCCAAC 900
 CTAGATCATG TATCTACCAA CTCTCCTGCA TTTTCAAAA GGCATTGAGC TTAATATTA 960
 55 GTCTTGCTTA GAGTAGGTTA TCCACTTACA TGCTGCGCTA AAGCCATGCC TTTGAACTC 1020
 CTTGTTTAAA ACATGATATG ATTTTGTGG GCAGTTTCAG AAAAGAAAAC AAACAAACAA 1080
 60 AAATCGACCC TTTAATTATT ACTTGCAACT CAACAGATCT CCCTGCCGTA CTGCCTTTTC 1140

CAGGAAC TTT ACTTCAGGGC TGTCCAGATT GCAGTTGTGC CCCGTGTATG TGGATCTAGT 1200
TCACAGAGTC TTTGGAAGCC AGCAGTCGTG CCCTCCGTAT ACTGTCCACT CATTTTATGT 1260
5 AGATTTGGTA TCCTCAGCAG CCAGTGTTAA CACCACTGTC ACGTAGTTAN CAGATTCATC 1320
TTTATGTAT TTAAAGTAAT CCATACTATG ATTTGGTTTT TCCCTGCACC ATTAATTCTG 1380
10 GCATCAGATC AGTTTTTGTG TTGTGAAGTT CTA CTGTGGT TTGACCCAAG ACCACAACCA 1440
TGAGACCCCTG AAGTAAAGAT AAGGTACACA TACATTATTT GAGTAACTGT TTCCTTGGGG 1500
GCCAATCTGT GTATGCTTTT AGAAGTTTAC AGAATGCTTT TATTTTGTG TATAACAAAC 1560
15 AGTCTGTCAT TTATTTCTGT TGATAAACCA TTTGGACAGA GTGAGGACGT TTGCCCTGTT 1620
ATCTCCTAGT GCTAACAAATA CACTCCAGTC ATGAGCCGGG CTTTACAAAT AAAGCACTTT 1680
20 TGATGACTCA MAAAAAAAAA AAAAAAAMC YCGGGGGGGG GCCGGTAACC CATTTNNCCC 1740

25 (2) INFORMATION FOR SEQ ID NO: 200:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 1707 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

35 GCTTATAGAA GGGAGAGGAG CGAACATGGC AGCGCGTTGG CGGTTTTGGT GTGTCTCTGT 60
GACCATGGTG GTGGCGCTGC TCATCGTTTG CGACGTTCCC TCAGCCTCTG CCCAAAGAAA 120
GAAGGAGATG GTGTTATCTG AAAAGGTTAG TCAGCTGATG GAATGGACTA ACAAAGACC 180
40 TGTAATAAGA ATGAATGGAG ACAAGTTCCG TCGCCTTGTG AAAGCCCCAC CGAGAAATTA 240
CTCCGTTATC GTCATGTTCA CTGCTCTCCA ACTGCATAGA CAGTGTGTG TTTGCAAGCA 300
45 AGCTGATGAA GAATCCAGA TCCTGGCAAA CTCCTGGCGA TACTCCAGTG CATTACCAA 360
CAGGATATTT TTTGCCATGG TGGATTTTGA TGAAGGCTCT GATGTATTTC AGATGCTAAA 420
CATGAATCA GCTCCAAC TTTCATCAACT TCCTGCAAAA GGGAAACCA AACGGGGTGA 480
50 TACATATGAG TTACAGGTGC GGGGTTTTTC AGCTGAGCAG ATTGCCCGGT GGATCGCCGA 540
CAGAACTGAT GTCAATATTA GAGTGATTAG ACCCCCAAAT TATGCTGGTC CCCTTATGTT 600
55 GGGATTGCTT TTGGCTGTTA TTGGTGGACT TGTGTATCTT CGAAGAGTAA TATGGAATTT 660
CTCTTTAATA AAAGTGGATG GGCTTTTGCA GCTTTGTGTT TTGTGCTTGC TATGACATCT 720
GGTCAAATGT GGAACCATAT AAGAGGACCA CCATATGCCC ATAAGAATCC CCACACGGGA 780
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CATGTGAATT ATATCCATGG AAGCAGTCAA GCCCAGTTTG TAGCTGAAAC ACACATTGTT 840
 CTTCTGTTTA ATGGTGGAGT TACCTTAGGA ATGGTGCTTT TATGTGAAGC TGCTACCTCT 900
 5 GACATGGATA TTGGAAGCG AAAGATAATG TGTGTGGCTG GTATTGGACT TGTGTATTA 960
 TTCTTCAGTT GGATGCTCTC TATTTTGA TCTAAATATC ATGGCTACCC ATACAGCTTT 1020
 CTGATGAGTT AAAAAGGTCC CAGAGATATA TAGACACTGG AGTACTGGAA ATTGAAAAAC 1080
 10 GAAAATCGTG TGTGTTTGAA AAGAAGAATG CAACTTGAT ATTTGTATT ACCTCTTTT 1140
 TTCAAGTGAT TTAAATAGTT AATCATTTAA CCAAAGAAGA TGTGTAGTGC CTTAACAAGC 1200
 15 AATCCTCTGT CAAAATCTGA GGTATTGAA AATAATTATC CTCTTAACCT TCTCTCCCA 1260
 GTGAACTTTA TGGAACATTT AATTTAGTAC AATTAAGTAT ATTATAAAAA TTGTAAACT 1320
 ACTACTTGT TTTAGTTAGA ACAAAGCTCA AACTACTTT AGTTAACTTG GTCATCTGAT 1380
 20 TTTATATTGC CTTATCCAAA GATGGGGAAA GTAAGTCCTG ACCAGGTGTT CCCACATATG 1440
 CCTGTTACAG ATAACTACAT TAGGAATTCA TTCCTAGCTT CTCATCTTT GTGTGGATGT 1500
 25 GTATACTTTA CGCATCTTTC CTTTGTAGTA GAGAAATTAT GTGTGTCATG TGGTCTCTG 1560
 AAAATGGAAC ACCATTCTTC AGAGCACAG TCTAGCCCTC AGCAAGACAG TTGTTTCTCC 1620
 TCCTCCTGC ATATTCTTA CTGAAATACA GTGCTGTCTA TGATGTTT TGTGTTGTG 1680
 30 TTTTPTYGAG ATCACGYTAC TGGGCTC 1707

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(2) INFORMATION FOR SEQ ID NO: 201:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 779 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

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CTGTCCCCAG TGTTCAGG TAATGACTTG GCACTCCAGA GAAAGTTTCA TRCTGTGCG 60
 TGTGGTGGCT CCAAGCÁAG CACCTGGCAT GCAGGTCAGC CTTCCCAGC GGGCGTGGCG 120
 50 TCGTCCTCTT CACAGATGCC ACGTGCAGC CCCAAGGCCT CACCATTTTG CGTTTTTTAG 180
 AAACCAATT TCTTGGTCAT TTATAAGCT GCTTTATAGA TATCTTTGAT CCTGGCATGC 240
 CTTGGTTTCC TCTCCCTCC CTCTTTCCAA TCCTGGTTTC CTAACCTCCT CTGTAGTAA 300
 55 TTCTCAACTC AACTCAAAGT CCCAAGAATT TGAATGGTA GGATGCTGTG CGGGAGCTC 360
 GAGGCTGAGG CATAATCACT GCTTCGGTTC TGCTCATCAG GGGACACGCT CCCTTACTCA 420
 60 TGGCAGCCAT GTTGATTGT CACAGAGCCC CCCGAATACT CTGTCTATAG TGACACACTG 480

	TAGGTGTCAT AAATTTTAAG AAACCTGCTT TTAAGTACTA TTTATAGGTT TTCTGTTAT	540
	ACTTGCAACC TAGTTTAA ATACATGAGG ATTTTATGAA AGCTTTATAC AGACATTTAT	600
5	AGGAAACTCA TTCCTTGATT TTAGGTGCCA TTAAATTGA TAACACTTAC TTTATAAAAA	660
	GATGCTTTTT GTCGGATAG AGCCTTATAG TTAAATAT CTTCATATAT TGCCATTTGA	720
10	TCAAATAAAT TTCTACTTA GAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAACTCGA	779
15	(2) INFORMATION FOR SEQ ID NO: 202:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 1617 base pairs	
	(B) TYPE: nucleic acid	
20	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:	
25	GGCACAGCTT TCTGTCTCTT CCTCGCTCCC TCTCTTCTC TCCTCCCTCT GCCTTCCCAG	60
	TGCATAAAGT CTCTGTCGCT CCCGGAACCT GTTGGCAATG CCTATTTTTT GGCTTTCCCC	120
	CGCGTCTCT AACTAACTA TTAAAGGTC TCGGTCGCA AATGGTTTGA CTAAACGTAG	180
30	GATGGGACTT AAGTTGAACG GCAGATATAT TTCACTGATC CTCGCGGTGC AAATAGCGTA	240
	TCTGGTGCAG GCCGTGAGAG CAGCGGGCAA GTGCGATGCG GTCTTCAAGG GCTTTTCGGA	300
35	CTGTTTGCTC AAGCTGGGCG ACACATGGCC AACTACCCGC AGCCTGGGAC GACAAGACGA	360
	ACATCAAGAC CGTGTGCACA TACTGGGAGG ATTTCCACAG CTGCACGGTC ACAGCCCTTA	420
	CGGATGCCA GGAAGGGGCG AAAGATATGT GGGATAAACT GAGAAAAGAA TCCAAAAACC	480
40	TCAACATCCA AGGCAGCTTA TTCGAACTCT GCGGCAGCGG CAACGGGGCG GCGGGTCCC	540
	TGCTCCCGGC GTTCCCGGTG CTCTGGTGT CTCTCTCGGC AGCTTTAGCG ACCTGGCTTT	600
45	CCTTCTGAGC GTGGGGCCAG CTCCCCCCGC GCGCCACCC AACTCACTC CATGCTCCCG	660
	GAAATCGAGA GGAAGATCCA TTAGTTCTTT GGGACGTTG TGATTCTCTG TGATGCTGAA	720
	AACACTCATA TAGGATTGTG GGAAATCCTG ATTCTCTTTT TTATTTCTGTT TGATTTCTTG	780
50	TGTTTTATTT GCCAAATGTT ACCAATCAGT GAGCAAGCAA GCACAGCCAA AATCGGACCT	840
	CAGCTTTAGT CCGTCTTCAC ACACAAATAA GAAAACGGCA AACCACCCC ATTTTTTAAT	900
55	TTTATTATTA TTAATTTT TTGTTGGCAA AAGAATCTCA GGAACGGCCC TGGGCACCTA	960
	CTATATTAAT CATGCTAGTA ACATGAAAAA TGATGGGCTC CTCCTAATAG GAAGCGGAGG	1020
60	AGAGGAGAAG GCCAGGGGAA TGAATTCAAG AGAGATGTCC ACGGACGAAA CATACGGTGA	1080

ATAATTCACG CTCACGTCGT TCTTCCACAG TATCTTGTTT TGATCATTTT CACTGCACAT 1140
 TTCTCCTCAA GAAAAGCGAA AGGACAGACT GTTGGCTTTG TGTGTGGAGG ATAGGAGGGA 1200
 5 GAGAGGGAAG GGGCTGAGGA AATCTCTGGG GTAAGAGTAA AGGCTTCCAG AAGACATGCT 1260
 GCTATGGTCA CTGAGGGGTT AGCTTTATCT GCTGTTGTTG ATGCATCCGT CCAAGTTCAC 1320
 TGCCTTTATT TTCCCTCCTC CCTCTTGTTT TAGCTGTAC ACACACAGTA ATACCTGAAT 1380
 10 ATCCAACGGT ATAGATCACA AGGGGGGAT GTTAAATGTT AATCTAAAAT ATAGCTAAAA 1440
 AAAGATTTTG ACATAAAGA GCCTTGATTT TAAAAAAGAG AGAGAGAGAG ATGTAATTTA 1500
 15 AAAAGTTTAT TATAAATTAA ATTACAGCAA AAAAGATTG CTACAAAGTA TAGAGAAGTA 1560
 TAAATAAAAA GTTATTGTTT GAAAAAAGAG AAAAAAAGAG CTCGACCGCA AGGGAAT 1617

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(2) INFORMATION FOR SEQ ID NO: 203:

(i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 1974 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

GAATTCGGCA CGAGGCTGAG GGAGCTGCAG CGCAGCAGAG TATCTGACGG CGCCAGGTTG 60
 CGTAGGTGCG GCACGAGGAG TTTTCCCGGC AGCGAGGAGG TCCTGAGCAG CATGGCCCGG 120
 35 AGGAGCGCCT TCCCTGCCGC CGCGCTCTGG CTCTGGAGCA TCCTCCTGTG CCTGCTGGCA 180
 CTGCGGGCGG AGGCCGGGCC GCCGCAGGAG GAGAGCCTGT ACCTATGGAT CGATGCTCAC 240
 40 CAGGCAAGAG TACTCATAGG ATTTGAAGAA GATATCCTGA TTGTTTCAGA GGGGAAAATG 300
 GCACCTTTTA CACATGATTT CAGAAAAGCG CAACAGAGAA TGCCAGCTAT TCCTGTCAAT 360
 ATCCATTCCA TGAATTTTAC CTGGCAAGCT GCAGGGCAGG CAGAATACTT CTATGAATTC 420
 45 CTGTCCTTGC GCTCCCTGGA TAAAGGCATC ATGGCAGATC CAACCGTCAA TGTCCCTCTG 480
 CTGGGAACAG TGCCTCACA GGCATCAGTT GPTCAAGTTG GTTCCCATG TCTTGAAAAA 540
 50 CAGGATGGGG TGGCAGCATT TGAAGTGGAT GTGATTGTTA TGAATTCTGA AGGCAACACC 600
 ATTCTCCAAA CACCTCAAAA TGCTATCTTC TTTAAAACAT GTCAACAAGC TGAGTGCCCA 660
 GGCGGGTGCC GAAATGGAGG CTTTGTGAAT GAAAGACGCA TCTGCGAGTG TCCTGATGGG 720
 55 TTCCACGGAC CTCACTGTGA GAAAGCCCTT TGTACCCAC GATGTATGAA TGGTGGACTT 780
 TGTGTGACTC CTGGTTTCTG CATCTGCCCA CCTGGATTCT ATGGAGTGAA CTGTGACAAA 840
 60 GCAAACTGCT CAACCACCTG CTTTAATGGA GGGACCTGTT TCTACCCTGG AAAATGTATT 900

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TSCCCTCCAG GACTAGAGGG AGAGCAGTGT GAAATCAGCA AATGCCACACA ACCCTGTCGA 960
 AATGGAGGTA AATGCATTGG TAAAGCAAA TGTAAGTKTT CCAAAGGTTA CCAGGGAGAC 1020
 5 CTCTGTTCAA AGCCTGTCTG CGAGCCTGGC TGTGGTGCAC ATGGAACCTG CCATGAACCC 1080
 AACAAATGCC AATGTCAAGA AGGTTGGCAT GGAAGACACT GCAATAAAAG GTACGAAGCC 1140
 10 AGCCTCATAC ATGCCCTGAG GCCAGCAGGC GCCAGCTCA GGCAGCACAC GCCTTCACTT 1200
 AAAAAGGCCG AGGAGCGGCG GGATCCACCT GAATCCAATT ACATCTGGTG AACTCCGACA 1260
 TCTGAAACGT TTTAAGTTAC ACCAAGTTCA TAGCCTTTGT TAACCTTTCA TGTGTTGAAT 1320
 15 GTTCAAATAA TGTTCATTAC ACTTAAGAAT ACTGGCCTGA ATTTTATTAG CTTCAATTATA 1380
 AATCACTGAG CTGATATTTA CTCTTCCTTT TAAGTTTCT AAGTACGTCT GTAGCATGAT 1440
 20 GGTATAGATT TTCTTGTTTC AGTGCTTTGG GACAGATTTT ATATTATGTC AATTGATCAG 1500
 GTTAAATTT TCAGTGTGTA GTTGGCAGAT ATTTTCAAAA TTACAATGCA TTTATGGTGT 1560
 CTGGGGCAG GGAACATCA GAAAGTTAA ATTGGGCAAA AATGCGTAAG TCACAAGAAT 1620
 25 TTGGATGGTG CAGTTAATGT TGAAGTTACA GCATTTTCTA TTTTATTGTC AGATATTTAG 1680
 ATGTTTGTTA CATTTTAAA AATTGCTCTT AATTTTAAA CTCTCAATAC AATATATTTT 1740
 30 GACCTTACCA TTATTCCAGA GATTCACTAT TAAAAAATA AAAATTACAC TGTGGTAGTG 1800
 GCATTTAAAC AATATAATAT ATTCTAAACA CAATGAAATA GGAATATAA TGTATGAACT 1860
 TTTTGCATTG GCTTGAAGCA ATATAATATA TTGTAAACAA AACACAGCTC TTACCTAATA 1920
 35 AACATTTTAT ACTGTTTGTA TGTATAAAAT AAAGGTGCTG CTTTAGTTT CTGA 1974

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(2) INFORMATION FOR SEQ ID NO: 204:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1057 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

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CGGCCCTCCG GGGCAACCGT TCGTCCCAAC NCGGAAAGG GTCCTGGAGN CGGGAACCTAG 60
 GAGCCTCGGA AGTCCAAGGG CGGAGCGCCC TTTGCTAATA AGCCAATCAG AACGTGAGAC 120
 55 GCTCCGGTGG GNCGGTGCCG TCGAGCGCGG GGTGGAGTCT GGGTGACTTG GCTGGCGGGA 180
 TCAAGTGCAG CTGCTTCAGG CTGAGGTGGC AGATAGTGAG CGCTGGTGGC GGAGTTAAAG 240
 TYAAAGCAGG AGAGTAATWA TGAATAGCGC AGCGGATTC TCACACCTAG ACCGTCGCGA 300
 60

GCGGGTCTC AAGTTAGGG AGAGTTTCGA GAAGCAGCCG CGCTGCGCTT CCACACTGTG 360
 CGCTATGACT TCAAACCTGC TTCTATTGAC ACTTCTTCTG AAGGATACCT TGAGKTTGGC 420
 5 GAAGKTGAAC AGKTGACCAT WACTCTGCCM AATATAGAAA GTTGAAGGAA GCAGTAAAT 480
 TCAGTATCGT AAAGAACAAC AGCAACAACA ATGTGGAATT CASCAGGAC TCCCAATCTT 540
 GTAAACATT CTCCATCTGA AGATAAGATG TCCCCAGCAT CTCCAATAGA TGATATCGAA 600
 10 AGAGAAGTGA AGGCAGAAGC TAGTCTAATG GACCAGATGA GTAGTTGTGA TAGTTCATCA 660
 GATTCCAAAA GTTCATCATC TTCAAGTAGT GAGGATAGTT CTAGTGACTC AGAAGATGAA 720
 15 GATTGCAAAT CCTCTACTTC TGATACAGG NAATTGTGTC TCAGGACATC CTACCATGAC 780
 ACAGTACAGG ATTCCTGATA TAGATGCCAG TCATAATAGA TTTCGAGACA ACAGTGGCCT 840
 TCTGATGAAT ACTTTAAGAA ATGATTTGCA GCTGAGTGAA TCAGGAAGTG ACAGTGATGA 900
 20 CTGAAGAAAT ATTTAGCTAT AAATAAAAT TTATACAGCA TGTATAATTT ATTTTGTATT 960
 AACATAAAA ATTCCTAAGA CTGAGGAAA TATGTCTTAA CTTTGTATGA TAAAGAAAT 1020
 25 TAAATTTGAT TCAGAAAAA AAAAAAAAAA AACTCGA 1057

30 (2) INFORMATION FOR SEQ ID NO: 205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 721 base pairs
 (B) TYPE: nucleic acid
 35 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

40 GAATTCGGCA CGAGTCATCC CTCTCCCTCT TCACTCCCT TACTCTTACT CTGTTTTTTG 60
 TGCTCCAGAC AGACAGACCC TACCTCTTTT GCTTCTTTT TGTGTTTG TTTTGAGATG 120
 GAGTGTGCT CTGTGTGCCC AGGCTGGAGT GCAGTGGCGC AATCTCGGCT CACCACAACC 180
 45 TCTGCCTCCC GGGTTCAAGC AATTCTCCTG CCTCAGCCTC CCGAGAAGCT GGGGATTACA 240
 GGCATGCGCC ACCACACCCA GCTNAATTTT ATATTTTATG TAGAGATGGT GTTCTCCAT 300
 50 GTTGGTCAGG CTGGCCTCAA ACTCCCAACC TCAGGTGATN CCGCCTGCTT TGGCCTCCCC 360
 AAAGTGCTGG GATTACAGGC GTGAGCCACT GCGCCAGCC TCTTTTGCTC CTTTATACTC 420
 ATTAATCAC GCCTGTAATC CCTGTTTTGG GAGGCCAAAG TGAGAAGGTT GCTTGAGGCC 480
 55 AAGAGTTTGA GACTAGCCTG GGCAACACAG CAAGATGCCA TCTTTATAAT AAAAATAAAA 540
 ATAAAAATCA ATTAGCTGGG CATGGTGGAA CGCACCTGTA GTCCAGCCA ATTGAGAGGC 600
 60 TGAAGTGGGA GGATCATTGA GCCCAGGAGT TGAGGTGCA GTGAGCCATG ATCATGTCAC 660

TACACTCAGC CTGGGCAATA GAGGACATG TTGTCTCTAA AAAAAAAAAA AAAAAACTCG 720

A 721

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(2) INFORMATION FOR SEQ ID NO: 206:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2465 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

CCACCATTTA TCCAAGTAA GAGGAGTAC AGGCAGTTCA GAAATTTGTT TCTATTACTG 60
AACCTGCTTT AAAACTCGTT TCAGACAGTT TGTCTGAACA TGAGAAGAAC AAGAACAAAG 120
AGGGAGATGA TAAGAAAGAG GGAGGTAAAG ACAGAGCTTT GAAAGGAGTT TTGCGAGTGG 180
GAGTATTGGC AAAAGGATTA CTTCTCCGAG GAGATAGAAA TGTCAACCTT GTTTTGCTGT 240
GCTCAGAGAA ACCTTCAAAG ACATTATTAA GCCGTATTGC AGAAAACCTA CCCAAACAGC 300
TTGCTGTTAT AAGCCCTGAG AAGTATGACA TAAATGTGC TGTATCTGAA GCGGCAATAA 360
TTTTGAATTC ATGTGTGGAA CCCAAATGC AAGTCACTAT CACTGACA TCTCCAATTA 420
TTCGAGAAGA GAACATGAGG GAAGGAGATG TAACCTCGGG TATGGTGAAA GACCCACCGG 480
ACGTCTTGA CAGGCAAAAA TGCTTGACG CTCTGGCTGC TCTACGCCAC GCTAAGTGGT 540
TCCAGGCTAG AGCTAATGGT CTGCAGTCCT GTGTGATTAT CATACGCATT CTTGAGAGC 600
TCTGTCAGCG AGTTCCAAGT TGGTCTGATT TTCCAAGCTG GGCTATGGAG TTACTAGTAG 660
AGAAAGCAAT CAGCAGTGCT TCTAGCCCTC AGAGCCCTGG GGATGCACTG AGAAGAGTTT 720
TTGAATGCAT TTCTTCAGG ATTATTCTTA AAGGTAGTCC TGGACTTCTG GATCCTTGTG 780
AAAAGGATCC CTTTGATACC TTGCAACAA TGAAGTACCA GCAGCGTGAA GACATCACAT 840
CCAGTGACA GTTTGCATTG AGACTCCTTG CATTCGCCCA GATACACAAA GTTCTAGGCA 900
TGGATCCATT ACCGCAAATG AGCCAACGTT TTAACATCCA CAACAACAGG AAACGAAGAA 960
GAGATAGTGA TGGAGTTGAT GGATTGAAG CTGAGGGGAA AAAAGACAAA AAAGATTATG 1020
ATAACTTTTA AAAAGTGTCT GTAAATCTTC AGTGTAAAA AAACAGATGC CCATTTGTG 1080
GCTGTTTTTC ATTCATAATA ATGTCTACAT TGAAAAATTT ATCAAGAATT TAAAGGATTT 1140
CATGGAAGAA CCAAGTTTTT CTATGATATT AAAAAATGTA CAGTGTTAGG TATTATTGTA 1200
ATGGAAAGAC ACCCAAAAAA AAAAATGTGC TCCGACTAGG GGGAAAACAG TAGTTCGGAT 1260

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	TTTTTCCCAT TATTTTATT TTATTTTCTG GTTGCCCTAG CTCCCCCCC TATTTTGTG	1320
	TCTTTTATTA ACTAGTGCAT TGTCITATTA AATCTTCACT GTATTTAATG CAGGATGTGT	1380
5	GCTTCAGTTG CTCTGTGTAT TTTGATATTT TAATTTAGAG GTTTTGTGTTG CTTTTTGACA	1440
	CTAGTTGTAA GTTACTTTGT TATAGATGGT ATCCTTTACC CCTTCTTAAT ATTTTACAGC	1500
	AGTACGTTTT TTTGTAACGT GAGACTGCAG AGTTTGTTTT TCTATATGTG AAGGATTACA	1560
10	ACACAAAAAG TTATCCTGCC ATTCGAGTGC TCAGAACTGA ATGTTTCTGC AGATCTTGTG	1620
	GCATTTGTCT CTAGTGTGAT ATATAAAGGT GTAATTAAGA CAGAGTCTG TTAATCTAAT	1680
15	CAAGTTTGCT GTTAGTTGTG CATTAGCAGT ATAAAAGCTA ATATATACTA TATGGTCTTG	1740
	CAACAGTTTT AAAGCCTCTG CATAATIGAT AATAAAAATG CATGACATTC TTGTTTTTAA	1800
	TAGACTTTTA AAATCATAAT TTTAGGTTTA ACACGTAGAT CTTGTACAG TTGACTTTTT	1860
20	GACATAGCAA GGCCAAAAAT AACTTTCTGA ATATTTTTTT CTTGTGTATA AGTGAAAGG	1920
	GCATTTTCA CATATAAGTG GGCTAACCAA TATTTTCAA AGAACTTCAT CATTTGTACAA	1980
25	CTAACACAG TAACTAGCCC TTAATTATGG TGACAGTTCC TTATTGGTGT GTGTGAGATT	2040
	ACTCTAGCAA CTATTACAGT ATAACACAGA TGATCTTCTC CACACACCCC ATCACCAGA	2100
	TAATTTACAG TTCTGTAAAC AGTGAGGTG ATAAAGTATT ACTGATAAAA AATTATCTAA	2160
30	GGAAAAAAC AGAAAATTAT TTGGTGTGGC CATCTTACCT GCTTATGTCT CCTACACAAA	2220
	GCTAAATATT CTAGCAGTGA TGTAATGAAA AATTACATCT TACTGTTGAT ATATGTATGC	2280
35	TCTGGTACAC AGATGTCATT TTGTTGTCAC AGCACTACAG TGAAATACAC AAAAAATGAA	2340
	ATTCATATAA TGACTTAAAT GTAPTATATG TTAGAATTGA CAACATAAAC TACTTTTGCT	2400
	TTGAAATGAT GTATGCTTCA GTAAATCAT ATTCAAATTT AAAAAAAAAA AAAAAAAAAA	2460
40	CTCGA	2465

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(2) INFORMATION FOR SEQ ID NO: 207:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

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GAATTCGGCA CGAGCTCAAG CTGGCAGGTG GTCGGGGGAG CGGCCGGAGA GGAGCTGCCG	60
GGAGTTCGTG CCTGCAGGA CATGACACCA GTGGCATATC ACGGCCATGG GGTCTCAGCA	120
TTCCGCTGCT GTCGCCCCCT CTCCTGCAG GCGAAAGCAA GAAGATGACA GGGACGGTTT	180

460

GCTGGCTGAA CGAGAGCAGG AAGAAGCCAT TGCTCAGTTC CCATATGTGG AATTCACCGG 240
GAGAGATAGC ATCACCTGTC TCACGTGCCA GGGGACAGGC TACATTCCAA CAGAGCAAGT 300
5 AAATGAGTTG GTGCGTTTGA TCCCACACAG TGATCAGAGA TTGCGCCCTC AGCGAACTAA 360
GCAATATGTC CTCCTGTCCA TCCTGCTTTG TCTCCTGGCA TCTGGTTTGG TGGTTTTCIT 420
10 CCTGTTTCCG CATTCAGTCC TTGTGGATGA TGACGGCATC AAAGTGGTGA AAGTCACATT 480
TAATAAGCAA GACTCCCTTG TAATTCTCAC CATCATGGCC ACCCTGAAAA TCAGGAACTC 540
CAACTTCTAC ACGGTGGCAG TGACCAGCCT GTCCAGCCAG ATTCAGTACA TGAACACAGT 600
15 GGTGAATTTT ACCGGAAGG CCGAGATGGG AGGACCGTTT TCCTATGTGT ACTTCTTCTG 660
CACGGTACCT GAGATCCTGG TGCACAACAT AGTGATCTTC ATGCGAACTT CAGTGAAGAT 720
20 TTCATACATT GGCCTCATGA CCCAGAGCTC CTTGGAGACA CATCACTATG TGGATTGTGG 780
AGGAAATTC ACAGCTATTT ACAAAGTCTT ATGGGTCTTT CCACACAGCG CCTGTAGAAG 840
AGAGCACAGC ATATGTTCCC AAGGCCTGAG TTCTGGACCT ACCCCCACGT GGTGTAAGCA 900
25 GAGGAGGAAT TGGTTCACTT AACTCCAGC AAACATCCTC CTGCCACTTA GGAGGAAACA 960
CCTCCCTATG GTACCATTTA TGTTCCTCAG AACCAGCAGA ATCAGTGCCT AGCCTGTGCC 1020
30 CAGCAAATAG TTGGCACTCA ATAAAGATTG GCAGAAATTA ATACAGATCT TTTCAGCTGT 1080
TCTTAGGGCA TTATAAATGG AAATCATAAC GTGGTTCTAG GTTATCAAAC CATGGAGTGA 1140
TGTGGAGCTA GGATTGTGAG TGACCTGCAG GCCATTATCA GTGCCTCATC TGTGCAGAAG 1200
35 TCGCAGCAGA GAGGGACCAT CCAATACCT AAGAGAAAAC AGACCTAGTC AGGATATGAA 1260
TTTGTTCAG CTGTTCCCAA AGGCCTGGGA GCTTTTGTAA AAGAAAGAAA AAAGTGTGTT 1320
40 GGCTTTTTTT TTTTITAGAA AGTTAGAATT GTTTITACCA AGAGTCTATG TGGGGCTTGA 1380
TTCACCTTC ATCCATTGGC TGAACATGG ATTGGGGATT TGATAGAAAA ATAAACCCTG 1440
45 CTTTGTATTC AAAAAAAAAA AAAAAWAAA AAAAAGTCGA 1480

(2) INFORMATION FOR SEQ ID NO: 208:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 872 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

CAGTATTTC CTCAGTACTG TAAGCAAAAG TGGTATGTTT TTCTTTCTTT ATGTCTACTC

60

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TGTCTCTGT GGCCTCTGG TGTACCCCTC TCTTCCTAGC CATTCACTCT CTCTAGTCAC 120
 CTCCTAGTA GCTAGTGCTC TCTAAGTTT TATTTAATTA GAACAACTCC ATTTCCATTT 180
 5 CAAGGTAGGT CAATGGGGG AAAAGCCTCA TGATTTAAAC TGAAGTTAAC AACACAGCTT 240
 TTAAATGAA AACTCATACT CCAACTTCTA AAGTATATTT GAGCTGATTT GTTCCAAAA 300
 CAAAGATATG CTGTACCTAA AACTGCTAAA AAAAAATAT AAAGACAAGG ACTAGGTGAT 360
 10 TAAGGGGAGA GAAAAATCAT YCTTTTCCA GGAAACCTTT GCTAAAATAA GCAAAACTTG 420
 ANTCTATGCT TCA'TGGAAAC TGACACAAAG AAAAGAACT GATGGATTGC ACAGGCCTTG 480
 15 TTATAGAAAT AGATCTATAA AAAGATCTGT CCACAGGAAA TATACACCTT CTCCTGGTTC 540
 TGAACPTCAA TGGGGATTG TCACCTAGGT CTCCATCTAT AGGAATACCT TCACATACCT 600
 ATCTATTCAT GCACATATTC TGAAACAGG TACATACAAA ATTACAACAA AGGAAAAAAA 660
 20 TTCTATTGAA CACTTAAAA TAGAAACAGG CCAGGCACGG TGGCTCATGC TGTAATCCCA 720
 ACAATTTGGG AGGCTGAGGC TGGTGGATCA CCTGAGGTCA GGAGTGTGAG ACCAGCTTGG 780
 25 CCAACATGGT GAAACCCGT CACTACTAAA AATACAAAAA AAATTAGCCT GTGTGGTGGC 840
 ACACTCNTAC AATCCNGGCT GACTCGGGAA AN 872

30

(2) INFORMATION FOR SEQ ID NO: 209:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1779 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

AATTGCCAAG ACTGCACAAA ATTACAGTGC TAATGTATAT GGTTCAGTT CACATAAAGA 60
 CAAAAGCATC TGTATGAAA TGAGTAGTAA TATTGGGTGG TTGATTGTT CTTAGCAGAC 120
 45 TTGGCTTCAT WTTGGTCTTG AGATAAAATG GCCAGCATAA ATGCTGTTTA TATTCACGTT 180
 TTCTAGGTG TGTGTGTGCA GGCCACAGCA GCATGCCCTT GGTTAGTCA GTGCCGAAAS 240
 50 GGGTCTGTTT CTTCTTGAGC CTGCCTGCAG GGATGGTCTC CTTTAAAGC AGGTGTGTG 300
 CAGCATTCAG TAACTGAAG GTAAGCTAAA CCATCAACAT CTCTGGTGT TTAAGATGTT 360
 ATTTTATTGG AACAACTGAC AATGAGGGA TGTAGCTTT GTGCAGAAT TCCCTGCATG 420
 55 TGTGATAACT GATCTGTTT TATTTTTTGG CATTGCAACT GTGCATAGT TACAATTTCT 480
 GTTGKTCAT CACATTTAAA ATTGGRAGAG AACGCGCTTG AKGGATAGAG CGCCTTCAGK 540
 60 GTACTGTTT TATTAACTT TACTTTTTTT AAATCAACTT GCTATAGACT TTATATACAT 600

TTTGTAAAT ATAGTTCCTA GTGACATAGA AACGATGCGT AGTTTTCATT TACTAATTAC 660
AAATGTTGAG GCCTAATTCT GAAAGTCCTC ATATTTAAAG GCTAGACAAC GTAATGAAAT 720
5 TTTTAACTAT TTGTATGTCA TTTTGAAAGT GTACTGCTTT ATGGTAAAAG TGTMTTTCAT 780
TTGTTTCATTG TTTTCATTAT TTGTGATCAT GTTGTCTTTC AATACAGGCA TAAACCTTCC 840
10 ACTCTTGAAC AAAGCAGCTG CTTTTTAAAA GCGGTAATTG CTTCTTTACC TTTTATTTCT 900
TTTGTAATG AAGCTTTTCT TTAAGAATGT GACITTTAAAG TGTGTCTAT TGCATAAAAC 960
AGTTGACACT CACTTATGT AAAGTGAAGA TTGTTCTACT GCATGTGAAG TGGACCATGC 1020
15 AGATTCTGT ATGTTCTCAG TATGCATCAC TAGATAATAA AGTCTTTTGT GAACAAGGCA 1080
TTTGTAGCCA TTTTAAAAAG TTTTGTCTT CAGTGCTGGT AAGTCAGGTA AACCATAAAT 1140
20 AGTTAAAAGC AACCTTTTGT TTTTTCCTG AAAGTTTITA ATTGAAAGTA TTATTAGTTA 1200
AAGATGTAAA CCTAGCCAAA ATTACCAGTT TATTAATAAT TAGGATCCTA ATTATTTCAA 1260
AAAATCCTAC AAATATTGTC AGCTTTCAGT GTAGTGAGAT TATTCCTGTA GGTATATGGG 1320
25 TATAATTCAG GATTTAACTA ATGTTTCTGC TATTTTCTCA CTTTTCCTTT TGATGGTGCG 1380
GAAAGAGAAA AAGGAAAACG GGGCACAGGC CATTGACGC CTTCTCCAAG GGGTCTGATT 1440
30 TGCTGAGACA CCAGCTTCAC CTTCTTAACA AGGCACCTAA TTACAACAAG CATGCACATT 1500
TTGGTGCATT CAAGAATGGA AAATCAGAAT AGCAGCATTG ATTCTTCTGG TGCAGCTCAG 1560
TGGAAGATGA TGACAACCAG AAGACATGAG CTAAGGGTAA GGGACTGTTC TGAAGAACCT 1620
35 TTCCATTTAG TGATCAAGAT ATGGAAGCTG ATTTCTGAAA ATGCTCAGTG TGTACTCTAA 1680
TTATTTATGG TACCATTGA ATTGTAACCT GCATTTTAGC AGTGCATGTT TCTAATTGAC 1740
40 TTACTGGGAA ACTGAATAAA ATATGCCTCT TATTATCAA 1779

45 (2) INFORMATION FOR SEQ ID NO: 210:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2110 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

55 GCGGCCGCTG CAGCCCGAG CTGAGCTAGC CGTCCGAGCC GAGCCGTCCG AGCCGGGGAA 60
GCCGGCGCGT GCTGCCGCTC GTGGCGCCA GAGGAGAGGA GAGGCAGCAG CATGGCGAGT 120
60 GTCTGTCCC GACGCTTGG AAAGCGGTCC CTCCTGGGAG CCCGGGTGTT GGGACCCAGT 180

	GCCTCGGAGG GGCCTCGGCT GCGCCACCCT CGGAGCCACT GCTAGAAGGG GCCGCTCCCC	240
	AGCCTTTCAC CACCTCTGAT GACACCCCTT GCCAGGAGCA GCCCAAGGAA GTCCTTAAGG	300
5	CTCCCAGCAC CTCGGGCTT CAGCAGGTGG CCTTTMAGCC TGGGCAGAAG GTTTATGTGT	360
	GGTACGGGGG TCAAGAGTGC ACAGGACTGG TGGWGCAGCA CAGCTGGATG GAGGGTCAGG	420
	TGACCGTCTG GCTGCTGGAG CAGAAGCTGC AGGTCTGCTG CAGGGTGGAG GAGGTGTGGC	480
10	TGGCAGAGCT GCAGGGCCCC TGTCCCCAGG CACCACCCCT GGAGCCCGGA GCCCAGGCCC	540
	TGGCCTACAG GCCCGTCTCC AGGAACATCG ATGTCCCAA GAGGAAGTCG GACGCATGGA	600
15	AATGGATGAG ATGATGGCGG CCATGGTGCT GACGTCCCTG TCCTGCAGCC CTGTTGTACA	660
	GAGTCCTCCC GGGACCGAGG CCAACTTCTC TGCTTCCCGT GCGGCTGCG ACCCATGGAA	720
	GGAGAGTGGT GACATCTCGG ACAGCGGCAN CAGCACTACC AGCGGTCACT GGAGTGGGAG	780
20	CAGTGGTGTC TCCACCCCTT CGCCCCCCA CCCCAGGCC AGCCCCAAGT ATTTGGGGGA	840
	TGCTTTTGGT TCTCCCCAAA CTGATCATGG CTTTGAGACC GATCCTGACC CTTTCCTGCT	900
25	GGACGAACCA GCTCCACGAA AAAGAAAGAA CTCTGTGAAG GTGATGTACA AGTGCCTGTG	960
	GCCAAACTGT GGCAAAGTTC TGCCTCCAT TGTGGGCATC AAACGACACG TCAAAGCCCT	1020
	CCATCTGGGG GACACAGTGG ACTCTGATCA GTTCAAGCGG GAGGAGGATT TCTACTACAC	1080
30	AGAGGTGCAG CTGAAGGAGG AATCTGCTGC TGCTGCTGCT GCTGCTGCCG CAGACCCCA	1140
	GTCCCTGGGA CTCCCACCTC CGAGCCAGCT CCCACCCCA GCATGACTGG CCTGCCTCTG	1200
35	TCTGCTCTC CACCACCTCT GCACAAAGCC CAGTCCTCCG GCCCAGAACA TCCTGGCCCC	1260
	GAGTCCTCCC TGCCCTCAGG GGCTCTCAGC AAGTCAGCTC CTGGGTCCCT CTGGCACATT	1320
	CAGGCAGATC ATGCATACCA GGCTCTGCCA TCCTTCCAGA TCCCAGTCTC ACCACACATC	1380
40	TACACCAATG TCAGCTGGGC TGCTGCCCCC TCCGCCGCTT GCTCTCTMTC TCCGGTCCGG	1440
	AGCCGGTTCG TAAGCTTCAG CGAAGCCCCA GCAGCCAGCA CCTGCGATGA AATCTCATCT	1500
45	GATCGTCACT TCTCCACCCC GGGCCAGAG TGGTGCCAGG AAAGCCCGAG GGGAGGCTAA	1560
	GAAGTGCCCG AAGTGTATGG CATCGAGCAC CGGGACCACT GGTGCACGGC CTGCCGGTGG	1620
	AAGAAGGCCT GCCAGCGCTT TCTGGACTGA GCTGTGCTGC AGGTTCCTACT CTGTTCTCTG	1680
50	CCCTGCCCGC AGCCACTGAC AAGAGGCCAG TGTGTACCA GCCCTCAGCA GAAACCGAAA	1740
	GAGAAAGAAC GGAAACACGG AGTTTGGGCT CTGTTGGCTA AGGTGTAACA CTAAAGCAA	1800
55	TTTTCTCCCA TTGTGCGAAC ATTTTATTTT TTAACAAAAA GAAACAAAAA TATTTTCCC	1860
	CCTAAAATAG GAGAGAGCCA AACTGACCA AGGCTATTCA GCAGTGAACC AGTGACCAA	1920
60	GAATTAATTA CCCTCCGTTT CCCACATCCC CACTCTCTAG GGGATTAGCT TGTGCGTGTC	1980

AAAAGAAGGA ACAGCTCGTT CTGCTTCCTG CTGAGTCGGT GAATTCTTTG CTTTCTAAAC 2040
TCTTCCAGAA AGGACTGTGA GCAAGATGAA TTTACTTTTC TTAAAAAAA AAAAAAAAAA 2100
5 AAAAACTCGA 2110

10 (2) INFORMATION FOR SEQ ID NO: 211:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 938 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

20 GGCACAGGAA AAAAAAGAAA AAAGAAAAA GAAAAAGTT TTTGTACCCA CAGATTAGCA 60
TTTTCTTGAT GTTTGAAAA AGTTTAAGCT ATGTCCTAAT TTAAAAATGA GCACAAACTA 120
CTTAACAGAT GTCTGTTCCC TCTTCTCTTA CTTAAATTAT CTTTATTTTC ACCATCACCT 180
25 CCCAGTGCCG AACACCTGAN CTCTGTGTTT TGTGGTTGGA TCCTGGGTTG CCAAGTTCCT 240
ATTTGGTCAG TCCCTGGCCT GTGGGGCGGT CTCAGGAAGT GGCATGCTCT TCAMGRAGGA 300
30 TCGTTTCATYT CCAGTATAAC CAWTTTGTTA ATAATAGTTG ATAATTCCCA GCTTTTACCA 360
GATGARTTTT GACTTATTTT TCCTCCTTTG ACCTGTTCAA AGCTAACATA TCTCGGTCAG 420
TTCGGAGAGG GTGGGGGATT TGAGAATGTG AGGAGGAGTG GGGTTAGAAT GGGTTTGCCT 480
35 ATCTGGGCAA GGAAAGAGTT CCTAGTCGAT TGGGCACAAT GACAAAATGA TTCCATGGAT 540
AGAATCGTCC CATGTTGCTG GAACACCTCA CGTGTGTGA ACGCCTTAAA TTCTTGCCAT 600
40 CCCTTCTCTG ATTCCCCACC TCCCTGTAGT TTCCACAGGA TTTATCTCTC TGTACCCCCG 660
TCCTCCAAC TACTCTGTC AGCCTCTCCT CCATCCCTTA CTTCCCTTCT AAATTCCAGG 720
AGATGACCTC ACTTTGCAAA GCAAATTGGA GCCACCAAAT TGTAGCTCTC CTCGGTGGAA 780
45 ACTGCATCTG TGCTCATCCC TGCACCTTCT TGCAGAAAGC CGCCCCCTCA GGCCAAGATG 840
AGTGCTGGC CCCCATGGGA GACTCAGACA CTTTGACCCC TTGTGACTTC AGCATCTCCC 900
50 TCTTTAAAGA TTCTCTCCA ACATTCAGTC GTGCTCGA 938

55 (2) INFORMATION FOR SEQ ID NO: 212:

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 1551 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

5	AGGCTGGACT AAGCATAGAG AACCAGGAGA GAAAGAAAGA TTAAAGAGAC TGAGTAATAT	50
	TTTTTGACAG ATCATTAAAG AAAGTGAAGT ATTTTTTTTT TCTCCAAAAG GGCATGGGTT	120
	TTTTTTTTGT TTGTTTTTTT CTCTATTTGG CACTTTCTAG GGATGGTCT ATAAATTTTT	130
10	TGAAAGATCA TAGGATAAAT TTCTTTGTAG CAACTTCCTA TTTTAGTGT TATGTTAGGG	240
	GARCCCCARG TGTCCTTGCT GATACGCCAT TAGGGCCACT TCTCAGCCTC TGGCTACATC	300
15	ATAATGCTTT TTTTCTATC TTGCCAAAGT TTCCMGAAAA TTKAKGTTTT CTAAATTTAA	350
	AAAAATTGGT TGTGGAGATG GGATGGGACC TCTTTATAAG CCCTGAAAAT AAGTGATTN	420
	TTTTAAGTGC TATCTGCTA TAAACCTGAT TCTCACTTTT TTCTGTAGAC AACAGTTTTT	430
20	TATAATATAT CTATTTTGTG TGGACATTAT TTCCTTTTAA CCAATACTGA AATTCCATAG	540
	TGTAWACTTT CTCCACATTT TCTTTGATTA ATACTTYCTT AAAATAGACA CTGGGATTGG	630
25	CACCAGCTGT CACCAATAAA GCTGCCCTGA ACATGTGCAA TCAATCCTGT TAAACCAATT	650
	GAGAATTTTT CTGGAATGCT TAGTTAGGGA TGAAATGCT GGGTTATAGG TATGAGTATG	720
	CTTGATATAC TTTTCTCCAG AATGTCTACA CCTGTGTGTA CACCACATCT CCAGAGATAG	730
30	GGGAATCTTA TGTCCTGCT AACTGCTCTC GTTATTTAAT TTTCTGACAT TTGCCGCCGC	840
	CGCCGCCCCC TGCCCCAAC ACACACATGG TATAAAGTGG TAGTTTCTTG TTTTAAATG	930
35	AACTTTGAAG TGATTGAAT TTGGGCATTT CTTGTATCC TGAGTTATTT TGGTTTCCCG	950
	TTATGTGAAT ATCCTTTTCC TATGCTTTAA CTACTTTTCT AATTGTCCC TTTTTNGGT	1020
	TATCAAATTC CAGGCCATTG TCTATTCCAT CGTCACTTTT GGGTATTGGA AACATCTTTC	1030
40	CATTCTGTAG CCTGTCTGTT GAACATAAAT CTGATTTTT ATGTAATCAG ATTTTCTCC	1140
	TTACGGTTAT GTTCTTGGA TTTTATTTAA GAAATCTTT TCTATCCTGA GACCACAAAA	1200
45	ATGTCCCCAC CATTTTCTTC TGTTTCATAG TTTGCTTG TATGTTAAT CCTTTAAGGC	1250
	ATGTGTAGTT CATTTTATAT GGTGTGAAAT AGTCTTATT CATTTATTCA ACACATATTG	1320
	GTGGAGTGCC TGCTGATGGT AGTACTCTTC AGAGTACTTT GTATATATTT GTGAACACAT	1330
50	ATTCTTGCCC TGGAAGCTTA TGTGTCTNTT CAAGGTAGAT CCNACTCGG TTCCACCTG	1440
	TTTTCTTCAG CCCTCAGGAT GAATCCACA ATTTTACACA TAGCACCAGT TAAGGAATAG	1500
55	GCTTTATTGG AGAAAAGGAA GGCTTATTAG ACCAGCATCA GCAAAAAAAA A	1551

60 (2) INFORMATION FOR SEQ ID NO: 213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 997 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

10 AGAGAGTCCT CAACAGAACC TAATCATGCT GGCACCCTAA TGTGATCTT CTAGCCTCCA 50
 GAACTGAGAG AACATAAACT CCAGTTGTTT AAGCTACCCA GGTATGGTA TTGTTATTA 120
 TAGCCCAAGC TAAGTCAGGT GGAAAGGCAG AAATAPTTTG AGAGATCTA TTCTACAAA 180
 15 AACAGAGTTG TTCTAAATGA AATGGCCAGA TATTCATCT TCTTCTACT AGTATTTATG 240
 AAAGTTTCAT TAAACACCAC TTGGCCAGCA CCCAGGCGTG CCACTCTCAG AACGGCAAC 300
 20 AAAAGCAAAT GATTTGAGGA ACAAAGAGT GGACACAGAG CTTCTCAGAA GATGGCTCCA 360
 TCTTCTGAGA TGATCTTCTG AGATCATCAA TTTTCTGCAC CTGATGCTCT ACTCCAATTG 420
 TAGTAGATAA GAGCAAAGAC ACTTCTGAT CCTGTGGAAA ATGCTGAGC CCTGCTGATG 480
 25 GAGAGGCTGA CACTGGGACC AACAGAAGGC CGGACATTTA TTGCTGCAG CCTTCTGCA 540
 CCTGGGCCCT CTTCAGGCT TGTACCTTGC ACTCCCCATG CCACTGTAGC ACCTGGTAG 600
 30 CTGAAGTTAG GTATTTGAAG AGATAATTGG CCCCCAACAA AGATTACTT AAAAGAAAA 660
 GGAAACCACT AAATCCACT TGACAAACCA GTTGTTCAG TTTTGACTTT TGCAAATTG 720
 AAACTTTCTC TTTGGCACCA TATGATCTG TTACATTAGG GTCATCAAT CTAAGATAC 780
 35 ACAGCTAGGT CTACCAGCTG CCAGTGGTCA AGAATGAPAG AACCTCTCAG AGAGAGATCA 840
 GTTTCTAATA ACCTAACAGT TTTCCTTGGG TATTACMAA AAAAAAAA TTAGAATAAA 900
 40 ATGTCAGTGC CATGCAGGCA AGTACAGATA TGAATGAA AGCTTGTCT ACAACTGCA 960
 GATTTGTTTG TTAATAAAAT TGATTGGGAT CACTCGA 997

45

(2) INFORMATION FOR SEQ ID NO: 214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1496 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

50 GAATTCGGCA CGAGTGACCA CAGATATCTT TGGCTTTCAG COTCACCACA ATGCTGTCCA 60
 CTATGTTTTT TTTAATCGAT TGACATCTCA TGAATCCACA AATTAGCCG CTTTTCATC 120

60

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TTTTCCATCT TTGTCATAGC TTCATCACGC ACGATGGAGG TCACTTCAGC ACTATCCGGA 180
GCGGCCTCAC GGACAGATCR GTGAATTGCC TTTTCCTTTT TCTTGATGTA CCGGATTGTC 240
5 GACTCGTTAA CATTGAGCTC ATGGCCAACA GCACTGTAAC TCATGCCTGA TTGGAGCTTA 300
TCCAACACGC GGAMTTTCTC CGTAAGGSAM ATCAMGGTCT TCTTTCGCTT AGGAACACTG 360
GGCARARCTT AARCACTACG CTTGGGGGCC ATTTTAGAAA GCAAAACCAC CCACAAAAAG 420
10 CAGAAAAAAA AGTGTGAGTA AACAGACTGN NGANAGGACT CTTGTGTTAC AGCACAGGAG 480
CTGCGACTAG AAGGCGGCGC TTCTCCCCAG TTCAAACCTC AGCTGGGAAC CTTACCTCCG 540
15 CCAACTCCAA ATTTTCACCC TCTGCGCATG CCCGGGAAAS AAACCCCCAG AACAGTACCG 600
TGATGATTGA TTTTAGGGTT ACAAATACAT TTTAGCAAGT AAGTGAATTT GGCATTACGA 660
ATTAATGATT AATGAAGGTC ACCTGTATTT CCATAGATAT GTAATTTTAT TTAAGCAGGT 720
20 TTATTATATT AAGGCGGSGA GGCAGCGCCG AAGACTACAA GTTCCAGCAT GCACCGCGTC 780
CGGGCGGGTT CGGGCTCCCA GCGAGGGCTT CAGGGACGCC AGCCCGGAGG CATCGGCCGG 840
25 AAGTGTCGTA GGGCAACCAC GTAGTACTCT CTGCGCATGT GCAAAGCGCT GTCGGGGGCC 900
GCCCTAGCTG CCGTCGCCGC CGCCGGGGCT CTATGGTCTC TCCCTAGAGC TTTGCCGTTG 960
GAGGCGGCTG CTGCGGTCTT GTGAGTTTGA CCAGCGTCGA GCGGCAGCAA CATGGAGGAA 1020
30 TTCGACTCCG AAGACTTCTC TACGTCCGAG GAGGACGAGG ACTACGTGCC GTCGGGTGAG 1080
CGATTCCGCC TGAGGCGAGA AGCGAATGCG CCCGCCCCAC GCCTCACGTG AGGCGCGCTC 1140
35 TGCCCCCGCG GCGGTCTGCC CTGTGGCCCA GGTGGTCCAG GGGGGCTCCT GTTCTCGAGC 1200
GTCCGCTCCC TCAGGCCCTT CATCCTCGGC CGCTCCGGCC CGAGGCGTGT GCGCGTGGCG 1260
GTTCTGTGCT CCCCTCCCGT TGGGCAGCTC CGGCCGCCGC CCCCTCTTGC AGCGCGGAA 1320
40 CGGCACATGG ACACGGCCCC TTGTCGCTAG GGACGCTCGT CGGTCAGCCC CGAACGACAA 1380
CGCTGCTTCA GAAGTCGGGG CGGCAGTTCT AGCCTTGGAA GTTTTTTTCA GCCCTGGCCC 1440
45 GAGAGAGCTG CTGGCCAACA ACCCGTCCAA GATAGAGCTG TCCGNTCTCC GNCTGG 1496

50 (2) INFORMATION FOR SEQ ID NO: 215:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1308 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

60 TTGGCANCNG GGAGAGGGAA AGAGGAGGAA ATGGGGTTTG AGGACCATGG CTTACCTTTC 60

CTGCCTTTGA CCCATCACAC CCCATTTCCT CCTCTTTCCC TCTCCCCGCT GCCAAAAAAA 120
 AAAAAAAGG AAACGTTTAT CATGAATCAA CAGGGTTTCA GTCCTTATCA AAGAGAGATG 180
 5 TGGAAAGAGC TAAAGAAACC ACCCTTIGTT CCCAACTCCA CTTTACCCAT ATTTTATGCA 240
 ACACAAACAC TGTCTTTTGG GGTCCCTTTC TTACAGATGG ACCTCTTGAG AAGAATTATC 300
 10 GTATTCCACG TTTTGTAGCC TCAGGTTACC AAGATAAATA TATGTATATA TAACCTTTAT 360
 TATTGCTATA TCTTGTGGA TAATACATTC AGGTGGTGCT GGGTGATTTA TTATAATCTG 420
 AACCTAGGTA TATCCTTTGG TCTTCCACAG TCATGTTGAG GTGGGCTCCC TGGTATGGTA 480
 15 AAAAGCCAGG TATAATGTAA CTTCACCCCA GCCTTGTAC TAAGCTCTTG ATAGTGATA 540
 TACTCTTTTA AGTTTAGCCC CAATATAGGG TAATGGAAAT TTCCTGCCCT CTGGGTTCCT 600
 20 CATTTTTACT ATTAAGAAGA CCAGTGATAA TTTAATAATG CCACCAACTC TGGCTTAGTT 660
 AAGTGAGAGT GTGAACTGTG TGGCAAGAGA GCCTCACACC TCACTAGGTG CAGAGAGCCC 720
 AGGCCTTATG TTTAAATCAT GCACTTGAAA AGCAAACCTT AATCTGCAA GACAGCAGCA 780
 25 AGCATTATAC GGTCACTCTG AATGATCCCT TTGAAATTTT TTTTGTGTTT GTTTGTTTAA 840
 ATCAAGCCTG AGGCTGGTGA ACAGTAGCTA CACACCCATA TTGTGTGTTT TGTGAATGCT 900
 30 AGCTCTCTTG AATTTGGATA TTGGTTATTT TTTATAGAGT GTAAACCAAG TTTTATATTC 960
 TGCAATGCGA ACAGGTACCT ATCTGTTTCT AAATAAACT GTTTACATTC ATTATGGGGT 1020
 ATGTATGACC TTCATTTTCC AAGAAATAGA ACTCTAGCTT AGAATTATGG ATGCTCTAAA 1080
 35 ATGTCAGAAT GGGAACTCTC CTCGAAGTTC TCCCAAATC AGAGACAGCA CTGCCTTCTC 1140
 CTAAATGATT ATTCTTTTCT CCCTGTTTTC TGGTATTTTC TAGGCATCCT TCTCACCACA 1200
 40 GCCATAACCC TTTTCTACTT CCATTAGGCC GTATAACTGG NGGACNGCT GGTGCGTATA 1260
 TAATACTGGT WCCAACAMAG GGGTCTGGA TGTACACMAG GTTATCTT 1308

45

(2) INFORMATION FOR SEQ ID NO: 216:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1705 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

TGGCCATGGA AGCGCTAGAA GGTTAGATT TTGAAACAGC AAAGAAGGAT TTCCTTGAT 60
 CTGGAGACCC CAAAGAAACA AAGATGCTAA TCACCAAACA GGCTGACTGG GCCAGAAATA 120
 60

	TCAAGGAGCC CAAAGCCGCC GTGGAGATGT ACATCTCAGC AGGAGAGCAC GTCAAGGCCA	180
	TCGAGATCTG TGGTGACCAT GGCTGGGTG ACATGTTGAT CGACATCGCC CGCAAACCTGG	240
5	ACAAGGCTGA GCGCGAGCCC CTGCTGCTGT GCGCTACCTA CCTCAAGAAG CTGGACAGCC	300
	CTGGCTATGC TGCTGAGACC TACCTGAAGA TGGGTGACCT CAAGTCCCTG GTGCAGCTGC	360
	AGTGGAGACC CAGCGCTGGG ATGAGGCCTT TGCTTTGGGT GAGAAGCATC CTGAGTTTAA	420
10	GGATGACATC TACATGCCGT ATGCTCAGTG GCTAGCAGAG AACGATCGCT TTGAGGAAGC	480
	CCAGAAAGCG TTCCACAAGG CTGGGCGACA GAGAGAAGCG GTCCAGGTGC TGGAGCAGCT	540
15	CACAAACAAT GCCGTGGCGG AGAGCAGGTT TAATGATGCT GCCTATTATT ACTGGATGCT	600
	GTCCATGCAG TGCCTCGATA TAGCTCAAGA TCCTGCCCAG AAGGACACAA TGCTTGCAA	660
	GTTCTACCAC TTCCAGCGTT TGGCAGAGCT GTACCATGGT TACCATGCCA TCCATCGCCA	720
20	CACGGAAGAT CCGTTCAGTG TCCATCGTCC TGAAACTCTT TTCAACATCT CCAGGTTCTT	780
	GCTGCACAGC CTGCCCAAGG ACACCCCTC GGGCATCTCT AAAGTGAAAA TACTCTTCAC	840
25	CTTGCCAAG CAGAGCAAGG CCCTCGGTGC CTACAGGCTG GCCCGGCACG CCTATGACAA	900
	GCTGCGTGGC CTGTACATCC CTGCCAGATT CCAAAAGTCC ATTGAGCTGG GTACCCCTGAC	960
	CATCCGCGCC AAGCCCTTCC ACGACAGTGA GGAGTTGGTG CCCTMTGTCT ACCGCTGCTC	1020
30	CACCAACAAC CCGCTGCTCA ACAACCTGGG CAACGTCTGC ATCAACTGCC GCCAGCCCTT	1080
	CATCTTCTCC GCCTCTTCTT ACGACGTGCT ACACCTGGTT GAGTTCTACC TGGAGGAAGG	1140
35	GATCACTGAT GAAGAAGCCA TCTCCCTCAT CGACCTGGAG GTGCTGAGAC CCAAGCGGGA	1200
	TGACAGACAG CTAGAGATTT GCAAACAACA GCTCCCAGAT TCTTGCGGCT AGTGGGAGAC	1260
	CAAGGGACTC CATCGGAGAT NAGGACCCGT TCACAGCTAA GCTRAGCTTT GAGCAAGGTG	1320
40	GCTCARAGTT CGTGCCAGTG GTGGTGAGCC GGCTGGTGCT GCGCTCCATG AGCCGCCGGG	1380
	ATGTCTCAT CAAGCGATGG CCCCCACCCC TGAGGTGGCA ATACTTCCGC TCACTGCTGC	1440
45	CTGACGCCTC CATTACCATG TGCCCCTCCT GCTTCCAGAT GTTCCATTCT GAGGACTATG	1500
	AGTTGCTGGT GCTTCAGCAT GGCTGCTGCC CCTACTGCCG CAGGTGCAAG GATGACCCTG	1560
	GCCCATGACC AGCATCCTGG GGACGGCCTG CACCCTCTGC CCGCCTTGGG GTCTGCTGGG	1620
50	CTGTGAAGGA GAATAAAGAG TTAAACTGTC AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1680
	AAAAAAAAA AAAAAAAAAA AAANA	1705
55		

(2) INFORMATION FOR SEQ ID NO: 217:

60 (i) SEQUENCE CHARACTERISTICS:

470

- (A) LENGTH: 999 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

AGCAAATCAC CTTAACGATC TGGAATGAAA CTGTGACCAG TGCCGCCCTG GGTGGTCTG 60
10 GAGAGACTGC CGTCTTCTTG TTTGGCCATA GGTGCTGGGG CCCC GGCTTC AGTCACTGTC 120
TCAGACAGKA GTCCCCATAA GCAGATCACC AGTCCTCCAC TGTCTTCCT GTCGGCCTTG 180
CTGCATGAGA AGATAGCTGC TTCCTCCCTC TTTTCTTACA CTGTAAATTA TTGTTTACA 240
15 ATTGAGTGYC TTAATAATAG TYTACAAATA CTATGTATTT ATGCAAAACT GTTAAAGTTC 300
TCATCTGTTA TGATTGGATA CTTGGTCTTG TCAGTAGTGG TCAGCATTGG GTTGTGAGCT 360
20 TGTCTACTC CATACGTGTT TATCCTGCTA TGCATTTTAC ATTGTGTGTT CACATCTATT 420
CCAAGGAGCC TTGCTAGAAA CAACACTGGC GGTTCCTGCA GGCCAGGCAG GCATGGCCCC 480
ATGCTGTGTC CCATAGGAGC CAATGGAAAG AACGTAGCTT GGTCTGCTAG CCAGCCGTGG 540
25 GGTGGCGCAG GCCAGGCAGC CTCGTCACCA GAGTCCAGCA CCTGCCCATTT CCCCAGTCAC 600
ACAATCATAC TCTTCTTTCA TAGAGATTTT ATTACCACCT AGACCACCCT AGTTTTCCTC 660
30 TCTGTTAGTG TCCTGAGCTC TTTTGCAACA AAATGTAGGT ACAGACCAAT CCCTGTCCCT 720
TCCCCAATCA GGAGCTCCAC ACCATGAGTT GPTTGGTTTT CCAGAAGCTG CCAGTGGGTT 780
CCCGTGAATT GCGTTAAGAT ATCGATGATK TTTTTTATTG TTTTCTTCT TGTTTTPTA 840
35 AATAATATAT TTAAAGGCAG TATCTTTTGT ACTGTGAATT TGCAGTAGAA GATGCAGAA 900
GCACTTTTTT TTTACTTCTG TTGGTGTGTA TTGTATATAG TGTGTGTGCT TCTGTGATG 960
40 AAAATAAACT TTTTCTTTAT AAAAAAAAAA AAAAAAAC 999

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(2) INFORMATION FOR SEQ ID NO: 218:

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 941 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

55 GGCACGAGTA GCATTTTCATT TAATCTGCAG GTATATTCTC CCAACAGTTT ATTGTCATGT 60
GATGTCCTCA GCCAAGATTG TRAGGCAGAG AGGAGCTGTC CCAACCTACT ATACCACCGA 120
GGCTGGAGAG ATCATATTTT TGGTATTAAA CTGGAGTCTC TCCATCCTTC ACATTGTTGA 180
60

471

TGTCTCTGT AGCAAACCGG AAAAGTCAGT GACAGAAGAT GCCGCTAGCG GTTTGAGCCA 240
 GAGAATGACA GCTCTGGTTT GGAGAAAAGG GCCGGATGGT GGCTCTAGAA AGCCCATCCT 300
 5 TCTGCTCTTC TTTTTCCTCC CCTTATATF GTGCTTTCAT TCATTCATTC ATTCATCAAA 360
 CATTGTGTTGA GCACCTATTA TGTGTCAAGC TCTGTGCTAG CCTCTGAAA ACCTGCCCTC 420
 ATGTAGCTCA CTGTGGAGTA GGAGAAACAA TGACTACACT ATGATAAGCA CGGGTGTGCA 480
 10 GGGTCTCACA GAGCAGTGGC CCTCATCCA GACCGATGAG GTCAAAGAAG GCATCCAGGC 540
 GAGGATGGTG TCAGAGCTAA CTGAAGAATG AGAGGGAGCT GCACCASCAG GGGTTGGAAC 600
 15 TGAAGGTGCC AGTGCCTGGA GTCTTGATTC CAGCAGAGGG AGAGCAGTCT GTGAAAAGGC 660
 ACCAAGGGTG GGAGAGGGCA GAGCACATGG AGGAACTTCA GGTAGTCTG GATGGCCTG 720
 GGGCAAAGCT AGAGAGGTAA GAAGAATCTA CAAATGTTCC TCGAGTTACA TGAACCTCCA 780
 20 TCCCAATAAA CCCATTGAA ACGAAAAATT TAAGTCAGAA GTGCATTAA GGCTGGTCCG 840
 AGTAGAATGA TTTTACAAC GAATTGATCA CAACAGTTA CAGATGTCTT TGTTCCTTCT 900
 25 CCACTCCAC TGCTTCACCT GACTAGCCTT TAAAAAAA A 941

30 (2) INFORMATION FOR SEQ ID NO: 219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 575 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

40 TAAGTGAAT CCCCCGGGT TGCAGGAAT TCGGCACGAG GCATTCTGAG AAGCTTAAGA 60
 CATACTTTGA AGACAACCCT AGGGACCTCC AGCTGCTGCG GCATGACCTA CCTTGCACC 120
 CCGCAGTGGT GAAGCCCCAC CTGGGCCATG TTCCTGACTA CCTGGTTCCT CTGCTCTCC 180
 45 GTGGCCTGGT RCGCCCTCAC AAGAAGCGGA AGAAGCTGTC TTCCTCTGT AGGAAGGCCA 240
 AGAGAGCAAA GTCCAGAAC CCACTGCGCA GCTTCAAGCA CAAAGGAAAG AAATTCAGAC 300
 50 CCACAGCCAA GCCCTCCTGA GGTGTGTTGG CCTCTCTGGA GCTGAGCACA TTGTGAGCA 360
 CAGGCTTACA CCTTTCGTGG ACAGGCGAGG CTCTGGTGCT TACTGCACAG CCTGAACAGA 420
 CAGTTCCTGGG GCCGGCAGTG CTGGGCCCTT TAGCTCCTTG GCACTTCCAA GCTGGCATCT 480
 55 TGCCCCTTGA CAACAGAATA AAAATTTAG CTGCCCAAA AAAAAAAAAA AAAAAAAAAA 540
 CTCGAGGGGG GCGCCGTACC CAATTCGCCC TATAA 575

60

(2) INFORMATION FOR SEQ ID NO: 220:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3018 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

GCCAGCCTTA CAGGTTTTCAC GTGAAATGAA AGCCATTGGA ATAGAACCCT CGCTTGCAAC 60
15 ATATCACCAT ATTATTCGCC TGTTCGATCA ACCTGGAGAC CCTTTAAAGA GATCATCCTT 120
CATCATTTAT GATATAATGA ATGAATTAAT GGGAAAGAGA TTTTCTCCAA AGGACCCGGA 180
20 TGATGATAAG TTTTTCAGT CAGCCATGAG CATATGCTCA TCTCTCAGAG ATCTAGAACT 240
TGCCTACCAA GTACATGGCC TTTTAAAAAC CGGAGACAAC TGGAAATTCA TTGGACCTGA 300
TCAACATCGT AATTTCATTT ATTCCAAGTT CTTCGATTG ATTTGTCTAA TGGAAACAAAT 360
25 TGATGTTACC TTGAAGTGGT ATGAGGACCT GATACCTTCA GCCTACTTTC CCCACTCCCA 420
AACAATGATA CATCTTCTCC AAGCATTGGA TGTGGCCAAT CGGCTAGAAG TGATTCCTAA 480
AATTGGGAA AGATAGTAAA GAATATGGTC ATACTTTCCG CAGTGACCTG AGAGAAGAGA 540
30 TCCTGATGCT CATGGCAAGG GACAAGCACC CACCAGAGCT TCAGGTGGCA TTTGCTGACT 600
GTGCTGCTGA TATCAAATCT GCGTATGAAA GCCAACCCAT CAGACAGACT GCTCAGGATT 660
35 GGCCAGCCAC CTCTCTCAAC TGTATAGCTA TCCTCTTTT AAGGGCTGGG AGAACTCAGG 720
AAGCCTGGAA AATGTTGGG CTTTTCAGGA AGCATAATAA GATTCCTAGA AGTGAGTTGC 780
TGAATGAGCT TATGGACAGT GCAAAAGTGT CTAACAGCCC TTCCAGGCC ATTGAAGTAG 840
40 TAGAGCTGGC AAGTGCCTTC AGCTTACCTA TTTGTGAGG CCTCACCCAG AGAGTAATGA 900
GTGATTTTGC AATCAACCAG GAACAAAAGG AAGCCCTAAG TAATCTAACT GCATTGACCA 960
45 GTGACAGTGA TACTGACAGC AGCAGTGACA GCGACAGTGA CACCAGTGAA GGCAATGAA 1020
AGTGGAGATT CAGGAGCAGC AATGGTCTCA CCATAGCTGC TGGAAACACA CCTGAGAACT 1080
GAGATATACC AATAATTAAC ATGTTTACAA AGAAGAAAAG ATACAGATTT GGTGAATTTG 1140
50 TTAATGTGAG GTACAGTCAG TACACAGCTG ACTTATGTAG ATTTAAGCTG CTAATATGCT 1200
ACTTAACCAT CTATTAATGC ACCATTAAAG GCTTAGCATT TAAGTAGCAA CATTGCGGTT 1260
55 TTCAGACACA TGGTGAGGTC CATGGCTCTT GTCATCAGGA TAAGCCTGCA CACCTAGAGT 1320
GTCGGTGAGC TGACCTCACG ATGCTGTCCT CGTGGGATTG CCCTCTCCTG CTGCTGGACT 1380
TCTGCCTTTG TTGGCCTGAT GTGCTGCTGT GATGCTGGTC CTTCATCTTA GGTGTTTCATG 1440
60

	CAGTTCCTAAC ACAGTTGGGG TTGGGTCAAT AGTTTCCCAA TTTCAGGATA TTTCGATGTC	1500
	AGAAATAACG CATCTTAGGA ATGACTAAAC AAGATAATGG CAGTTTAGGC TGCACAACCTG	1560
5	GTAAAATGAC TGTAGATAAA TGTGTAAATT AGTGTACACG TTTGTATTTT TGTTAATATA	1620
	GCCGCTGCCA TAGTTTCTTA ACTTGAACAG CCAATGAATGT TTCATGTCTC CCTTTTTTTT	1680
10	TTGTCTATAG CTGTACCTA TTTTAGTGGT TGAAATGAGA GCTAGTGATG ACAGAAGGAT	1740
	GTGGAATGTC TTCTTGACAT CATGTGTAT TGCTGGTAAT CAAGTTGGTA ACGACTACTT	1800
	CTAGCAGCTC TTACCACTAT GACTTAAAGT GTCCTGGAAG GCAGTAAGTG GAGGTTTGCA	1860
15	GCATTCTGCG CTTTCATGAGG GCTTCTACCA CTGACCACTT TGCACGTACC TGGCTCCCAG	1920
	ATTTACTTAG GTACCCACG AGTCGTCCAC ATAAGCAGCT TCATCTTTAC CTTGCCAGAG	1980
20	TTGACAATTA TGGGATACTC TAGTCTACTT ATACTTGTGT TCCCATCTGT CTGCCATCCT	2040
	CTGAAGGCCA GGACCCAGTC ATACATCCTT AGAAACCAAA GTATGGTTTT TGTTTTCTCT	2100
	TGGAATGTCA GGTCTTAAGG CATTTAATTG AGGGACAAAA AAAAAAAAAA GCCGATATAG	2160
25	TAGCTAGCTA CTTAAGCATC CATGGGTATT GCTCCATATC AAAGCAGATT TGCAGGACAG	2220
	AAAGAGTAAA TTAGCCTTCA GTCTTGGTTT ACAGCTTCCA AGGAGAGCCT TGGSCACCTG	2280
30	AAATGTTAAC TCGGTCCCTT CCTGTCTCTA GTTCATCAGC ACCTGCAGAT GCCTGACTCT	2340
	TGTTAGCCTT ACTATTCAAT ACAGTCCTTA GATTACGGT ATGCCTCTTC CTATCCAGGC	2400
	ACCTATTCTG AATCACCATG TTGCTCTGCA GCTAGAGTTG ATAGGAGAAA ATCCATTGCG	2460
35	GTAGATGGCC TATGAATTTG TAGTAGACTT TCAAAATGAG TGATTTGTTA GCTTGGTACT	2520
	TTTAAGTTTG TGGTACAGAT CCTQCAAACC CATACTCTGA GCAATTAACT GCCTTGAACA	2580
40	TAGAGAAAAA TTAAGGCCTC ACAGGATGAG TCTCCATTCT CTGTAAATGC TTATTTTATC	2640
	ATAGTCTTTA GCCTCTAACT ATGAGTAAAA TGTCTCTTTC GGCCGGGTGT GGTGACTCAC	2700
	ACCTGTAACC TCAGCACTTT GGGAGGCAGA GGTGGGAGGA TCACTTAGGT CCAGGAGTTC	2760
45	GAGACTAGCC TGGGCAACAT AGTGAGACAC CGGATCTACA AAAAAATAAA AAGCCAGACT	2820
	GGTGGTATGT ATCTGTGTCC CAGCTAATTG GGAGGGTGAG ATGGGAGGAT TGTTTGAGCC	2880
50	TAGGAGAGGG AGGTTGCAGT GAGCCGTGAT CGCACCCTG CACTCCAGCC TGGGCAACAG	2940
	AGCAAGACCC TGTCTTGAG AAACCAGAAT TTTGGAAGAG CAAATGGGGC TGAGTGCACT	3000
	GGCTCATGCC TGTAATCC	3018
55		

(2) INFORMATION FOR SEQ ID NO: 221:

60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 968 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

	GGCACGAGGG CCGCGGGACA TCCACGGGGC GCGAGTGACA CGCGGGAGGG AGAGCAGTGT	60
10	TCTGCTGGAG CCGATGCCAA AAACCATGCA TTTCTTATTC AGATTCATTG TTTCTTTTA	120
	TCTGTGGGGC CTTTITACTG CTCAGAGACA AAAGAAAGAG GAGAGCACCG AAGAAGTGAA	180
	AATAGAAGTT TTGCATCGTC CAGAAAAGCT CTCTAAGACA AGCAAGAAGG GAGACCTACT	240
15	NAAATGCCCA TTATGACGGC TACCTGGCTA AAGACGGCTC GAAATTCTAC TGCAGCCGGA	300
	CACAAAATGA AGGCCACCCC AAATGGTTTG TTCTTGGTGT TGGCAAGTC ATAAAAGGCC	360
20	TAGACATTGC TATGACAGAT ATGTGCCCTG GAGAAAAGCG AAAAGTAGTT ATACCCCTT	420
	CATTTGCATA CGGAAAGGAA GGCTATGCAG AAGGCAAGAT TCCACCGGAT GCTACATTGA	480
	TTTTTGAGAT TGAACTTTAT GCTGTGACCA AAGGACCACG GAGCATTGAG ACATTTAAAC	540
25	AAATAGACAT GGACAATGAC AGGCAGCTCT CTAAGCCGA GATAAACCTC TACTTGCAAA	600
	GGGAATTGTA AAAAGATGAG AAGCCACGTG ACAAGTCATA TCAGGATGCA GTTTTAGAAG	660
30	ATATTTTAA GAAGATGAC CATGATGGTG ATGGCTTCAT TTCTCCAAG GAATACAATG	720
	TATACCAACA CGATGAACTA TAGCATATTT GTATTTCTAC TTTMTTTTTT TAGCTATTTA	780
	CTGTACTTTA TGTATWAAAC AAAGTCMCTT TTCTCCMAGT TGKATTTGCT ATTTTCCCC	840
35	TATGAGAAGA TATTTTGATC TCCCAATAC ATTGATTTTG GTATAATAAA TGTGAGGCTG	900
	TTTTCGCAAC TTAAAAAAA ATTAAAAAA ACTGGAGGGG GGCCCGTACC CAANTCGCCG	960
40	NATATGAT	968

45 (2) INFORMATION FOR SEQ ID NO: 222:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1404 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

55	CGTTTCCGG CCGTGCGTTT GTGGCCGTCC GGCTCCCTG ACATGCAGCC CTCTGGACCC	60
	CGAGGTGGA CCCTACTGTG ACACACCTAC CATGCGGACA CTCTCAACC TCCTCTGGCT	120
60	TGCCCTGGCC TGCAGCCTG TTCACACTAC CCTGTCAAAG TCAGATGCCA AAAAGCCGC	180

	CTCAAAGACG CTGCTGGAGA AGAGTCAGTT TTCAGATAAG CCGGTGCAAG ACCGGGGTTT	240
	GGTGGTGACG GACCTCAAAG CTGAGAGTGT GGTTCCTTGAG CATCGCAGCT ACTGCTCGGC	300
5	AAAGGCCCGG GACAGACACT TTGCTGGGGA TGTACTGGGC TATGTCACCTC CATGGAACAG	360
	CCATGGCTAC GATGTCACCA AGGTCTTTGG GAGCAAGTTC ACACAGATCT CACCCGTCTG	420
10	GCTGCAGCTG AAGAGACGTG GCCGTGAGAT GTTTGAGGTC ACGGGCCTCC ACGACGTGGA	480
	CCAAGGGTGG ATGCGAGCTG TCAGGAAGCA TGCCAAGGGC CTGCACATAG TGCCTCGGCT	540
	CCTGTTTGAG GACTGGACTT ACGATGATTT CCGGAACGTC TTAGACAGTG AGGATGAGAT	600
15	AGAGGAGCTG AGCAAGACCG TGGTCCAGGT GGCAAGAAG CAGCATTTTCG ATGGCTTCGT	660
	GGTGGAGGTC TGGAACCAGC TGCTAAGCCA GAAGCGCGTG GGCCTCATCC ACATGCTCAC	720
20	CCACTTGGCC GAGGCTCTGC ACCAGGCCCG GCTGCTGGCC CTCCTGGTCA TCCCGCCTGC	780
	CATCACCCCC GGGACCGACC AGCTGGGCAT GTTCACGCAC AAGGAGTTTG AGCAGCTGGC	840
	CCCCGTGCTG GATGGTTTCA GCCTCATGAC CTACGACTAC TCTACAGCGC ATCAGCCTGG	900
25	CCCTAATGCA CCCCTGTCCT GGGTTCGAGC CTGCGTCCAG GTCCTGGACC CGAAGTCCAA	960
	GTGGCGAAGC AAAATCCTCC TGGGGCTCAA CTTCTATGGT ATGGACTACG CGACCTCCAA	1020
30	GGATGCCCGT GAGCCTGTTG TCGGGGCCAG GTACATCCAG AACTGAAGG ACCACAGGCC	1080
	CCGATGGTG TGGGACAGCC AGGYCTCAGA GCACTTCTTC GAGTACAAGA AGAGCCGAG	1140
	TGGGAGGCAC GTCGTCTTCT ACCCAACCCT GAAGTCCCTG CAGGTGCGGC TGGAGCTGGC	1200
35	CCGGGAGCTG GCGGTTGGGG TCTCTATCTG GGAGCTGGCC AGGGCCTGGA CTACTTCTAC	1260
	GACCTGCTCT AGGTGGGCAT TGGGGCCTCC GCGGTGGACG TGTCTTTTC TAAGCCATGG	1320
40	AGTGAGTGAG CAGGTGTGAA ATACAGGCCT NCACTCCGTT TGCTGTGAAA AAAAAAAAAA	1380
	AAAAAAAAAA AAAAAAAAAA AAAA	1404

45

(2) INFORMATION FOR SEQ ID NO: 223:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 707 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

50	NGCGCGCCTG CAGTCGACAC TAGTGGATCC AAAGAATTTCG GCACGAGGGC AGGTCCAGGG	60
	CTCAGAAATC AGCTCTATTG ACGAATTCTG CCGCAAGTTC CGCCTGGACT GCCCGCTGGC	120
60	CATGGAGCGG ATCAAGGAGG ACCGGCCCAT CACCATCAAG GACGACAAGG GCAACCTCAA	180

CCGCTGCATC GCAGACGTGG TCTCGCTCTT CATCACGGTC ATGGACAAAC TCGGCTTGA 240
 GATCCGCGCC ATGGATGAGA TCCAGCCCGA CCTGCCGAG CTGATGAGA CCAATGCACCG 300
 5 CATGAGCCAC CTCCCACCCG ACTTTGAGGG CCGCCAGACG GTCAGCCAST GGCTGCAGAC 360
 CCTGAGCGGC ATGTCGGCGT CAGATGAGCT GGACGACTCA CAGGTGGCTC AGATGCTGTT 420
 10 CGACCTGGAG TCAGCCTACA ACGCCTTCAA CCGCTTCCTG CATGCCCTGAG CCGGGGGCAC 480
 TAGCCCTTGC ACAGAAGGGC AGAGTCTGAG GCGATGGCTC CTGTCCTCTT GTCCGCCACA 540
 CAGGCCGTGG TCATCCACAC AACTCACTGT CTGCAGCTGC CTGTCTGCTG TCTGCTTTTG 600
 15 GTGTCAAGAC TTTTGGGCCG GGGCCCTCCC CACAATAAAG ATGCTCTCCG ACCTTCAAAA 660
 AAAAAAAAAA AAAAATCRG GGGGGGCCCG GTCCCAATCC CCCCCT 707
 20

(2) INFORMATION FOR SEQ ID NO: 224:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1384 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

GGGGAAGTGC AGTGACAGCA GGAGTAAGAG TGGGAGGACG GACAGAGCTG GGACACAGGT 60
 35 ATGGAGAGGG GGTTCAGCGA GCCTAGAGAG GGCAGACTAT CAGGGTGGCG GCTGTGAGAA 120
 TCCAGGGAGA GGAGCGGAAA CAGAGAGGG GCGAAGACC GGGGCACTTG TGGTTGCAG 180
 40 AGCCCCTCAG CCATGTTGGG AGCCAAGCCA CACTGGGTAC CAGGTCTCTT ACACAGTCCC 240
 GGGTGTCCCT TGGTTCTGGT GCTTCTGGCT CTGGGGGCCG GGTGGGCCCC GAGGGGTCA 300
 GAGCCCGTCC TGCTGGAGGG GGAGTGCCTG GTGGTCTGTG AGCCTGGGCG AGTGTCTGCA 360
 45 GGGGGGCCCG GGGGAGCAGC CCTGGGAGAG GCACCCCTG GCGAGTGGC ATTGCTGGG 420
 GTCCGAAGCC AACCACATGA GCCAGCAGGG GAAACCGCA ATGGCACTAK TGGGGCCATC 480
 TACTTCGACC AGGTCTGGT GAACGAGGGC GGTGGCTTTG ACCGGGCTTC TGGCTCCTTC 540
 50 GTAGCCCTG TCCGGGGTGT CTACAGCTTC CGGTTCATG TGGTGAAGT GTACAACCGC 600
 CAAACTGTCC AGGTGAGCCT GATGCTGAAC ACGTGGCTG TCATCTCAGC CTTTGCCAAT 660
 55 GATCCTGACG TGACCCGGA GGCAGCCACC AGCTCTGTG TACTGCTCTT GGACCTGGG 720
 GACCGAGTGT CTCTGCGCT GCGTCGGGG AACTCTCTG GTGGTGGAA AACTCAAGT 780
 60 TTCTCTGGCT TCCTCATCTT CCTCTCTGA GGAACCAAGT YTTTCAAGCA CAAATCCA 840

477

GCCCCGTGACA ACTTTCTTCT GGCCTCTCTT GCCCCAGAAA CAGCAGAGGC AGGAGAGAGA 900
 CTCCCTCTGG YTCCTATCCC ACYTCTTTGC ATGGGAMCCT GTGCCAAACA CCCAAGTTTA 960
 5 AGARAAARARY ARARCTGWGG CAGGTATACA GAGCTGGAAG TGGACCATGG AAAACATSGA 1020
 TAACCATGCA TCYTCTTGCT TGGCCACCTC CTGAAACTGT CCACCTTTGA AGTTTGAAC 1080
 10 TTAGTCCCTC CAMACTCTGA CTGCTGCCTC CTTCTCCCA GCTCTCTCAC TGAGTTATYT 1140
 TCACTGTACC TGTTCCAGCA TATCCCACT ATCTCTCTTT CTCCTGATCT GTGCTGTCTT 1200
 ATTCTCTCC TTAGGCTTCC TATTACCTGG GATTCATGA TTCATTCCTT CAGACCCTCT 1260
 15 CCTGCCAGTA TGCTAAACCC TCCCTCTCTC TTTCTTATCC CGCTGTCCCA TTGGCCCAGC 1320
 CTGGATGAAT CTATCAATAA ACAAACCTAGA GAATGGTGGT CAAAAAAAAA AAAAAAAAAAC 1380
 TCGA 1384
 20

25 (2) INFORMATION FOR SEQ ID NO: 225:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 760 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

35 GGGTCGACCC ACGCGTCCGC TGACCACTCC GTTATAGATA CTCTTCCTA TACCAAACT 60
 GTTTAAACAG GTGCCACCAC AAGGGATGTC GTCCTTACTC TCTGCGGGTC TTCAAGCATC 120
 CCTTGTGGG AAARGTCTCT GGGCAAGCAC GTGGTATTG GTCTGCTGCT TGCTTCCCTT 180
 40 TTCCACCAG GGATGTTGTG ATCATAAGTC AAAACAACAG TATATTCCAA ATCTCAAAAG 240
 CTATTGTGGC CTGAGCACAA TTGAAATCTA GCAGAGTTTT TCCTATGTAG CTTTAGAGTA 300
 ACTCTTCTGC TTCTCTGTCA CTTACAATTC AGGTTCTGCC TTGCTTAAG AGCATGAGCA 360
 45 GAAGAGTCCT CATGTGACGC TTAGTTCTAT TGCAGTCCTG GGTGAAACTA TTTAAGCWAT 420
 GGGGCTGCTK CTCCCCANWT CCTCCCTAAC AATTGCTTGT GTGGACTTCT CATCTAAAAG 480
 50 GTTAGTGGCT TTTGCTTGGG ATCAGTGCTC TCTATTGATG TTCTTGCTGG TCTCCAGACA 540
 CATTCTGTT GCATTAAGAC TTGAAAGACT TGTAGATGTG TGATGTTTCA GCACAGGATG 600
 CTGAAAGCTA TGTTACTATT CTTAGTTTGT AAATGTCTCT TTTGATACCA TCATCTTGT 660
 55 TTCTTTTGT AGGTATAAAT AAAAACAACG TTGACAATAA AAAAAAAAAA AAAAAAAAAA 720
 AAAAAAAAAA AAAAAAAAAA NAAAAAAAAA AAAAAAAAAA 760

60

(2) INFORMATION FOR SEQ ID NO: 226:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2057 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

CCGAGCCGGC	TGCGCCGGGG	GAATCCGTGC	GGGCGCCTTC	CGTCCCRGTC	CCATCCTCGC	60
15	CGCGCTCCAG	CACCTCTGAA	GTTTTCACGC	GCCCAGAAAG	GAGGCGAGGA	120
	GTGTGAGAGG	AGGGAGCAAA	AAGCTCACCC	TAAAACATTT	ATTTCAAGGA	180
	AGGGGGGGCG	CAAAAATGGC	TGGGGCAATT	ATAGAAAACA	TGAGCACCAA	240
20	ATTGTTGGTG	GGATTCTGCT	CGTGTTCCAA	ATCATCGCCT	TTCTGGTGGG	300
	GCTCCAGGGC	CCACAACGGC	AGTGTCTTAC	ATGTCGGTGA	AATGTGTGGA	360
25	AACCATCACA	AGACAAAATG	GTTCTGTCCT	TGGGGACCCA	ATCATTGTGA	420
	GACATTGAAG	AGGCAATTCC	AAGGGAAATT	GAAGCCAATG	ACATCGTGTT	480
	ATTCCCCTCC	CCCACATGGA	GATGAGTCCT	TGGTTCCAAT	TCATGMTGTT	540
30	CTGGACATTG	CCTTCAAGCT	AAACAACCAA	ATCAGRGAAA	ATGCAGAAGT	600
	GTTTCCCTGG	CTTACCGTGA	TGACGCGTTT	GCTGAGTGGA	CTGAAATGGC	660
35	GTACCACGGA	AACTCAAATG	CACCTTCACA	TCTCCCAAGA	CTCCAGAGCA	720
	GTTACTATGA	ATGTGATGTC	CTTCTTTTCA	TGAAATTTGG	GTCTGTGGCC	780
	TACCTTTTAA	ACATCCGGCT	GCCTGTGAAT	GAGAAGAAGA	AAATCAATGT	840
40	GAGATAAAGG	ATATCCGTTT	GGTGGGGATC	CACCAAAATG	GAGGCTTCAC	900
	TTTGCCATGA	AGACCTTCCT	TACGCCCAGC	ATCTTCATCA	TTATGGTGTG	960
45	AGGATCACCA	TGATGTCCCG	ACCCCCAGTG	CTTCTGGAAA	AAGTCATCTT	1020
	ATTTCCATGA	CCTTTATCAA	TATCCCAGTG	GAATGGTTTT	CCATCGGGTT	1080
	TGGATGCTGC	TGTTTGGTGA	CATCCGACAG	GCATCTTCTA	TGCRATGCTT	1140
50	GGATCATCTT	CTGTGGCGAG	CACATGATGG	ATCAGCACGA	GCGGAACCAC	1200
	ATTGGAAGCA	AGTCGGACCC	ATTGCCGTTG	GTCTTCTGCG	CTCTTCATAT	1260
55	TGAGAGAGGG	GTACAACTCA	CGAATCCCTT	CTACAGTATC	TGGAATACAG	1320
	CAGAGCTGGC	CATGGCTTTC	ATCATCGTGG	CTGGAATCTG	CCTCTGCCTC	1380
60	TTTCTATGCT	TCATGGTATT	TCAGGTGTTT	CGGAACATCA	GTGGGAAGCA	1440

CCAGCTATGA GCAAAATCCG GGGGCTACAC TATGAGGGGC TAATTTTITAG GTTCAAGTTC 1500
 CTCATGCTTA TCACCTTGGC CTGGGCTGAC ATGACTGTCA TCTTCTTCAT CGTTAGTCAG 1560
 5 GTACCGGAG GCAATTGGGA AATGGGGGGG CGTCACATC CCAAGTGAAC AGTGCCTTTT 1620
 TCACAGGCAT CTATGGGATG TGGAACTGTG AATGCTTTGG TGTGATGTC TTGTATGCAC 1680
 CATCCCATTA AACTATGGA GAGACCACT CCAATGGAT GCAACTCCCA TGTAAATCGA 1740
 10 GGGAGGATG TGTCTGTTT GTTTCGGAC TTATCAAGA ATTGTTGAG GCTTCGAAAT 1800
 ATTCCTTCAT CATGACAC GAGCTTTTG GTATTGAGT CAACAAGGCA ACACATGTTT 1860
 15 ATCAGCTTG CATTTGAGT TTTACAGTC AATCGATTG TACTTGATA CGCACACAAA 1920
 TACACTCAT TACCTTTAT CTCAAATGT TAATATAAG GAAAAACCG TCAACAATAA 1980
 ATATCTTTG AATATCTGT TACTCTCTT AAAAAAAAA AAAAAACTC GTGCCGAATT 2040
 20 CGGCACGAGC GGCACGA 2057

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(2) INFORMATION FOR SEQ ID NO: 227:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2084 base pairs
 30 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (ii) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

GGCAGAGGGC CATTTCTGAC AAGAGGCCAA ACCCGCATTC CTCTGTGCCC CTCCTCTCCC 60
 ACCAAATGCT TTATATAAAT AACTCTTGTT ACCGGAATA ACTGTTCAAT TTTCACCTCT 120
 40 CCCTCCTAGG TCACACTTTT CAGAAAAAAG ATGTGCATCC TGGAAACCAG AAGAAAAATA 180
 TGAGACGGGG AATCATCGTG TGATGTGTGT SCTGCCCTTG GCTGAGTGTG TGGAGTCCTG 240
 CTCAGGTGTT AGGTACAGTG TGTTTGATCG TGGTGGCTTG ACGGGAACCG CTTGTTTACA 300
 45 GCTGTGACTG CGGCTGCACT GAGAGAAAC TCCCTTGGC TGCTCGTAGC GCCGGGCCTT 360
 CTCTCTCTGT CATCATCCAG ASCAGCCACT GTCCGGGAGG CAGAAGGTAC CGGGGCAGCT 420
 50 ACTGGAGGAC TGTGCGGGCC TGCCTGGGCT GCGCCCTCCG CCGTGGGGCC CTGTTGCTGC 480
 TGTCCATCTA TTTCTACTAC TCCCTCCCAA ATGGGGTGG CCGCCCTTC ACTTGATGTC 540
 TTGCCCTCCT GGGCCTCTC GAGGCACTG AACATCTCC TGGGCCTCAA GGGCCTGGCC 600
 55 CCAGCTGAGA TCTGTGCAAT GTGTGAAAA GGAATTTCA ACGTGGCCCA TGGGCTGGCA 660
 TGGTCATATT ACATCGGATA TGTGGGCTG ATCTTGCCAG AGCTCCAGGC CCGGATTCCA 720
 60 ACTTACAATC ASCATTACAA CAACCTGCTA CGGSGTGCAG TGAGCCAGCG GTGTNATATT 780

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CTCCTCCCAT TGGACTGTGG GGTGCCTGAT AACCTGAGTA TGGCTGACCC CAACATTGCG 840
TTCCTGGATA AACTGCCCCA GCAGACCGGT GACCGTGCTG GCATCAAGGA TCGGGTTTAC 900
5 AGCAACAGCA TCTATGAGCT TCTGGAGAAC GGGCAGCGGG CGGGCACCTG TGTCTGGAG 960
TACGCCACCC CCTGCGAGAC TTTGTTTGCC ATGTCACAAT ACAGTCAAGC TGGCTTTAGC 1020
10 GGGGAGGATA GGCTTGAGCA GGCCAAACTC TTCTGCCGGA CACTTGAGGA CATCCTGGCA 1080
GATGCCCTTG AGTCTCAGAA CAACTGCCGC CTCATTGCCT ACCAGGAACC TGCAGATGAC 1140
AGCAGCTTCT CGCTGTCCCA GGAGGTTCTC CGGCACCTGC GGCAGGAGGA AAAGGAAGAG 1200
15 GTTACTGTGG GCAGCTTGAA GACCTCAGCG GTGCCAGTA CCTCCACGAT GTCCCAAGAG 1260
CCTGAGCTCC TCATCAGTGG AATGAAAAG CCCCTCCCTC TCCGCACGGA TTTCTCTTGA 1320
20 GACCCAGGGT CACCAGGCCA GAGCCTCCAG TGGTCTCCAA GCCTCTGGAC TGGGGGCTCT 1380
CTTCAGTGGC TGAATGTCCA GCAGAGCTAT TTCCTTCCAC AGGGGGCCTT GCAGGGAAGG 1440
GTCCAGGACT TGACATCTTA AGATGCGTCT TGTCCCTTG GCCAGTCAT TCCCCCTCTC 1500
25 TGAGCCTCGG TGTCTTCAAC CTGTGAAATG GGATCATAAT CACTGCCTTA CCTCCCTCAC 1560
GGTGTGTG AGGACTGAGT GTGTGGAAGT TTTTCATAAA CTTTGGATGC TAGTGTACTT 1620
30 AGGGGGTGTG CCAGGTGTCT TTCATGGGGC CTTCCAGACC CACTCCCCAC CCTTCTCCCC 1680
TTCCTTTGCC CGGGGACGCC GAACTCTCTC AATGGTATCA ACAGGCTCCT TCGCCCTCTG 1740
GCTCCTGGTC ATGTTCCATT ATTGGGGAGC CCCAGCAGAA GAATGGAGAG GAGGAGGAGG 1800
35 CTGAGTTTGG GGTATTGAAT CCCCCGGCTC CCACCCTGCA GCATCAAGGT TGCTATGGAC 1860
TCTCCTGCCG GCAACTCTT CGGTAATCAT GACTATCTCT AGGATTCTGG CACCACTTCC 1920
40 TTCCCTGGCC CCTTAAGCCT AGCTGTGTAT CGGCACCCCC ACCCCACTAG AGTACTCCCT 1980
CTCACTTGCG GTTTCCTTAT ACTCCACCCC TTTCTCAACG GTCCTTTTTT AAAGCACATC 2040
45 TCAGATTAAA AAAAAAAAAA AAAAAAAAAA AGGGGGGGCN GCNT 2084

(2) INFORMATION FOR SEQ ID NO: 228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2143 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

TCGACCCACG CGTCCGGTTG AATTCCTTGA CCTGCAACA CATATTTATT AGCCTGACTC 60

	AAACAATGAA GCTATTAAAA CTTGCGAGGA ACATTGTAAA ACTCTCTTTG TATCGGCATT	120
	TCACCAACAC GCTTATTTTG GCAGTGGCAG CATCCATTGT GTTTATCATC TGGACAACCA	180
5	TGAAGTTCAG AATAGTGACA TGTCAGTCGG ACTGGCGGGA GCTGTGGGTA GACGATGCCA	240
	TCTGGCGCTT GCTGTTCTCC ATGATCCTCT TTGTCATCAT GGTTCCTCTG CGACCATCTG	300
10	CAAACAACCA GAGGTTTGCC TTTTCACCAT TGTCTGAGGA AGAGGAGGAG GATGAACAAA	360
	AGGAGCCTAT GCTGAAAGAA AGCTTTGAAG GAATGAAAAT GAGAAGTACC AAACAAGAAC	420
	CCAATGGAAA TAGTAAAGTT AACAAAGCAC AGGAAGATGA TTTGAAGTGG GTAGAAGAGA	480
15	ATGTTCTTTC TTCTGTGACA GATGTAGCAC TTCCAGCCCT TCTGGATTCA GATGAGGAAC	540
	GAATGATCAC AACTTTGAA AGGTCCAAAA TGGAGTAAGG AATGGGAAGA TTTGCAGTTA	600
20	AAGATGGCTA CCATCAGGGA AGAGATCAGC ATCTGTGTCA GTCTTCTGTA CGGCTCCATG	660
	GGATTAAAGG AAGCAATGAC ATCCTGATCT GTTCCTTGAT CTTTGGGCAT TGGAGTTGGC	720
	GAGAGGTGTC AGAACAAAGA GAACATCTTA CTGAAAACAA GTTCATAAGA TGAGAAAAAT	780
25	CTACGAGCTT CTTATTTACA AACTGTCTGC CCCCTTTCCT CCCAGACTCT GACATGGATG	840
	TTCATGCAAC TTAAGTGTGT TGTTCCTGAA CTTTCTGTAA TGTTCATTT TTTAAATCTG	900
30	ACAAACTAAA AAGTTTAACG TCTTCTAAAA GATTGTCATC AACACCATAA TATGTAATCT	960
	CCAGGAGCAA CTGCCTGTAA TTTTATTTTA TTTAGGGAGT TACATAGGTG ATGGGGGAAA	1020
	TTGTTAACTA CCTTTCATTT TCCTGGGAAG TCAAGGTTAC ATCTTGCAGA GGTGTGTTTG	1080
35	AGAAAAAAGG GCCCTTCTGA GTTAAGGAGC CATAGTTCTA TCAATGATCA AAAGAAAAAA	1140
	AAAAAAAGA GAAACTGTTA CAGTATGATT CAGATCATTT AAAAAAGCAA AATCAAGTGC	1200
40	AATTTTGTIT ACAAATGGTG TATAATTAAAG ATTTTCTAT TTCAGATGTA CTTTAAAGAG	1260
	AAATATTAGC TTAACCTCTT TGACATCTGC TATTGTGACA CATCCCATG CTGGCAATGT	1320
	GGTGACACT CCGAACTTT TAACTACTGT TTGTGAAGCC TCCAAGGGTG GCATTGCAGG	1380
45	GTCCCTAGGC AATGTTTGTG TTGCCTTTAT GCAGAGAGGT GCTCCAAGTG CTGTGATTGA	1440
	GCACCGTGCT AGAGGAACTG TAATGCTTCA GAAGTTGTAG CTTATACAAA GGAAACAGGT	1500
50	CCTGCTGGCT TAATTTAAAC AGTTATTGCA TGAAGTAGCG TGGAGGCCCT GGACTGCTGC	1560
	TCGTTCTTTA GGATGGACTG TTCTGGTATC TGGTATTGGT TTAGAGACTG TTAATAAGGG	1620
	ACATCACAAG GTGATGGGAT TCATTGAAG CACTCTATTT CTGTTTAAAT GGTTTTATCC	1680
55	AATTTTGCCT TCCCAAGATT TTTGTTCTAC ATAAAAAGTT CATGCCACTT TTTAATATAA	1740
	AAAAATTTAA CAAAATTAAT GTATTTTCT CATTTTTTC AACTTTTTTC TAAAGACTCT	1800
60	TTCTGTCAAA CTCATGAAAA ATTTCTTTCT ATGGCTTTTA TTCTAGATTG TCTTATTTTC	1860

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TGTTAAAACC AATGACCACA TGACCACAAT CTTCACTAAC TCATACTGCA GTGAAAGTGT 1920
TAACCCCTTAG GTAGTTTCTC TACAACTCTT TGCTATGGTG ATTTTAAAAA AAGTTTCCTA 1980
GGGAAGTATC TCTGAGGGAA CAGGCAATCT GAAGGAACTG ACTATATTCT CCATGGCTAA 2040
GTCCATTAGG CCAAAGNCT GGGTGGGTAT TGGTTGTCTCAN GCTGTCTATT GGCATATTAA 2100
AAACGTAGGC CGGANGGAAT AATTAGGTTG TNATGCCGGC GGG 2143

(2) INFORMATION FOR SEQ ID NO: 229:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1025 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

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CCTGGCCCAC ATTGCTTCAT TGGCCTGGCC ATGCGCCTGT ACTATGGCAG CCGCTAGTCC 60
CTGACAACTT CCACCCTGAT TCCGGACCCT GTAGATTGGG CGCCACCACC AGATCCCCCT 120
CCCAGGCCTT CCTCCTCTC CCATCAGCAG CCCTGTAACA AGTGCCTTGT GAGAAAAGCT 180
GGAGAAGTGA GGGCAGCCAG GTTATTCTCT GGAGGTGGT GGATGAAGGG GTACCCTAGG 240
AGATGTGAAG TGTGGGTTTG GTTAAGGAAA TGCTTACCAT CCCCCACCCC CAACCAAGTT 300
CTTCCAGACT AAAGAATTAA GGTAACATCA ATACCTAGGC CTGAGAAATA ACCCCATCCT 360
TGTGGGCAG CTCCCTGCTT TGTCTGTCAT GAACAGAGTT GATGAAAGTG GGGTGTGGGC 420
AACAAGTGGC TTTCTTGCC TACTTTAGTC ACCCAGCAGA GCCACTGGAG CTGGCTAGTC 480
CAGCCCAGCC ATGGTGCATG ACTCTTCCAT AAGGGATCCT CACCCTTCCA CTTTCATGCA 540
AGAAGGCCCA GTTGCCACAG ATTATACAAC CATTACCCAA ACCACTCTGA CAGTCTCCTC 600
CAGTTCCAGC AATGCCTAGA GACATGCTCC CTGCCCTCTC CACAGTGCTG CTCCCCACAC 660
CTAGCCTTTG TTCTGGAAAC CCCAGAGAGG GCTGGGCTTG ACTCATCTCA GGGAATGTAG 720
CCCCTGGGCC CTGGCTTAAG CCGACACTCC TGACCTCTCT GTTCACCCTG AGGGCTGTCT 780
TGAAGCCCGC TACCCACTCT GAGGCTCCTA GGAGGTACCA TGCTTCCCAC TCTGGGGCCT 840
GCCCTGCTT AGCAGTCTCC CAGCTCCCAA CAGCCTGGGG AAGCTCTGCA CAGAGTGACC 900
TGAGACCAGG TACAGGAAAC CTGTAGCTCA ATCAGTGTCT CTTTAACTGC ATAAGCAATA 960
AGATCTTAAT AAAGTCTTCT AGGCTGTAGG GTGGTTCCTA CAACCACAGC CAAAAAAAAA 1020
AAAAA 1025

(2) INFORMATION FOR SEQ ID NO: 230:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1250 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

5 GCCACGCGT CCGCCACGC GTCCGCGGT GCGAGTATG GGGCGCTGAT GGCCATGGAG 60
15 GGCTACTGGC GCTTCCTGGC GCGCTGGGG TCGGCACTGC TCGTCGGCTT CCTGTCGGTG 120
 ATSTTCGCCC TCGTCTGGGT CCTCCACTAC CGAGAGGGGC TTGGCTGGGA TGGGAGCGCA 180
20 CTAGAGTTTA ACTGGACCC AGTGCTSATG GTCACCGGT TCGTCTTCAT CCAGGGCATC 240
 GCATCATCGT CTACAGACTG CCGTGGACCT GGAAATGCAG CAAGCTCCTG ATGAAATCCA 300
 TCCATGCAGG GTTAAATGCA GTTGCTGCCA TTCTTGCAAT TATCTCTGTG GTGGCCGTGT 360
25 TTGAGAACCA CAATGTTAAC AATATAGCCA ATATGTACAG TCTGCACAGC TGGGTGGAC 420
 TGATAGCTGT CATATGCTAT TTGTTACAGC TTCTTTCAGG TTTTTCAGTC TTTCTGCTTC 480
30 CATGGGCTCC GCTTCTCTC CGAGCATTTC TCATGCCCAT ACATGTTTAT TCTGGAATTG 540
 TCATCTTTGG AACAGTGATT GCAACAGCAC TTATGGGATT GACAGAGAAA CTGATTTTTT 600
 CCCTGAGAGA TCCTGCATAC AGTACATTC CGCCAGAAGG TGTTCGTA AATACGCTTG 660
35 GCCTTCTGAT CCTGGTGTTT GGGGCCCTCA TTTTTCGGAT AGTCACCAGA CCGCAATGGA 720
 AACGTCCTAA GGAGCCAAAT TCTACCATTC TTCATCCAAA TGGAGGCACT GAACAGGGAG 780
 CAAGAGGTTT CATGCCAGCC TACTCTGGCA ACAACATGGA CAAATCAGAT TCAGAGTTAA 840
40 ACARTGAAGT AGCAGCAAGG AAAAGAACT TAGCTCTGGA TGAGGCTGGG CAGAGATCTA 900
 CCATGTAAAA TGTGTAGAG ATAGAGCCAT ATAACGTCAC GTTCAAAAC TAGCTCTACA 960
45 GTTTTCCTTC TCCTATTAGC CATATGATAA TTGGGCTATG TAGTATCAAT ATTTACTTTA 1020
 ATCACAAAGG ATGGTTTCTT GAAATAATTT GTATTGATTG AGGCCTATGA ACTGACCTGA 1080
 ATTGGAAAGG ATGTGATTAA TATAAATAAT AGCAGATATA AATTGTGGTT ATGTTACCTT 1140
50 TATCTGTGTG AGGACCACAA CATTAGCACG GTGCCTGTG CAAATAGAT ACTCAATATG 1200
 TGAATATGTG TCTACTAGTA GTTAATTGGA TAACTGGCA GCATCCCTGA 1250

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(2) INFORMATION FOR SEQ ID NO: 231:

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(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 1811 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

	CNGNCAGTAC CGGTCNGATT CCCGGGTCGA CCCACGCGTC CGCTGCATT CAGGGCCTTT	60
10	CAGTGGCTTT CATCTGAAG TTCCTGGATA ACATGTTCCA TGTCTTGATG GCCCAGGTTA	120
	CCASTGTCAT TATCACAACA GTGTCTGTCC TGGTCTTTGA CTTCAGGCCC TCCCTGGAAT	180
	TTTTCTTGA AGCCSCATCA GTCSTYCTCT CTATATTTAT TTATAATGCC AGCAAGCCTC	240
15	AAGTTCGGA ATACGCACCT AGGCAAGAAA GGATCCGAGA TCTAAGTGGC AATCTTTGGG	300
	AGCGTTCCAG TGGGGATGGA GAAGAACTAG AAAGACTTAC CAAACCCAAG AGTGATGAGT	360
20	CAGATGAAGA TACTTTCTAA CTGGTACCCA CATAGTTTGC AGCTCTCTTG AACCTTATTT	420
	TCACATTTTC AGTGTMTGTA ATATTTATCT TTTCACTTTG ATAAACCAGA AATGTTTCTA	480
	AATCCTAATA TTCTTTGCAT ATATCTAGCT ACTCCCTAAA TGGTTCCATC CAAGGCTTAG	540
25	AGTACCCAAA GGCTAAGAAA TTCTAAAGAA CTGATACAGG AGTAACAATA TGAAGAATTC	600
	ATTAATATCT CAGTACTTGA TAAATCAGAA AGTTATATGT GCAGATTATT TTCCTTGGCC	660
30	TTCAAGCTTC CAAAAAATT GTAATAATCA TGTTAGCTAT AGCTTGATA TACACATAGA	720
	GATCAATTTG CCAAATATTC ACAATCATGT AGTTCTAGTT TACATGCCAA AGTCTTCCCT	780
	TTTTAACATT ATAAAGCTA GGTGTCTCT TGAATTTTGA GGCCTAGAG ATAGTCATTT	840
35	TGCAAGTAAA GAGCAACGGG ACCCTTTCTA AAAACGTTGG TTGAAGGACC TAAATACCTG	900
	GCCATACCAT AGATTTGGGA TGATGTAGTC TGTGCTAAAT ATTTTGCTGA AGAAGCAGTT	960
40	TCTCAGACAC AACATCTCAG AATTTTAATT TTAGAAATT CATGGGAAAT TGGATTTTGT	1020
	TAATAATCTT TTGATGTTT AAACATTGGT TCCCTAGTCA CCATAGTTAC CACTTGATTT	1080
	TTAAGTCATT TAAACAAGCC ACGGTGGGGC TTTTCTCTCC TCAGTTTGAG GAGAAAAATC	1140
45	TTGATGTCAT TACTCCTGAA TTATTACATT TTGGAGAATA AGAGGGCATT TTATTTTATT	1200
	AGTTACTAAT TCAAGCTGTG ACTATGTAT ATCTTTCCAA GAGTTGAAAT GCTGGCTTCA	1260
50	GAATCATACC AGATTGTCAG TGAAGCTGAT GCCTAGGAAC TTTTAAAGG ATCCTTTCAA	1320
	AAGGATCACT TAGCAAACAC ATGTTGACTT TTAAGTATG TATGAATATT AATACTCTAA	1380
	AAATAGAAAG ACCAGTAATA TATAAGTCAC TTTACAGTGC TACTTCACAC TTTAAAGTGC	1440
55	ATGGTATTTT TCATGGTATT TTGCATGCAG CCAGTTAACT CTCGTAGATA GAGAAGTCAG	1500
	GTGATAGATG ATATTAAAAA TTAGCAAACA AAAGTGACTT GCTCAGGGTC ATGCAGCTGG	1560
60	GTGATGATAG AAGAGTGGGC TTAACTGGC AGGCCTGTAT GTTTACAGAC TACCATACTG	1620

	TAAATATGAG CTTTATGGTG TCATTCTCAG AAACCTTATAC ATTTCTGCTC TCCTTTCTCC	1680
	TAAGTTTCAT GCAGATGAAT ATAAGGTAAT ATACTATTAT ATAATTCATT TGTGATATCC	1740
5	ACAATAATAT GACTGGCAAG AATTGGTGGA AATTGTGAAT TAAATAATT ATTAAACCTA	1800
	AAAAAAAAAN N	1811
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	(2) INFORMATION FOR SEQ ID NO: 232:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 2271 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:	
	CTGACCTCAT GCGGTAGAGC CTAGCAACAG CGCAGGCTCC CAGCCGAGTC CGTTATGGCC	60
25	GCTGCCGTCC CGAAGAGGAT GAGGGGGCCA GCACAAGCGA AACTGCTGCC CGGGTCGGCC	120
	ATCCAAGCCC TTGTGGGGTT GGCGCGGCCG CTGGTCTTGG CGCTCCTGCT TGTGTCCGCC	180
	GCTCTATCCA GTGTGTATC ACGGACTGAT TCACCGAGCC CAACCGTACT CAACTCACAT	240
30	ATTTCTACCC CAAATGTGAA TGCTTTAACA CATGAAAACC AAACCAAACC TTCTATTTCC	300
	CAAATCAGCA CCACCTCCC TCCCACGACG AGTACCAAGA AAAGTGGAGG AGCATCTGTG	360
35	GTCCCTCATC CCTCGCCTAC TCCTCTGTCT CAAGAGGAAG CTGATAACAA TGAAGATCCT	420
	AGTATAGAGG AGGAGGATCT TCTGATGCTG AACAGTTCTC CATCCACAGC CAAAGACACT	480
40	CTAGACAATG GCGATTATGG AGAACCAGAC TATGACTGGA CCACGGGCCC CAGGGACGAC	540
	GACGAGTCTG ATNGACACCT TGAAGAAAA CAGGGGTTAC ATGGAATTG AACAGTCAGT	600
	GAAATCTTTT AAGATGCCAT CCTCAAATAT AGAAGAGGAA GACAGCCATT TCTTTTTC	660
45	TCTTATTATT TTGCTTTT GCATTGCTGT TGTTTACATT ACATATCACA ACAAAGGAA	720
	GATTTTCTT CTGGTTCAAA GCAGGAAATG GCGTGATGGC CTTTGTTC	780
	ATACCATCGC CTAGATCAGA ATGTTAATGA GGCAATGCCT TCTTTGAAGA TTACCAATGA	840
50	TTATATTTT TAAAGCACTG TGATTTGAAT TTGCTTATGT AATTTTATTT GCTTGACTTT	900
	TTATATGATA TTGTGCAAAT GTTTGCCATA GGCAATTGGT ACTTAAATGA GAGGTGAGTC	960
55	TCTCTTTTGC CTTGGTGCTT TGGAAATTAA ATGTCACAAA CGAGTATATA ATTTTATC	1020
	TGTACTTTTA GAGCTGAGTT TAATCAGGTG TCCAAAATGT GAGTTAAACA TTACCTTATA	1080
60	TTTACACTGT TAGTTTTTAT TGTTTTAGAT TTATTATGCT TCTTCTGGAA GTATTAGTGA	1140

	TGCTACTTTT AAAAGATCCC AAACCTGTAA CTAAATTCTG ACATATCTGT TACTGCTGAC	1200
	TCACATTCAT TCTCCGCCAT TCAAATACTA TTTTATATCC ACATTTTTTT TTGTTCCCAA	1260
5	ACTGTAATGT ACAAGGATAT GTGTGATAAT GCTTTGGATT TGAGTAATAT TTTTTTTTCT	1320
	TCCAAGAAAA CTGCTTTGGA TATTTTGTAGA TAATTTAAAC ATAATTTAGG ATAATGATAT	1380
10	TGCTCAATCT GACCACAATT TTAGGTAAAA CATTAAATGT GTCAAGAAAT CTTGGCAACA	1440
	GAGACTCTGC AGCTTGCAGT GGACATAGAT AAAATGTTAC AGAGATACTA TTTTTTTGGT	1500
	TGGAATTACT ATATTAAATT TAGAAGCAGA AACTGGTAAA ATGTTAAATA CATGTACAAT	1560
15	TGCTTTTAGT TAGCAATTGA TTGTAGCATG GGTTCCTCCA AGGTTTCAAG CAATGGGCAG	1620
	AGTTTAAAT TATATCAGAT TCGTTTACTT CGTTTATTAT TTTACAGTAA ATTTGAATAA	1680
	ATCTTAGGGG TCATTATCAC TTAAATAATA CTGTACCTAG GTCTTTCAAA TTAAATTTAT	1740
20	ACCTGAATGA AGTTGTTTGT ATACATAAAG GATATTTGTG TACAATTACC TTTTTTCCCC	1800
	CACACTTGTT TTCCTTGTCT TGTCTTTTGA TGGCAACTGG AAAGTATTTA CTATGGGATT	1860
25	CATTTATGTC TGTCTTCTA TCATAAGAA TTGATCAATA TGTAAATATG TGATTGTAAC	1920
	CATGGTTGAC TTACAAGTGT CACTACAGCT TTTTAGAAAA CATAGCCCTA ATATATGTTA	1980
30	AGCAGGACCC GGGTGAGCCA GTGGGCTTGC GCTTTATGTA GAGCTGGAAG AAGGCCGTCC	2040
	ATCCTGTCTC TTGGGCGGAC AGTGTACTTT CCTAATAGGG AAGGAAGCA CAATGGAAAT	2100
	ACCCCTGAAC CGTTTATTG CAGTAATTTT TTTCATATCT GAACTATTA TTAAATATTT	2160
35	TGAATAAGAT TTTAAAAAAT AAATGGCAAA GATATAAATC TAAAAAATAA AAAAAAATAA	2220
	AAAAAATAA AAAAAAATAA AAAAAAATAA AAAAAAATAA AAAAAANANA N	2271

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(2) INFORMATION FOR SEQ ID NO: 233:

- 45 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1338 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

	CTTCCGGTTC TCCGGGCAGC TGCCACTGCT GTAGCTTCTG CCACCTGCCA CGACCGGGCC	60
	TCTCCCTGGC GTTTGGTCAC CTCTGCTTCA TTCTCCACCG CGCCTATGGT CCCTCTTGGA	120
55	GCCAGCGTGG CGNGCCTGGC GGCTCCGGG TGGTGAGAGA GCGGTCCGGG AACGATGAAG	180
	GCCTCGCAGT GCTGCTGCTG TCTCAGCCAC CTCTTGGCTT CCGTCCTCCT CCTGCTGTG	240
60	CTGCCTGAAC TAAGCGGGYC CCTGGMAGTC CTGCTGCAGG CAGCCGAGGC CGCGCCAGGT	300

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YTTGGGCCTC CTGACCCTAG ACCAGGACAT TACCGCCGCT GCCACCGGGC CCTWACCCCT 360
 GCCCAGCAGC CGGGCCGTGG TCTGGCTGAA GCTGCGGGGG CCGCGGGGCT CCGAGGGAGG 420
 5 CAATGGCAGC AACCTGTGG CCGGGCTTGA GACGGACGAT CACGGAGGGA AGGCCGGGGA 480
 ARGCTCGGTG GGTGGCGGCC TTGCTGTGAG CCCCAACCCT GCGGACAAGC CCATGACCCA 540
 10 GCGGGCCCTG ACCGTGTTGA TGGTGGTGAG CGGCGCGGTG CTGGTGACT TCGTGGTCAG 600
 GACGGTCAGG ATGAGAAGAA GAAACCGAAA GACTAGGAGA TATGGAGTTT TGGACACTAA 660
 CATAGAAAAT ATGGAATTGA CACCTTTAGA ACAGGATGAT GAGGATGATG ACAACACGTT 720
 15 GTTTGATGCC AATCATCCTC GAAGATAAGA ATGTGCCTTT TGATGAAAGA ACTTTATCTT 780
 TCTACAATGA AGAGTGAAT TTCTATGTTT AAGGAATAAG AAGCCACTAT ATCAATGTTG 840
 20 GGGGGGTATT TAAGTTACAT ATATTNAAAC AACCTTTAAT TTGCTGTTGC AATAAATACC 900
 GTATCCTTTT ATTATATCTT TATATGTATA GAAGTACTCT GTTAATGGGC TCAGAGATGT 960
 TGGGGATAAA GTATACTGTA ATAATTTATC TGTTTGAAAA TTAATAATAA ACGGTGTTTT 1020
 25 CTGRTCGGTT TTGTTTCCT GCTTACCATA TGATTGTAAA TTGTTTATG TATTAATCAG 1080
 TTAATGCTAA TTATTTTGC TGATGTCATA TGTTAAAGAG CTATAAATTC CAACAACCAA 1140
 30 CTGGTGTA AAAATAATTT AAAATYTCCT TTAAGTAAAG GTATTTCCCA TTTTGTGGG 1200
 GAAAAGAAGC CAAATTTATT ACTTTGTGTT GGGGTTTTTA AAATATTAAG AAATGTCTAA 1260
 GTTATTGTTT GCAAAACAAT AAATATGATT TTAAATCTC TTAATAAAAA AAAAAAAC 1320
 35 CCCGGGGGGG GGCCCGGN 1338

40

(2) INFORMATION FOR SEQ ID NO: 234:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

50

Met Leu Ser Thr Gly Ile Glu Val Ala Arg Pro Pro Ala Thr Leu Leu
 1 5 10 15

Gly Leu Met Phe Val Leu Thr Gly Met Pro Arg Gly Leu Arg Xaa
 20 25 30

55

(2) INFORMATION FOR SEQ ID NO: 235:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids

60

488

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

5 Met Asn Val Val Ile Val Ile Ile Leu Phe Ser Phe Asp Ser Val Gly
 1 5 10 15

Thr Met Phe Ser Cys Asn Arg Ile Pro Lys Ile Thr Val Leu Asn Lys
 20 25 30

10 Leu Lys Phe Xaa Cys Glu Val Leu Leu Arg Ile Gln Thr Ile Gln Gly
 35 40 45

15 Phe Tyr Arg Cys Thr Arg Ile Ser Arg Tyr Lys Gly Ile Phe Pro Asp
 50 55 60

Phe Cys Gln Ser Gln Cys Met Gly Cys Asn Pro Glu Ser Xaa Met Ala
 65 70 75 80

20 Val Pro Ala Leu Val Thr Pro Ile Leu Ala His Arg Lys Lys Glu Lys
 85 90 95

Gly Met Cys Leu Phe Thr Leu Ile Ile Ala Pro Thr Arg Cys Thr His
 100 105 110

25 Tyr Phe Cys Xaa
 115

30

(2) INFORMATION FOR SEQ ID NO: 236:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 103 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

35 Met Ser Ser Ala Lys Ile Val Arg Gln Arg Gly Ala Val Pro Thr Tyr
 1 5 10 15

Tyr Thr Thr Glu Ala Gly Glu Ile Ile Phe Leu Val Leu Asn Trp Ser
 20 25 30

45 Leu Ser Ile Leu His Ile Val Asp Val Leu Cys Ser Lys Pro Glu Lys
 35 40 45

Ser Val Thr Glu Asp Ala Ala Ser Gly Leu Ser Gln Arg Met Thr Ala
 50 55 60

50 Leu Val Trp Arg Lys Gly Pro Asp Gly Gly Ser Arg Lys Pro Ile Leu
 65 70 75 80

Leu Leu Phe Phe Phe Leu Pro Leu Ile Leu Cys Phe His Ser Phe Ile
 85 90 95

55 His Ser Ser Asn Ile Cys Xaa
 100

60

489

(2) INFORMATION FOR SEQ ID NO: 237:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 42 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

10 Met Ile Leu Phe Pro Gln Xaa Ala Leu Arg Leu Gly Xaa Trp Pro Arg
1 5 10 15
Thr Trp Ser Ile Leu Xaa Lys Tyr Ser Val Asn Phe Phe Ser Ala Tyr
20 25 30
15 Ser Pro Met Gly Ala Val Gly Thr Glu Phe
35 40

20

(2) INFORMATION FOR SEQ ID NO: 238:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 37 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

30 Met Ile Ile Leu Leu Leu Phe Met Leu Leu Asn Asn Val Val Leu Val
1 5 10 15
Gln Glu Asp Asn Cys Gln Arg Lys Asn Thr Val Gln Glu Arg Arg Xaa
20 25 30
35 Trp Ser Gln Trp Xaa
35

40

(2) INFORMATION FOR SEQ ID NO: 239:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 128 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

50 Met Ala Ala Xaa Pro Pro Gly Cys Thr Pro Pro Xaa Leu Leu Asp Ile
1 5 10 15
Ser Trp Leu Thr Glu Ser Leu Gly Ala Gly Gln Pro Val Pro Val Glu
20 25 30
55 Cys Arg His Arg Leu Glu Val Ala Gly Pro Arg Lys Gly Pro Leu Ser
35 40 45
Pro Ala Trp Met Pro Ala Tyr Ala Cys Gln Arg Pro Thr Pro Leu Thr
50 55 60
60 His His Asn Thr Gly Leu Ser Glu Leu Leu Glu His Gly Val Cys Glu

490

	65		70		75		80
	Glu Val Glu Arg Val Arg Arg Ser Glu Arg Tyr Gln Thr Met Lys Val						
			85		90		95
5	Arg Arg Ala Gly Leu Gly Pro Thr Pro Gly Met Ser Cys Pro Gly Asn						
		100		105		110	
10	Asp Asn Thr Val His Thr Met His Gly Glu Ala Asn Arg Gly Ser Xaa						
		115		120		125	

15

(2) INFORMATION FOR SEQ ID NO: 240:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

```

25 Met Ser Ile Leu Cys Cys Pro Xaa Leu Cys Leu Phe Phe Ser Phe Cys
    1          5          10          15

    Ile Ser Ser Gly Ser Cys Pro Phe Ser His Val Ser Gln Leu Ser Phe
    20          25          30

30 Ile Ala Thr Phe Ser Gln Ser Ser Pro Val Leu Leu Val Pro Ala Tyr
    35          40          45

    Asn Thr Tyr Leu Ser Phe Leu Ala Phe Leu Asp Cys Ala Ser Leu Thr
35  50          55          60

    Ser Thr Xaa
    65

```

40

(2) INFORMATION FOR SEQ ID NO: 241:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

50 Met Ser Thr Phe Gln Leu Leu Leu Leu Ile Leu Ala Gln Ser Thr Tyr
1 5 10 15

Lys Ile Lys Ser Lys Pro Leu His Met Thr Asn His Thr Leu Leu Asn
20 25 30

55 Ser Pro Gly Leu Asn Pro Ser Ser Pro Thr Leu Asn Phe Lys Thr Gln
35 40 45

Gln His Glu Ser Val Ser Tyr Ala Cys Cys His Met Arg Ser Leu His
50 55 60

491

His Ala Phe Ala Xaa
65

5

(2) INFORMATION FOR SEQ ID NO: 242:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 44 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

15 Met Val Ser Val Val Leu Ile Phe Ser Phe Leu Ser Leu Thr Ile Ser
 1 5 10 15
 Thr Thr Ala Ser Ala Tyr Asn Gly Asn Asp Thr Gln Gly Trp Asn Asp
 20 25 30
 20 Lys Phe His Xaa Xaa Ser Val Lys Thr Gln Thr Xaa
 35 40

25

(2) INFORMATION FOR SEQ ID NO: 243:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

35 Met Ile Ser Asp Ala Gly Ala Gly Phe Gly Val Phe Leu Leu Val Pro
 1 5 10 15
 Arg Ala Gly His Cys Trp Gly Ala Gly Lys Pro Leu Pro Ser Cys Pro
 20 25 30
 40 Ser Val Ala Ser Ile Pro Ser Trp Val Leu Pro Ser Phe Leu Glu Arg
 35 40 45
 Gly Arg Xaa
 50

45

(2) INFORMATION FOR SEQ ID NO: 244:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

55

Met Val Gln Thr Ile Gln Asp Phe Leu Ser Leu Phe Ser Thr Pro Ile
 1 5 10 15
 Phe Leu Leu Leu Met Phe Glu Thr Leu Ser Leu Ala Pro Ala Trp
 20 25 30
 60

492

Leu Lys Pro Leu Arg Val Thr Ser His Ser Xaa
 35 40

5

(2) INFORMATION FOR SEQ ID NO: 245:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

15

Met Ile Leu Met Pro Gly Leu Gly Thr Ser Arg Gln Arg Ser Val Pro
 1 5 10 15

Phe Val Pro Thr Leu Asn Ala Ser Thr Pro Gly Ala Met Thr Gly Pro
 20 25 30

20

Thr Ala Thr Leu Thr Ser Cys Gln Trp Thr Thr Ala Cys Arg Val Ser
 35 40 45

25

Trp Ala Asn Gly Trp Thr Ser Leu Arg Thr Phe Arg Xaa
 50 55 60

30

(2) INFORMATION FOR SEQ ID NO: 246:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

Met Ser His His Ala Gln Pro Arg Phe Leu Leu Ile Thr Met Leu Leu
 1 5 10 15

40

Gln Glu Ala Lys Pro Val Ser Asn Ile Pro His Leu Leu Glu Ser Trp
 20 25 30

Tyr Phe Gly Xaa
 35

45

(2) INFORMATION FOR SEQ ID NO: 247:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

55

Met Asn Ser Leu Phe Trp Met Ile Leu Leu Pro Val Ser Gln Asp Gln
 1 5 10 15

60

Val Val Glu Gly Leu Gln Gly Gly Phe Ser Gln Ile His Met Arg Ile
 20 25 30

493

Leu Arg Lys His Leu Xaa
35

5

(2) INFORMATION FOR SEQ ID NO: 248:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 211 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

15 Met Ser Arg Ser Xaa Asp Val Thr Asn Thr Thr Phe Leu Leu Met Ala
1 5 10 15
Ala Ser Ile Tyr Leu His Asp Gln Asn Pro Asp Ala Ala Leu Arg Ala
20 20 25 30
Leu His Gln Gly Asp Ser Leu Glu Cys Thr Ala Met Thr Val Gln Ile
35 40 45
Leu Leu Lys Leu Asp Arg Leu Asp Leu Ala Arg Lys Glu Leu Lys Arg
25 50 55 60
Met Gln Asp Leu Asp Glu Asp Ala Thr Leu Thr Gln Leu Ala Thr Ala
65 70 75 80
30 Trp Val Ser Leu Ala Thr Gly Gly Glu Lys Leu Gln Asp Ala Tyr Tyr
85 90 95
Ile Phe Gln Glu Met Ala Asp Lys Cys Ser Pro Thr Leu Leu Leu Leu
100 105 110
35 Asn Gly Gln Ala Ala Cys His Met Ala Gln Gly Arg Trp Glu Ala Ala
115 120 125
Glu Gly Leu Leu Gln Glu Ala Leu Asp Lys Asp Ser Gly Tyr Pro Glu
40 130 135 140
Thr Leu Val Asn Leu Ile Val Leu Ser Gln His Leu Gly Lys Pro Pro
145 150 155 160
45 Glu Val Thr Asn Arg Tyr Leu Ser Gln Leu Lys Asp Ala His Arg Ser
165 170 175
His Pro Phe Ile Lys Glu Tyr Gln Ala Lys Glu Asn Asp Phe Asp Arg
180 185 190
50 Leu Val Leu Gln Tyr Ala Pro Ser Ala Glu Ala Gly Pro Glu Leu Ser
195 200 205
Gly Pro Xaa
55 210

60

(2) INFORMATION FOR SEQ ID NO: 249:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 548 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

Met Glu Asp Ser Glu Ala Leu Gly Phe Glu His Met Gly Leu Asp Pro
 1 5 10 15
 10 Arg Leu Leu Gln Ala Val Thr Asp Leu Gly Trp Ser Arg Pro Thr Leu
 20 25 30
 Ile Gln Glu Lys Ala Ile Pro Leu Ala Leu Glu Gly Lys Asp Leu Leu
 35 40 45
 15 Ala Arg Ala Arg Thr Gly Ser Gly Lys Thr Ala Ala Tyr Ala Ile Pro
 50 55 60
 20 Met Leu Gln Leu Leu Leu His Arg Lys Ala Thr Gly Pro Val Val Glu
 65 70 75 80
 Gln Ala Val Arg Gly Leu Val Leu Val Pro Thr Lys Glu Leu Ala Arg
 85 90 95
 25 Gln Ala Gln Ser Met Ile Gln Gln Leu Ala Thr Tyr Cys Ala Arg Asp
 100 105 110
 Val Arg Val Ala Asn Val Ser Ala Ala Glu Asp Ser Val Ser Gln Arg
 115 120 125
 30 Ala Val Leu Met Glu Lys Pro Asp Val Val Val Gly Thr Pro Ser Arg
 130 135 140
 Ile Leu Ser His Leu Gln Gln Asp Ser Leu Lys Leu Arg Asp Ser Leu
 145 150 155 160
 Glu Leu Leu Val Val Asp Glu Ala Asp Leu Leu Phe Ser Phe Gly Phe
 165 170 175
 40 Glu Glu Glu Leu Lys Ser Leu Leu Cys His Leu Pro Arg Ile Tyr Gln
 180 185 190
 Ala Phe Leu Met Ser Ala Thr Phe Asn Glu Asp Val Gln Ala Leu Lys
 195 200 205
 45 Glu Leu Ile Leu His Asn Pro Val Thr Leu Lys Leu Gln Glu Ser Gln
 210 215 220
 Leu Pro Gly Pro Asp Gln Leu Gln Gln Phe Gln Val Val Cys Glu Thr
 225 230 235 240
 Glu Glu Asp Lys Phe Leu Leu Leu Tyr Ala Leu Leu Lys Leu Ser Leu
 245 250 255
 50 Ile Arg Gly Lys Ser Leu Leu Phe Val Asn Thr Leu Glu Arg Ser Tyr
 260 265 270
 Arg Leu Arg Leu Phe Leu Glu Gln Phe Ser Ile Pro Thr Cys Val Leu
 275 280 285
 60

495

Asn Gly Glu Leu Pro Leu Arg Ser Arg Cys His Ile Ile Ser Gln Phe
 290 295 300
 5 Asn Gln Gly Phe Tyr Asp Cys Val Ile Ala Thr Asp Ala Glu Val Leu
 305 310 315 320
 Gly Ala Pro Val Lys Gly Lys Arg Arg Gly Arg Gly Pro Lys Gly Asp
 325 330 335
 10 Lys Ala Ser Asp Pro Glu Ala Gly Val Ala Arg Gly Ile Asp Phe His
 340 345 350
 His Val Ser Ala Val Leu Asn Phe Asp Leu Pro Pro Thr Pro Glu Ala
 355 360 365
 15 Tyr Ile His Arg Ala Gly Arg Thr Ala Arg Ala Asn Asn Pro Gly Ile
 370 375 380
 Val Leu Thr Phe Val Leu Pro Thr Glu Gln Phe His Leu Gly Lys Ile
 20 385 390 395 400
 Glu Glu Leu Leu Ser Gly Glu Asn Arg Gly Pro Ile Leu Leu Pro Tyr
 405 410 415
 25 Gln Phe Arg Met Glu Glu Ile Glu Gly Phe Arg Tyr Arg Cys Arg Asp
 420 425 430
 Ala Met Arg Ser Val Thr Lys Gln Ala Ile Arg Glu Ala Arg Leu Lys
 435 440 445
 30 Glu Ile Lys Glu Glu Leu Leu His Ser Glu Lys Leu Lys Thr Tyr Phe
 450 455 460
 Glu Asp Asn Pro Arg Asp Leu Gln Leu Leu Arg His Asp Leu Pro Leu
 35 465 470 475 480
 His Pro Ala Val Val Lys Pro His Leu Gly His Val Pro Asp Tyr Leu
 485 490 495
 40 Val Pro Pro Ala Leu Arg Gly Leu Val Arg Pro His Lys Lys Arg Lys
 500 505 510
 Lys Leu Ser Ser Ser Cys Arg Lys Ala Lys Arg Ala Lys Ser Gln Asn
 515 520 525
 45 Pro Leu Arg Ser Phe Lys His Lys Gly Lys Lys Phe Arg Pro Thr Ala
 530 535 540
 50 Lys Pro Ser Xaa
 545

(2) INFORMATION FOR SEQ ID NO: 250:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 299 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

496

Met Thr Thr Val Pro Pro Ser Pro Arg Pro Met Ser Arg Pro Ser Glu
 1 5 10 15
 5 Arg Asn Met Arg Arg Pro Arg Gly Pro Ser Pro Leu Pro Ala Ser Pro
 20 25 30
 Arg Asn Ser Thr Pro Asp Glu Pro Asp Val His Phe Ser Lys Lys Phe
 35 40 45
 10 Leu Asn Val Phe Met Ser Gly Arg Ser Arg Ser Ser Ser Ala Glu Ser
 50 55 60
 Phe Gly Leu Phe Ser Cys Ile Ile Asn Gly Glu Glu Gln Glu Gln Thr
 15 65 70 75 80
 His Arg Ala Ile Phe Arg Phe Val Pro Arg His Glu Asp Glu Leu Glu
 85 90 95
 20 Leu Glu Val Asp Asp Pro Leu Leu Val Glu Leu Gln Ala Glu Asp Tyr
 100 105 110
 Trp Tyr Glu Ala Tyr Asn Met Arg Thr Gly Ala Arg Gly Val Phe Pro
 115 120 125
 25 Ala Tyr Tyr Ala Ile Glu Val Thr Lys Glu Pro Glu His Met Ala Ala
 130 135 140
 Leu Ala Lys Asn Ser Asp Trp Val Asp Gln Phe Arg Val Lys Phe Leu
 145 150 155 160
 Gly Ser Val Gln Val Pro Tyr His Lys Gly Asn Asp Val Leu Cys Ala
 165 170 175
 35 Ala Met Gln Lys Ile Ala Thr Thr Arg Arg Leu Thr Val His Phe Asn
 180 185 190
 Pro Pro Ser Ser Cys Val Leu Glu Ile Ser Val Arg Gly Val Lys Ile
 195 200 205
 40 Gly Val Lys Ala Asp Asp Ser Gln Glu Ala Lys Gly Asn Lys Cys Ser
 210 215 220
 His Phe Phe Gln Leu Lys Asn Ile Ser Phe Cys Gly Tyr His Pro Lys
 225 230 235 240
 Asn Asn Lys Tyr Phe Gly Phe Ile Thr Lys His Pro Ala Asp His Arg
 245 250 255
 50 Phe Ala Cys His Val Phe Val Ser Glu Asp Ser Thr Lys Ala Leu Ala
 260 265 270
 Glu Ser Val Gly Arg Ala Phe Gln Gln Phe Tyr Lys Gln Phe Val Glu
 275 280 285
 55 Tyr Thr Cys Pro Thr Glu Asp Ile Tyr Leu Glu
 290 295
 60

497

(2) INFORMATION FOR SEQ ID NO: 251:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

5 Leu Leu Tyr Leu Leu Lys Val Xaa Val Ile Phe Val Phe Ser Ser Ser
 10 1 5 10 15
 Lys Gly Val Thr Leu Val Ser Met Asn Leu Thr Ser Phe Phe Val Ser
 20 25 30
 15 Ser Val Leu Ala Cys Phe Ser Xaa
 35 40

20 (2) INFORMATION FOR SEQ ID NO: 252:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 594 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

25 Met Pro Ala Ser Ser Leu Glu Ser Arg Ser Phe Leu Leu Ala Lys Lys
 30 1 5 10 15
 Ser Gly Glu Asn Val Ala Lys Phe Ile Ile Asn Ser Tyr Pro Lys Tyr
 20 25 30
 35 Phe Gln Lys Asp Ile Ala Glu Pro His Ile Pro Cys Leu Met Pro Glu
 35 40 45
 Tyr Phe Glu Pro Gln Ile Lys Asp Ile Ser Glu Ala Ala Leu Lys Glu
 50 55 60
 40 Arg Ile Glu Leu Arg Lys Val Lys Ala Ser Val Asp Met Phe Asp Gln
 65 70 75 80
 Leu Leu Gln Ala Gly Thr Thr Val Ser Leu Glu Thr Thr Asn Ser Leu
 85 90 95
 45 Leu Asp Xaa Leu Cys Tyr Tyr Gly Asp Gln Glu Pro Ser Thr Asp Tyr
 100 105 110
 50 His Phe Gln Gln Thr Gly Gln Ser Glu Ala Leu Glu Glu Glu Asn Asp
 115 120 125
 Glu Thr Ser Arg Arg Lys Ala Gly His Gln Phe Gly Val Thr Trp Arg
 130 135 140
 55 Ala Lys Asn Asn Ala Glu Arg Ile Phe Ser Leu Met Pro Glu Lys Asn
 145 150 155 160
 Glu His Ser Tyr Cys Thr Met Ile Arg Gly Met Val Lys His Arg Ala
 165 170 175
 60

498

Tyr Glu Gln Ala Leu Asn Leu Tyr Thr Glu Leu Leu Asn Asn Arg Leu
 180 185 190
 5 His Ala Asp Val Tyr Thr Phe Asn Ala Leu Ile Glu Ala Thr Val Cys
 195 200 205
 Ala Ile Asn Glu Lys Phe Glu Glu Lys Trp Ser Lys Ile Leu Glu Leu
 210 215 220
 10 Leu Arg His Met Val Ala Gln Lys Val Lys Pro Asn Leu Gln Thr Phe
 225 230 235 240
 Asn Thr Ile Leu Lys Cys Leu Arg Arg Phe His Val Phe Ala Arg Ser
 245 250 255
 15 Pro Ala Leu Gln Val Leu Arg Glu Met Lys Ala Ile Gly Ile Glu Pro
 260 265 270
 20 Ser Leu Ala Thr Tyr His His Ile Ile Arg Leu Phe Asp Gln Pro Gly
 275 280 285
 Asp Pro Leu Lys Arg Ser Ser Phe Ile Ile Tyr Asp Ile Met Asn Glu
 290 295 300
 25 Leu Met Gly Lys Arg Phe Ser Pro Lys Asp Pro Asp Asp Asp Lys Phe
 305 310 315 320
 Phe Gln Ser Ala Met Ser Ile Cys Ser Ser Leu Arg Asp Leu Glu Leu
 325 330 335
 30 Ala Tyr Gln Val His Gly Leu Leu Lys Thr Gly Asp Asn Trp Lys Phe
 340 345 350
 35 Ile Gly Pro Asp Gln His Arg Asn Phe Tyr Tyr Ser Lys Phe Phe Asp
 355 360 365
 Leu Ile Cys Leu Met Glu Gln Ile Asp Val Thr Leu Lys Trp Tyr Glu
 370 375 380
 40 Asp Leu Ile Pro Ser Ala Tyr Phe Pro His Ser Gln Thr Met Ile His
 385 390 395 400
 Leu Leu Gln Ala Leu Asp Val Ala Asn Arg Leu Glu Val Ile Pro Lys
 405 410 415
 45 Ile Trp Lys Asp Ser Lys Glu Tyr Gly His Thr Phe Arg Ser Asp Leu
 420 425 430
 Arg Glu Glu Ile Leu Met Leu Met Ala Arg Asp Lys His Pro Pro Glu
 435 440 445
 50 Leu Gln Val Ala Phe Ala Asp Cys Ala Ala Asp Ile Lys Ser Ala Tyr
 450 455 460
 55 Glu Ser Gln Pro Ile Arg Gln Thr Ala Gln Asp Trp Pro Ala Thr Ser
 465 470 475 480
 Leu Asn Cys Ile Ala Ile Leu Phe Leu Arg Ala Gly Arg Thr Gln Glu.
 485 490 495
 60

499

Ala Trp Lys Met Leu Gly Leu Phe Arg Lys His Asn Lys Ile Pro Arg
 500 505 510

5 Ser Glu Leu Leu Asn Glu Leu Met Asp Ser Ala Lys Val Ser Asn Ser
 515 520 525

Pro Ser Gln Ala Ile Glu Val Val Glu Leu Ala Ser Ala Phe Ser Leu
 530 535 540

10 Pro Ile Cys Glu Gly Leu Thr Gln Arg Val Met Ser Asp Phe Ala Ile
 545 550 555 560

Asn Gln Glu Gln Lys Glu Ala Leu Ser Asn Leu Thr Ala Leu Thr Ser
 565 570 575

15 Asp Ser Asp Thr Asp Ser Ser Ser Asp Ser Asp Ser Asp Thr Ser Glu
 580 585 590

20 Gly Lys

(2) INFORMATION FOR SEQ ID NO: 253:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

Met Lys Leu Asn Leu Cys Ile Pro Asn Trp Ala Arg Cys Pro Leu Leu
 1 5 10 15

35 Leu Leu Phe Pro Gln Leu Leu Pro Phe Gln Gly Glu Asp Asp Asp Pro
 20 25 30

Leu Lys Ala Lys Ala Ala Asn Leu Val Glu Ala Val Pro Trp Gly Ile
 35 40 45

40 Lys Ala Pro Ser Phe Gln Val Thr Cys Leu Val Arg Val Gln Leu Gln
 50 55 60

45 Ser Cys Thr Pro Ser Arg Pro Ser Thr Leu Leu Ala Thr Ser Gln Ser
 65 70 75 80

Pro Gly Arg Ile Ser Cys Tyr Ser Pro Leu Ser His Leu Pro Pro Val
 85 90 95

50 Thr Thr Ser Ile Gln Pro Ser Pro Val Met Val Pro Phe Gln Tyr Gln
 100 105 110

Ala Phe Leu Leu Gln Val Lys Glu Pro Ala Ala Gln Thr Leu Leu Gly
 115 120 125

55 Gln Gln Xaa
 130

60

500

(2) INFORMATION FOR SEQ ID NO: 254:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

Met Arg Tyr His Ala Gln Leu Ile Phe Cys Ile Phe Cys Xaa Phe Val
 1 5 10 15
 Phe Val Xaa Lys Xaa
 20

(2) INFORMATION FOR SEQ ID NO: 255:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

Met Asn Asp Asn Ser Pro Asn His Ser Ser Ser Tyr Leu Pro Leu Pro
 1 5 10 15
 Leu Thr Ile Val Ile Leu Gln Thr Gly His Lys Gly Thr Leu Xaa
 20 25 30

(2) INFORMATION FOR SEQ ID NO: 256:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

Met His Phe Leu Phe Arg Phe Ile Val Phe Phe Tyr Leu Trp Gly Leu
 1 5 10 15
 Phe Thr Ala Gln Arg Gln Lys Lys Glu Glu Ser Thr Glu Glu Val Lys
 20 25 30
 Ile Glu Val Leu His Arg Pro Glu Asn Cys Ser Lys Thr Ser Lys Lys
 35 40 45
 Gly Asp Leu Leu Asn Ala His Tyr Asp Gly Tyr Leu Ala Lys Asp Gly
 50 55 60
 Ser Lys Phe Tyr Cys Ser Arg Thr Gln Asn Glu Gly His Pro Lys Trp
 65 70 75 80
 Phe Val Leu Gly Val Gly Gln Val Ile Lys Gly Leu Asp Ile Ala Met
 85 90 95
 Thr Asp Met Cys Pro Gly Glu Lys Arg Lys Val Val Ile Pro Pro Ser
 100 105 110

501

Phe Ala Tyr Gly Lys Glu Gly Tyr Ala Glu Gly Lys Ile Pro Pro Asp
 115 120 125
 5 Ala Thr Leu Ile Phe Glu Ile Glu Leu Tyr Ala Val Thr Lys Gly Pro
 130 135 140
 Arg Ser Ile Glu Thr Phe Lys Gln Ile Asp Met Asp Asn Asp Arg Gln
 145 150 155 160
 10 Leu Ser Lys Ala Glu Ile Asn Leu Tyr Leu Gln Arg Glu Phe Glu Lys
 165 170 175
 Asp Glu Lys Pro Arg Asp Lys Ser Tyr Gln Asp Ala Val Leu Glu Asp
 15 180 185 190
 Ile Phe Lys Lys Asn Asp His Asp Gly Asp Gly Phe Ile Ser Pro Lys
 195 200 205
 20 Glu Tyr Asn Val Tyr Gln His Asp Glu Leu Xaa
 210 215

25 (2) INFORMATION FOR SEQ ID NO: 257:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

Met Trp Val Ile Arg Val Phe Gln Lys Thr Phe Leu Phe Phe Val Leu
 1 5 10 15
 35 Phe Trp Ser Val His Cys Ile Ser Asp Lys Phe Gly Cys Leu Trp His
 20 25 30
 Val Cys Met Lys Arg Glu Gly Asp Xaa Asn Cys Leu Ser Phe Ser Xaa
 40 35 40 45
 Leu Xaa
 50

45

(2) INFORMATION FOR SEQ ID NO: 258:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

55 Met Pro Ser Gln Thr Glu Xaa Phe Ala Ala Cys Gly Gly His Ser Leu
 1 5 10 15
 Leu Leu Val Xaa Leu Pro Leu Gly Leu Pro Phe Cys Pro Arg Ala Ala.
 20 25 30
 60

502

Leu Cys Asp Leu Pro Phe Ser Leu Pro Ser Phe Pro Gly Gln Ala Arg
 35 40 45
 5 Arg Gly Gly Ala Glu Lys Gln Gly Ala Glu Gly Arg Gly Leu Gln Val
 50 55 60
 Lys Pro Arg Gly Gln Arg Thr Phe Gln Val Ser Arg Thr Ala Pro Ala
 65 70 75 80
 10 Ala Pro Arg Ser Arg Gln Pro Arg Pro Pro Ala Ala Leu Pro Ala Leu
 85 90 95
 Gly Phe Gly Gly Arg Gly Val Ala Lys Gly Arg Phe Leu Cys Phe Trp
 100 105 110
 15 Cys Leu Tyr Met Leu Arg Ile Asp Gln Xaa
 115 120

20

(2) INFORMATION FOR SEQ ID NO: 259:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 88 amino acids
 25 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

30 Met Thr Ala Phe Cys Ser Leu Leu Leu Gln Ala Gln Ser Leu Leu Pro
 1 5 10 15
 Arg Thr Met Ala Ala Pro Gln Asp Ser Leu Arg Pro Gly Glu Glu Asp
 20 25 30
 35 Glu Gly Met Gln Leu Leu Gln Thr Lys Asp Ser Met Ala Lys Gly Ala
 35 40 45
 Arg Pro Gly Ala Xaa Arg Gly Arg Ala Arg Trp Gly Leu Ala Tyr Thr
 50 55 60
 40 Leu Leu His Asn Pro Thr Leu Gln Val Phe Arg Lys Thr Ala Leu Leu
 65 70 75 80
 Gly Ala Asn Gly Ala Gln Pro Xaa
 45 85

50 (2) INFORMATION FOR SEQ ID NO: 260:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

Met Ile Gln Val Ser Val Pro Leu Leu Thr Ile Met Ile Phe Leu Leu
 1 5 10 15
 60 Tyr Leu Gln Ile Gly Pro Gly Lys Leu Xaa

20

25

5 (2) INFORMATION FOR SEQ ID NO: 261:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

Met Leu Leu Asp Pro Phe Ile Leu Leu Phe Cys Leu Phe Ser Thr Ala

1 5 10 15

15

Ala Gln Ser Cys Leu Glu Phe Ile Tyr Ile Gln Phe Xaa

20 25

20

(2) INFORMATION FOR SEQ ID NO: 262:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

25 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

Met Lys Phe Leu Ser Ile Leu Leu Asp Asp Asn Asn Phe Xaa Leu Met

30 1 5 10 15

Leu Met Leu Ala Pro Phe Gly Cys Leu Ala Phe Glu Arg Ser Met Lys

20 25 30

35

Met Arg Asn Gly Ala Leu Gly Leu Glu Glu Val Xaa

35 40

40

(2) INFORMATION FOR SEQ ID NO: 263:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 363 amino acids

(B) TYPE: amino acid

45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro

50 1 5 10 15

Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala Ala Ser Lys

20 25 30

55

Thr Leu Leu Glu Lys Ser Gln Phe Ser Asp Lys Pro Val Gln Asp Arg

35 40 45

Gly Leu Val Val Thr Asp Leu Lys Ala Glu Ser Val Val Leu Glu His

50 55 60

60

Arg Ser Tyr Cys Ser Ala Lys Ala Arg Asp Arg His Phe Ala Gly Asp

504

	65		70		75		80
	Val Leu Gly Tyr	Val Thr Pro Trp Asn Ser His Gly Tyr Asp Val Thr					
		85		90		95	
5	Lys Val Phe Gly Ser Lys Phe Thr Gln Ile Ser Pro Val Trp Leu Gln						
		100		105		110	
	Leu Lys Arg Arg Gly Arg Glu Met Phe Glu Val Thr Gly Leu His Asp						
10		115		120		125	
	Val Asp Gln Gly Trp Met Arg Ala Val Arg Lys His Ala Lys Gly Leu						
		130		135		140	
15	His Ile Val Pro Arg Leu Leu Phe Glu Asp Trp Thr Tyr Asp Asp Phe						
		145		150		155	
	Arg Asn Val Leu Asp Ser Glu Asp Glu Ile Glu Glu Leu Ser Lys Thr						
20		165		170		175	
	Val Val Gln Val Ala Lys Asn Gln His Phe Asp Gly Phe Val Val Glu						
		180		185		190	
	Val Trp Asn Gln Leu Leu Ser Gln Lys Arg Val Thr Asp Gln Leu Gly						
25		195		200		205	
	Met Phe Thr His Lys Glu Phe Glu Gln Leu Ala Pro Val Leu Asp Gly						
		210		215		220	
30	Phe Ser Leu Met Thr Tyr Asp Tyr Ser Thr Ala His Gln Pro Gly Pro						
		225		230		235	
	Asn Ala Pro Leu Ser Trp Val Arg Ala Cys Val Gln Val Leu Asp Pro						
35		245		250		255	
	Lys Ser Lys Trp Arg Ser Lys Ile Leu Leu Gly Leu Asn Phe Tyr Gly						
		260		265		270	
	Met Asp Tyr Ala Thr Ser Lys Asp Ala Arg Glu Pro Val Val Gly Ala						
40		275		280		285	
	Arg Tyr Ile Gln Thr Leu Lys Asp His Arg Pro Arg Met Val Trp Asp						
		290		295		300	
45	Ser Gln Xaa Ser Glu His Phe Phe Glu Tyr Lys Lys Ser Arg Ser Gly						
		305		310		315	
	Arg His Val Val Phe Tyr Pro Thr Leu Lys Ser Leu Gln Val Arg Leu						
50		325		330		335	
	Glu Leu Ala Arg Glu Leu Gly Val Gly Val Ser Ile Trp Glu Leu Gly						
		340		345		350	
	Gln Gly Leu Asp Tyr Phe Tyr Asp Leu Leu Xaa						
55		355		360			

(2) INFORMATION FOR SEQ ID NO: 264:

60

505

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

Leu Pro Thr Lys Ile Leu Val Lys Pro Asp Arg Thr Phe Glu Ile Lys
 1 5 10 15
 10 Ile Gly Gln Pro Thr Val Ser Tyr Phe Leu Lys Ala Ala Ala Gly Ile
 20 25 30
 Glu Lys Gly Ala Arg Gln Thr Gly Lys Glu Val Ala Gly Leu Val Thr
 35 40 45
 15 Leu Lys His Val Tyr Glu Ile Ala Arg Ile Lys Ala Gln Asp Glu Ala
 50 55 60
 Phe Ala Leu Gln Asp Val Pro Leu Ser Ser Val Val Arg Ser Ile Ile
 20 65 70 75 80
 Gly Ser Ala Arg Ser Leu Gly Ile Arg Val Val Lys Asp Leu Ser Ser
 85 90 95
 25 Glu Glu Leu Ala Ala Phe Gln Lys Glu Arg Ala Ile Phe Leu Ala Ala
 100 105 110
 Gln Lys Glu Ala Asp Leu Ala Ala Gln Glu Glu Ala Ala Lys Lys Xaa
 115 120 125
 30

35

(2) INFORMATION FOR SEQ ID NO: 265:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

45 Met Leu Leu Gln Ile His Pro Leu Leu Pro Ser Pro Thr Ile Pro His
 1 5 10 15
 Ile Leu Leu Leu Phe Leu Tyr Pro Thr Phe Ser Ile Leu Glu His Ser
 20 25 30
 50 Cys Ser Tyr Cys Ile Glu Tyr Leu Trp Val Cys Leu Leu Phe Cys Leu
 35 40 45
 Ser Leu Trp Phe Leu Xaa
 50
 55

60

(2) INFORMATION FOR SEQ ID NO: 266:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

5

Met Cys Leu Trp Cys Cys Gly Asp Val Cys Ser Gly Leu Ser Ser Leu
 1 5 10 15

10

Leu Ser Leu Cys Val Cys Cys Val Val Leu Ala Val Cys
 20 25

(2) INFORMATION FOR SEQ ID NO: 267:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

Glu Gly Leu Arg Leu Leu Leu Ser Leu Pro Ala Ala Leu Pro Arg Ser
 1 5 10 15

25

Cys Cys His Pro Arg Trp Leu Pro Val Xaa
 20 25

30

(2) INFORMATION FOR SEQ ID NO: 268:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 221 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

Met Phe His Gly Ile Pro Ala Thr Pro Gly Ile Gly Ala Pro Gly Asn
 1 5 10 15

40

Lys Pro Glu Leu Tyr Glu Glu Val Lys Leu Tyr Lys Asn Ala Arg Glu
 20 25 30

45

Arg Glu Lys Tyr Asp Asn Met Ala Glu Leu Phe Ala Val Val Lys Thr
 35 40 45

Met Gln Ala Leu Glu Lys Ala Tyr Ile Lys Asp Cys Val Ser Pro Ser
 50 55 60

50

Glu Tyr Thr Ala Ala Cys Ser Arg Leu Leu Val Gln Tyr Lys Ala Ala
 65 70 75 80

Phe Arg Gln Val Gln Gly Ser Glu Ile Ser Ser Ile Asp Glu Phe Cys
 85 90 95

55

Arg Lys Phe Arg Leu Asp Cys Pro Leu Ala Met Glu Arg Ile Lys Glu
 100 105 110

60

Asp Arg Pro Ile Thr Ile Lys Asp Asp Lys Gly Asn Leu Asn Arg Cys
 115 120 125

507

Ile Ala Asp Val Val Ser Leu Phe Ile Thr Val Met Asp Lys Leu Arg
 130 135 140

5 Leu Glu Ile Arg Ala Met Asp Glu Ile Gln Pro Asp Leu Arg Glu Leu
 145 150 155 160

Met Glu Thr Met His Arg Met Ser His Leu Pro Pro Asp Phe Glu Gly
 165 170 175

10 Arg Gln Thr Val Ser Gln Trp Leu Gln Thr Leu Ser Gly Met Ser Ala
 180 185 190

Ser Asp Glu Leu Asp Asp Ser Gln Val Arg Gln Met Leu Phe Asp Leu
 15 195 200 205

Glu Ser Ala Tyr Asn Ala Phe Asn Arg Phe Leu His Ala
 210 215 220

20

(2) INFORMATION FOR SEQ ID NO: 269:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

30 Met Lys Xaa
 1

35 (2) INFORMATION FOR SEQ ID NO: 270:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 49 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

Met Gln Ala Pro Phe Xaa His Phe Ser Phe Arg Met Phe Ser Asn Leu
 1 5 10 15

45 Tyr Cys Phe Ser Asp Phe Gln Pro Asn Ile Ser Pro Cys Pro Leu Cys
 20 25 30

His Cys Ile Leu Pro Xaa His His His Val Phe Leu Leu Leu Ala Val
 50 35 40 45

Xaa

55

(2) INFORMATION FOR SEQ ID NO: 271:

60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 amino acids

508

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

5 Met Lys Leu Val Thr Met Phe Asp Lys Leu Ser Arg Asn Arg Val Ile
 1 5 10 15

Gln Pro Met Gly Met Ser Pro Arg Gly His Leu Thr Ser Leu Gln Asp
 20 25 30

10 Ala Met Cys Glu Thr Met Glu Gln Gln Leu Ser Ser Asp Pro Asp Ser
 35 40 45

Asp Pro Asp Xaa
 15 50

(2) INFORMATION FOR SEQ ID NO: 272:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

Met Ala Val Gly Glu Ala Val Phe Val Pro Leu Gln His Pro Pro Leu
 1 5 10 15

30 Leu His Gly Ser Pro Ile Pro Lys Leu Leu Pro Gly Pro Leu Leu Xaa
 20 25 30

35

(2) INFORMATION FOR SEQ ID NO: 273:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

Met Asn Gly Cys His Arg Arg Lys Arg Leu His Leu Cys Lys Thr Ile
 1 5 10 15

50 Tyr Leu Leu Trp Phe Val Phe Ser Phe Leu Leu Ser Asn Glu Val Val
 20 25 30

Ser Ser His Trp His Ile Leu Arg Ala Val Gln Ile Ile Cys Thr Leu
 35 40 45

55 Phe His Arg Xaa Ile Ser Ala Phe Xaa
 50 55

60

(2) INFORMATION FOR SEQ ID NO: 274:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

Met Gly Trp Val Ser Ser Pro His Val Lys Arg Arg Glu Cys Val Leu
 1 5 10 15
 Lys Lys Pro Phe Phe Xaa
 20

(2) INFORMATION FOR SEQ ID NO: 275:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

Met Phe Asn Phe Phe Lys Asn Pro Leu Leu Thr Cys Leu Phe Ile Ser
 1 5 10 15
 Cys Tyr Leu Tyr Leu Ser Leu Leu Val Asn Lys Val Leu Phe Ala Glu
 20 25 30
 Glu Gly Leu Cys Cys Thr Tyr Cys Thr Thr Ser Asn Thr Gly Glu Gly
 35 40 45
 Gly Val Xaa
 50

(2) INFORMATION FOR SEQ ID NO: 276:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

Met Xaa
 1

(2) INFORMATION FOR SEQ ID NO: 277:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

Met Leu Cys Thr Ile Leu Thr Val Val Ile Ile Ala Ala Gln Thr
 1 5 10 15

510

Thr Arg Thr Thr Gly Ile Pro Lys Asn Ala Pro Gly Pro Ala Pro Leu
 20 25 30
 5 Cys Ala Pro Arg Ser Pro Arg Leu Phe Leu Gln Xaa Tyr Arg Gly Pro
 35 40 45
 Asn Gly Arg Pro Ala His Pro Phe Leu Gly Pro Ser Asp Leu Asp Thr
 50 55 60
 10 Ser Xaa
 65
 15
 (2) INFORMATION FOR SEQ ID NO: 278:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 257 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:
 20
 25 Met Leu Gly Ala Lys Pro His Trp Leu Pro Gly Pro Leu His Ser Pro
 1 5 10 15
 Gly Leu Pro Leu Val Leu Val Leu Leu Ala Leu Gly Ala Gly Trp Ala
 20 25 30
 30 Gln Glu Gly Ser Glu Pro Val Leu Leu Glu Gly Glu Cys Leu Val Val
 35 40 45
 Cys Glu Pro Gly Arg Ala Ala Ala Gly Gly Pro Gly Gly Ala Ala Leu
 50 55 60
 35 Gly Glu Ala Pro Pro Gly Arg Val Ala Phe Xaa Ala Val Arg Ser His
 65 70 75 80
 40 His His Glu Pro Ala Gly Glu Thr Gly Asn Gly Thr Ser Gly Ala Ile
 85 90 95
 Tyr Phe Asp Gln Val Leu Val Asn Glu Gly Gly Gly Phe Asp Arg Ala
 100 105 110
 45 Ser Gly Ser Phe Val Ala Pro Val Arg Gly Val Tyr Ser Phe Arg Phe
 115 120 125
 His Val Val Lys Val Tyr Asn Arg Gln Thr Val Gln Val Ser Leu Met
 130 135 140
 50 Leu Asn Thr Trp Pro Val Ile Ser Ala Phe Ala Asn Asp Pro Asp Val
 145 150 155 160
 Thr Arg Glu Ala Ala Thr Ser Ser Val Leu Leu Pro Leu Asp Pro Gly
 165 170 175
 Asp Arg Val Ser Leu Arg Leu Arg Arg Gly Xaa Ser Thr Gly Trp Leu
 180 185 190
 60 Glu Ile Leu Lys Phe Leu Trp Leu Pro His Leu Pro Ser Leu Lys Asp

511

195 200 205

Pro Ser Leu Ser Ser Thr Arg Ile Gln Pro Leu Thr Thr Phe Phe Cys
 210 215 220

5 Pro Leu Leu Pro Xaa Lys Gln Xaa Lys Gln Xaa Xaa Xaa Ser Leu Trp
 225 230 235 240

10 Leu Leu Ser His Leu Phe Ala Trp Glu Pro Val Pro Asn Thr Gln Val
 245 250 255

Xaa

15

(2) INFORMATION FOR SEQ ID NO: 279:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 103 amino acids

(B) TYPE: amino acid

(C) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

25 Met Ala Pro Arg Ala Leu Pro Gly Ser Ala Val Leu Ala Ala Ala Val
 1 5 10 15

 Phe Val Gly Gly Ala Val Ser Ser Pro Leu Val Ala Pro Asp Asn Gly
 20 25 30

30 Ser Ser Arg Thr Leu His Ser Arg Thr Glu Thr Thr Pro Ser Pro Ser
 35 40 45

35 Asn Asp Thr Gly Asn Gly His Pro Glu Tyr Ile Ala Tyr Ala Leu Val
 50 55 60

 Pro Val Phe Phe Ile Met Gly Leu Phe Gly Val Leu Ile Xaa Pro Xaa
 65 70 75 80

40 Xaa Xaa Lys Lys Lys Gly Tyr Arg Cys Thr Thr Glu Ala Glu Gln Asp
 85 90 95

 Ile Glu Glu Glu Lys Gly Xaa
 100

45

(2) INFORMATION FOR SEQ ID NO: 280:

50 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

55

Met Pro Val Thr Leu Ser Ser Leu Gly Phe Trp Val Leu Leu Ser Leu
 1 5 10 15

60 Leu Phe Pro Trp Arg Thr Asp Gln Gly Cys Gly Pro Ala Thr Cys Tyr
 20 25 30

Xaa

5

(2) INFORMATION FOR SEQ ID NO: 281:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

15

Met Val Leu Gly Leu Leu Leu Leu Xaa Phe Phe Ser Phe Ser Ser
 1 5 10 15

Ser Pro Ser Pro Ser Ser Ser Leu Leu Leu Leu Ser Ser Phe Phe Phe
 20 25 30

20

Gln Ser Leu Ala Leu Ser Pro Arg Leu Glu Xaa
 35 40

25

(2) INFORMATION FOR SEQ ID NO: 282:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

30

Glu Trp Leu Val Phe Thr Phe Leu Leu Val Phe Gly Ser Pro Leu Gly
 1 5 10 15

Lys Gly Pro Leu Xaa
 20

40

(2) INFORMATION FOR SEQ ID NO: 283:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

45

Met Ile Arg Ala Leu Ser Leu Phe Leu Leu Ile Phe Asp Ala Ala Leu
 1 5 10 15

Phe Ser Leu Ser Val Phe Val Phe Ile Gly His Leu Leu Pro Met Pro
 20 25 30

55

Lys Gly Thr Gly Leu His Ser Cys Ala Lys His Leu Ile Lys Ser Leu
 35 40 45

60

Lys Glu Asn Val Leu Pro Leu Met Asn Tyr Pro Asp Cys Lys Leu Lys
 50 55 60

Ile Asn Ile Ser Pro Xaa
65 70

5

(2) INFORMATION FOR SEQ ID NO: 284:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

15

Met Gly Lys Leu Ile Arg Leu Ser Val Met Val Met Ser Val Arg Arg
1 5 10 15

Leu Phe Ser Ile Tyr Trp Val Leu Ser Thr Val Pro Asp Ala Val Gly
20 25 30

20

Ser Arg Gly Gly Met Glu Glu Glu Cys Ser Arg Gly Leu Cys Cys Val
35 40 45

25

Ala Gly Gln His Lys Gln Ala Lys Gly Lys Arg Gln Ala Trp Asn Lys
50 55 60

Gly Gly Glu Tyr Gln Cys Val Thr Tyr Cys Xaa
65 70 75

30

(2) INFORMATION FOR SEQ ID NO: 285:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

40

Met Pro Ala Leu Val Thr Leu Leu Leu Leu Phe Pro Leu Leu Pro Leu
1 5 10 15

Met Glu Ala Ser Cys His Val Met Arg Cys Pro Met Glu Arg Pro Thr
20 25 30

45

Xaa

50

(2) INFORMATION FOR SEQ ID NO: 286:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

55

Glu Ala Pro Trp Gly Leu Leu Lys Leu Leu Leu Leu Ala Val Phe
1 5 10 15

60

Xaa

5

(2) INFORMATION FOR SEQ ID NO: 287:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

15

Met Gln Gln Lys Gln Lys Lys Ala Asn Glu Lys Lys Glu Glu Pro Lys
1 5 10 15

Xaa

20

(2) INFORMATION FOR SEQ ID NO: 288:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

30

Met Gln Arg Lys Val Ser Asp Phe Ile Ile His Gln Arg Leu Thr Val
1 5 10 15

35

Asn Leu Cys Val Ile Ser Phe Phe Phe Phe Leu Pro Ile Cys Ile Phe
20 25 30

Ser Leu Ala Lys Lys Xaa
35

40

(2) INFORMATION FOR SEQ ID NO: 289:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

50

Met Ala Leu Leu Ile Ser Ser Leu Ile Trp Ser Xaa
1 5 10

55

(2) INFORMATION FOR SEQ ID NO: 290:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

(B) TYPE: amino acid

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

5 Met Gln Met Phe Thr Val Ser Leu Leu Leu Ser Leu Leu Leu Arg Ser
 1 5 10 15
 Thr Asp Gln Asn His Leu Gln Leu Leu Val Gly Arg Glu Asp His Tyr
 20 25 30
 10 Gly Gly Xaa
 35

(2) INFORMATION FOR SEQ ID NO: 291:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

25 Met Ser Glu Ser Ala Cys Ile Leu Asn Asn Gln Lys Glu Leu Xaa
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 292:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

35 Met Asp Leu Asp Arg Val Lys Ala Glu Ala Thr Glu Asp Ile Thr Ser
 1 5 10 15
 Gly Val Leu Cys Leu Leu Phe Leu Arg Leu Pro Pro Asn Ser Cys Ile
 20 25 30
 40 Phe Pro Ser Ala Val Leu Gly Ser Thr Arg Thr Xaa
 35 40

(2) INFORMATION FOR SEQ ID NO: 293:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

55 Val Val Gly Thr Gly Thr Ser Leu Ala Leu Ser Ser Leu Leu Ser Leu
 1 5 10 15
 Leu Leu Phe Ala Gly Met Gln Met Tyr Ser Arg Gln Leu Ala Ser Thr
 20 25 30
 60 Glu Trp Leu Thr Ile Gln Gly Gly Leu Leu Gly Ser Gly Leu Phe Val

516

35 40 45
 Phe Ser Leu Thr Ala Phe Asn Asn Leu Glu Asn Leu Val Phe Gly Lys
 50 55 60
 5 Gly Phe Gln Ala Lys Ile Phe Pro Glu Ile Leu Leu Cys Leu Leu Leu
 65 70 75 80
 10 Ala Leu Phe Ala Ser Gly Leu Ile His Arg Val Cys Val Thr Thr Cys
 85 90 95
 Phe Ile Phe Ser Met Val Gly Leu Tyr Tyr Ile Asn Lys Ile Ser Ser
 100 105 110
 15 Thr Leu Tyr Gln Ala Ala Ala Pro Val Leu Thr Pro Ala Lys Val Thr
 115 120 125
 Gly Lys Ser Lys Lys Arg Asn Xaa
 130 135
 20

(2) INFORMATION FOR SEQ ID NO: 294:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln Glu
 1 5 10 15
 35 Glu Tyr Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys Phe Gly Cys Leu
 20 25 30
 Arg Xaa

40

(2) INFORMATION FOR SEQ ID NO: 295:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 137 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

50 Met Arg Thr Pro Gly Pro Leu Pro Val Leu Leu Leu Leu Ala Gly
 1 5 10 15
 Ala Pro Ala Ala Arg Pro Thr Pro Pro Thr Cys Tyr Ser Arg Met Arg
 20 25 30
 55 Ala Leu Ser Gln Glu Ile Thr Arg Asp Phe Asn Leu Leu Gln Val Ser
 35 40 45
 60 Glu Pro Ser Glu Pro Cys Val Arg Tyr Leu Pro Arg Leu Tyr Leu Asp
 50 55 60

517

Ile His Asn Tyr Cys Val Leu Asp Lys Leu Arg Asp Phe Val Ala Ser
 65 70 75 80

5 Pro Pro Cys Trp Lys Val Ala Gln Val Asp Ser Leu Lys Asp Lys Ala
 85 90 95

Arg Lys Leu Tyr Thr Ile Met Asn Ser Phe Cys Arg Arg Asp Leu Val
 100 105 110

10 Phe Leu Leu Asp Asp Cys Asn Ala Leu Glu Tyr Pro Ile Pro Val Thr
 115 120 125

Thr Val Leu Pro Asp Arg Gln Arg Xaa
 15 130 135

20 (2) INFORMATION FOR SEQ ID NO: 296:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

Met Trp Leu Leu Lys Pro Ser Ala His Ser Pro Val His Xaa Leu Val
 1 5 10 15

30 Leu Leu Phe Pro Arg Gly Trp Ser Gln Pro Gly Thr His Lys Arg Gln
 20 25 30

Ile Leu Val Asn Xaa Ala Ser Leu Pro Gly Gly Cys Leu Leu Pro Trp
 35 35 40 45

35 Ile Trp Ser Gly Ala Ala Leu Arg Phe Xaa
 50 55

40

(2) INFORMATION FOR SEQ ID NO: 297:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

Met Ser Arg Arg Ala Glu Ala Ser Ile Phe Val Leu Pro Lys Thr Leu
 50 1 5 10 15

Leu Phe Val Leu Phe Pro Ala Phe Pro Ser Pro Ala Val Gly Cys Pro
 20 25 30

55 Val Pro Xaa
 35

60 (2) INFORMATION FOR SEQ ID NO: 298:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

5 Ser Cys Tyr Ile Thr Pro Trp Ser Lys Ile Gln Ser Phe Ser Leu Ser
 1 5 10 15
 10 Leu Phe Gln Phe Ile Leu Gln Glu Val Asn Ile Thr Leu Pro Glu Asn
 20 25 30
 15 Ser Val Trp Tyr Glu Arg Tyr Lys Phe Asp Ile Pro Val Phe His Leu
 35 40 45
 Asn Gly Gln Phe Leu Met Met His Arg Val Asn Thr Ser Lys Leu Glu
 50 55 60
 20 Lys Gln Leu Leu Lys Leu Glu Gln Gln Ser Thr Gly Xaa Xaa
 65 70 75

(2) INFORMATION FOR SEQ ID NO: 299:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

30 Met Phe Val Leu Phe Ser Leu Pro Lys Tyr Ala Gly Leu Arg Leu Pro
 1 5 10 15
 35 Ile Pro Gly Leu Ser Ala Leu Leu Val Phe Leu Leu Ser Leu Phe Ser
 20 25 30
 40 Arg Arg Ala Gln Val Glu Leu Thr Thr Gly Arg Glu Thr Leu Pro Lys
 35 40 45
 Asn Leu Gln Gly Tyr Phe Pro Glu Phe Gly Phe Gln Val Gln Asn Phe
 50 55 60
 45 Leu Ser Cys Lys Ile Tyr Ala Ala Ser Gln Lys Gln Pro Leu Pro Pro
 65 70 75 80
 Leu Tyr Gln Leu Arg Phe Tyr Leu Lys His Met Gly Leu Pro Xaa
 85 90 95
 50

(2) INFORMATION FOR SEQ ID NO: 300:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

60

519

Met Ser Ser His Trp Thr Leu Lys Ile Leu Leu Val Pro Leu Phe Tyr
 1 5 10 15
 5 Leu Ser Leu Glu Phe Pro Ser Gly Phe Val Leu Cys Leu Ala Asn Asp
 20 25 30
 Leu Gly Tyr His Phe Ser Ser Arg Val Arg Ser Xaa
 35 40

10

(2) INFORMATION FOR SEQ ID NO: 301:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

20 Met Leu Val Val Asn Ile Asn Leu Val Phe Leu Leu Phe Phe Ile Phe
 1 5 10 15
 Leu Cys Tyr Leu Asp Ala Cys Ile Asn Val Phe Cys Phe Tyr Xaa
 20 25 30
 25

(2) INFORMATION FOR SEQ ID NO: 302:

(i) SEQUENCE CHARACTERISTICS:
 30 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

35 Met Pro Val Leu Pro Gly Arg Thr Thr Ala Leu Leu Ser Leu Thr Leu
 1 5 10 15
 40 Ala Phe Ala Val Pro Cys Ser Gly Val Glu Ala Gly Pro Cys Val Pro
 20 25 30
 Arg Ser His Gly Cys Ser Ser Trp Glu Ala Ser Val Cys Val Thr Ser
 35 40 45
 45 Ser Thr Pro Gly Gly Ser Trp Arg Ala Arg Ala Leu Phe Pro Ser Ala
 50 55 60
 50 Ala Trp His Arg Xaa Ala Ala Trp Asp Ser Pro Trp Thr Gln Thr Gly
 65 70 75 80
 Asp Phe Ala Arg Gly Ala Met Gly Gly Ala Gly Ala Leu Pro Gly Gly
 85 90 95
 55 Cys Val Cys Ile Ser Gly Arg Pro Arg Ala Gln Lys Leu Pro Ala Leu
 100 105 110
 Xaa

60

(2) INFORMATION FOR SEQ ID NO: 303:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

10 Thr His Ile His Thr His Ile Ile Ile Cys Ser Ser Val Xaa
1 5 10

15 (2) INFORMATION FOR SEQ ID NO: 304:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

20 Met Glu Asn Phe Phe Phe Ser Phe Tyr Leu Phe Leu Ile Thr Leu Ile
1 5 10 15

25 Pro Asn Gly Arg Thr Leu Ser Thr Thr Ala Asp His Cys Lys Ile Pro
20 25 30

30 Cys Ile Xaa
35

35 (2) INFORMATION FOR SEQ ID NO: 305:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

40 Met Glu Leu Trp Glu Leu Ala Leu Cys Leu Leu Val Ala Leu Ser Ala
1 5 10 15

45 His Met Phe Thr Val Gln Leu Leu Ala Asp Leu Gly Phe Leu Phe Gly
20 25 30

50 Gly Phe Xaa
35

(2) INFORMATION FOR SEQ ID NO: 306:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

60

521

Met Gly Ala Gly Ile Leu Ala Leu Leu Leu Pro Leu Glu Ser Val Leu
 1 5 10 15

Thr Cys Ser Trp Ile Ser Val Ser Thr Ser Glu Arg Gln Leu Trp Gln
 5 20 25 30

Ser Ser Gln Lys Ala Thr Ile Leu Ser Leu Lys Leu Asp Ser Cys Phe
 35 40 45

Cys Gly His Ser Gly Leu Lys Gly Lys Asn Glu Asp Thr Asp Ser Ser
 10 50 55 60

Val Pro Ile Ile Pro Ser Lys Thr His Thr His Leu Gly Lys His Leu
 55 70 75 80

15 Ile Xaa

20

(2) INFORMATION FOR SEQ ID NO: 307:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 72 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

Met Phe Tyr Phe Val Leu Phe Ile Tyr Ser Ser Ser Glu Thr Trp Ser
 30 1 5 10 15

Gly Ser Val Ala Gln Asp Gly Val His Gly Val Ile Ile Gly His Cys
 20 25 30

35 Ser Val Glu Leu Pro Gly Ser Gly Asp Pro Pro Ala Ser Ala Xaa Leu
 35 40 45

Val Ala Gly Thr Ile Gly Thr Cys Pro Thr Met Pro Gly Phe Val Tyr
 50 55 60

40 Phe Leu Asn Asp Val Xaa Asn Xaa
 65 70

45

(2) INFORMATION FOR SEQ ID NO: 308:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

Met Asp Ser Thr Leu Arg Gln Gly Arg Xaa Leu Leu Thr Leu Val Pro
 55 1 5 10 15

Ala Ser Leu Phe Ser Leu Thr Leu Gly Pro Gly Pro Trp Lys Asp
 20 25 30

60 Pro Xaa

5 (2) INFORMATION FOR SEQ ID NO: 309:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

Met Gln Val Val Gly Ser Trp Pro Gly Arg Val Gly Val Val Gly Leu
 1 5 10 15

Ala Phe Ser Leu Val Ile Pro Pro Pro Ala Ile Cys Ile Ala Gly Pro
 20 25 30

Ala Pro Gly Leu Gly Gly Gly Glu Arg Gln Gln Lys Gly Leu Gly Arg
 35 40 45

Gly Gly Gly Gly Leu Arg Asn Cys Pro Gly Arg Val Gly Met Ala Ala
 50 55 60

Glu Pro Gly Ala Leu Leu Cys Leu Thr Ser Arg Asp Gly Ser Leu Leu
 65 70 75 80

Leu Ser Cys Val Arg Pro His His Val Ile Lys Pro Lys Gly Thr Ala
 85 90 95

Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Xaa Xaa
 100 105 110

Gly Gly Xaa
 115

40 (2) INFORMATION FOR SEQ ID NO: 310:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

Met Asp Leu Pro Gln Phe Ile Tyr Leu Phe Ile Phe Cys Phe Cys Cys
 1 5 10 15

Leu Ala Ile Val Asn Asn Ala Ser Ile Asn Ile His Ile Gln Val Ser
 20 25 30

Met Trp Leu Tyr Val Phe Ile Ser Leu Gly Tyr Leu His Gly Ser Arg
 35 40 45

Ile Leu Gly His Asn Ile Ile Leu Cys Leu Thr Ser Gln Arg Ile Ala
 50 55 60

Lys Arg Phe Phe Ile Val Ala Ala Ser Phe Thr Phe Pro Pro Ala Met
 65 70 75 80

523

Tyr Lys Asp Phe Tyr Phe Ser Ile Ser Leu His Leu Pro Thr Leu Leu
 85 90 95

5 Phe Xaa Xaa Xaa Phe Val Phe Ser Leu Leu Pro Pro
 100 105

10 (2) INFORMATION FOR SEQ ID NO: 311:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

Met Cys Ser Pro Ser Leu Ser Ser Ser Pro Pro Pro Leu Leu Gln Val
 1 5 10 15

20 Phe Phe Phe Phe Phe Phe Ser Pro His Trp Ala Ala Lys Val Val Pro
 20 25 30

25 Gln Trp Lys Xaa Arg His Pro Gln Val Ser Ser Gln Leu Leu Leu Cys
 35 40 45

Phe Leu Arg Val Asn Cys Gln Phe Leu Phe Leu Gln Glu Ile Leu Phe
 50 55 60

30 Xaa
 65

35 (2) INFORMATION FOR SEQ ID NO: 312:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

Met Cys Leu Ser Arg Trp Lys Ile Phe Tyr Thr Leu Leu Ile Leu Phe
 1 5 10 15

45 Xaa Xaa Phe Ser Ile Thr Ser Glu Xaa Glu Thr Phe Tyr Met Ile Ile
 20 25 30

50 Ile His His Asn Pro Thr Gln Ile Thr Ala Ser Cys Ser Phe Thr Phe
 35 40 45

Leu Xaa
 50

55

(2) INFORMATION FOR SEQ ID NO: 313:

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 293 amino acids

524

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

5 Met Glu Arg Pro Asp Trp Glu Thr Ala Ile Gln Lys Pro Leu Cys Ser
 1 5 10 15
 Leu Pro Ala Gly Ser Gly Asn Ala Leu Ala Ala Ser Leu Asn His Tyr
 20 25 30
 10 Ala Gly Tyr Xaa Gln Val Thr Asn Glu Asp Leu Leu Thr Asn Cys Thr
 35 40 45
 Leu Leu Leu Cys Arg Arg Leu Leu Ser Pro Met Asn Leu Leu Ser Leu
 15 50 55 60
 His Thr Ala Ser Gly Leu Arg Leu Phe Ser Val Leu Ser Leu Ala Trp
 65 70 75 80
 20 Gly Phe Ile Ala Asp Val Asp Leu Glu Ser Glu Lys Tyr Arg Arg Leu
 85 90 95
 Gly Glu Met Arg Phe Thr Leu Gly Thr Phe Leu Arg Leu Ala Ala Leu
 100 105 110
 25 Arg Thr Tyr Arg Gly Arg Leu Ala Tyr Leu Pro Val Gly Arg Val Gly
 115 120 125
 Ser Lys Thr Pro Ala Ser Pro Val Val Val Gln Gln Gly Pro Val Asp
 130 135 140
 Ala His Leu Val Pro Leu Glu Glu Pro Val Pro Ser His Trp Thr Val
 145 150 155 160
 35 Val Pro Asp Glu Asp Phe Val Leu Val Leu Ala Leu Leu His Ser His
 165 170 175
 Leu Gly Ser Glu Met Phe Ala Ala Pro Met Gly Arg Cys Ala Ala Gly
 180 185 190
 40 Val Met His Leu Phe Tyr Val Arg Ala Gly Val Ser Arg Ala Met Leu
 195 200 205
 Leu Arg Leu Phe Leu Ala Met Glu Lys Gly Arg His Met Glu Tyr Glu
 210 215 220
 Cys Pro Tyr Leu Val Tyr Val Pro Val Val Ala Phe Arg Leu Glu Pro
 225 230 235 240
 50 Lys Asp Gly Lys Gly Val Phe Ala Val Asp Gly Glu Leu Met Val Ser
 245 250 255
 Glu Ala Val Gln Gly Gln Val His Pro Asn Tyr Phe Trp Met Val Ser
 260 265 270
 55 Gly Cys Val Glu Pro Pro Pro Ser Trp Lys Pro Gln Gln Met Pro Pro
 275 280 285
 Pro Glu Glu Pro Leu
 60 290

(2) INFORMATION FOR SEQ ID NO: 314:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

Met Pro Leu Glu Gly Phe Cys Leu Val Leu Asp Ile Gly Phe Leu Leu
 1 5 10 15

15

Val Met Leu Ile Ser Leu Ala Ser Glu Cys Phe Thr Thr Cys Leu Asp
 20 25 30

20

Ser Phe Ser Thr Thr Glu Pro Gly Cys Lys Phe Tyr Lys Leu Leu His
 35 40 45

Ser Val Ser Leu Leu Asn Ile Asn Phe Asn Val Lys Ser Leu Leu Cys
 50 55 60

25

Ser His Ile Xaa
 65

(2) INFORMATION FOR SEQ ID NO: 315:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

Met Pro Leu Gln Leu Ser Gly Gln Tyr Trp Ile Ser Leu Leu Val Phe
 1 5 10 15

40

Leu Ser Leu Gln Pro Phe Pro Gln Ala Ala Ile Pro Cys Ala Leu Thr
 20 25 30

45

Asp Val Gly Gly Ser Cys Val Ile Cys His Ile Leu Leu Asn Cys Leu
 35 40 45

Cys Ile Leu Phe Thr Leu Thr Ala Pro Ser Leu Ser His Val Leu Leu
 50 55 60

50

Ile Lys Met Ser Leu Ser Val Cys Tyr Glu Pro Gly Ala Asp Leu Ser
 65 70 75 80

Asp Arg Ala Ala Thr Gly Asn Lys Lys Leu Thr Arg Ser Thr Cys Leu
 85 90 95

55

Leu Met His Ser Asn Lys Leu Cys Xaa
 100 105

60

(2) INFORMATION FOR SEQ ID NO: 316:

526

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

Met Trp Gly Cys Ser Gly Leu Gly His Arg Thr Val Ser Phe Leu Leu
 1 5 10 15

Leu Leu Pro Cys Ser Phe Pro Arg Pro Cys Xaa Leu Phe Gly Leu Ile
 20 25 30

Pro Ile Ser Arg Pro Cys Lys Val Glu Ala Pro Arg Leu Ser Val Pro
 35 40 45

Xaa Leu Ser Cys Ala Ser His Pro Tyr Cys Asn Cys Pro Met Ser Thr
 50 55 60

Ser Cys Pro Leu Pro Arg Xaa
 65 70

(2) INFORMATION FOR SEQ ID NO: 317:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

Met Leu Asn Val Leu Ser Lys Val Gln Gln Leu Val Ser Xaa Leu Gly
 1 5 10 15

Leu Val Thr Phe Leu Leu Asn His Ser Ala Ala Gly Gly Ser Pro Gln
 20 25 30

His Arg Trp Leu Leu Leu Xaa
 35

(2) INFORMATION FOR SEQ ID NO: 318:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

Met Lys Ala Ile Ala Arg Ala Cys Leu Leu Leu Ser Leu Leu Val Leu
 1 5 10 15

Pro His Val Val Ser Glu His Leu Phe Trp His His Asn Pro Arg His
 20 25 30

Pro Val Ile Trp Pro Phe Pro Pro Phe His Leu Ile Ser Cys Ser Val
 35 40 45

527

Ser Ala Ser Thr Trp His Leu Gly Glu Xaa Leu Leu Leu Val Pro
 50 55 60

5 Ile Ala Pro Ser Val Trp Ser Xaa
 65 70

10 (2) INFORMATION FOR SEQ ID NO: 319:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 62 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

Met Glu Gln Gly Gly Gly Pro Arg Leu Leu Leu Ile Pro Gly Leu
 1 5 10 15

20 Leu His Asn Thr Tyr Leu Ala Arg Pro Gly Asp Phe Pro Ala Gln Gly
 20 25 30

Thr Thr Glu Asn Thr Glu Cys Gln Gly Ser Pro Ser Pro Ile Ser His
 35 40 45

25 Leu Gly Lys Val Arg Ser Leu Asp Ser Asn Thr Gln Ile Xaa
 50 55 60

30 (2) INFORMATION FOR SEQ ID NO: 320:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 286 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

40 Met Pro Leu Leu Phe Phe Ser Val Ser Thr Leu Phe Ser Gly Ser Val
 1 5 10 15

Thr Leu Gln Gln Arg Gly Met Phe Leu Pro Trp Thr Gly Thr Gly Glu
 20 25 30

45 Gln Val Leu Ala Leu Leu Trp Pro Arg Phe Glu Leu Ile Leu Glu Met
 35 40 45

Asn Val Gln Ser Val Arg Ser Thr Asp Pro Gln Arg Leu Gly Gly Leu
 50 55 60

50 Asp Thr Arg Pro His Tyr Ile Thr Arg Arg Tyr Ala Glu Phe Ser Ser
 65 70 75 80

55 Ala Leu Val Ser Ile Asn Gln Thr Ile Pro Asn Glu Arg Thr Met Gln
 85 90 95

Leu Leu Gly Gln Leu Gln Val Glu Val Glu Asn Phe Val Leu Arg Val
 100 105 110

60 Ala Ala Glu Phe Ser Ser Arg Lys Glu Gln Leu Val Phe Leu Ile Asn

528

115 120 125

Asn Tyr Asp Met Met Leu Gly Val Leu Met Glu Arg Ala Ala Asp Asp
130 135 140

5 Ser Lys Glu Val Glu Ser Phe Gln Gln Leu Leu Asn Ala Arg Thr Gln
145 150 155 160

10 Glu Phe Ile Glu Glu Leu Leu Ser Pro Pro Phe Gly Gly Leu Val Ala
165 170 175

Phe Val Lys Glu Ala Glu Ala Leu Ile Glu Arg Gly Gln Ala Glu Arg
180 185 190

15 Leu Arg Gly Glu Glu Ala Arg Val Thr Gln Leu Ile Arg Gly Phe Gly
195 200 205

Ser Ser Trp Lys Ser Ser Val Glu Ser Leu Ser Gln Asp Val Met Arg
210 215 220

20 Ser Phe Thr Asn Phe Arg Asn Gly Thr Ser Ile Ile Gln Gly Ala Leu
225 230 235 240

25 Thr Gln Leu Ile Gln Leu Tyr His Arg Phe His Arg Val Leu Ser Gln
245 250 255

Pro Gln Leu Arg Ala Leu Pro Ala Arg Ala Glu Leu Ile Asn Ile His
260 265 270

30 His Leu Met Val Glu Leu Lys Lys His Lys Pro Asn Phe Xaa
275 280 285

35 (2) INFORMATION FOR SEQ ID NO: 321:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

Met Phe Arg Ala Leu Arg Asp Leu Leu Thr His Tyr Pro Gln Gln Ile
1 5 10 15

45 Leu Leu Gln Val Leu Val Val Met Tyr Gln Val Leu Gln Val Trp Glu
20 25 30

50 Leu Pro Trp Pro Glu Leu Ile His Leu Gln Gly Ile Val Pro Thr Asp
35 40 45

Gln Leu His Leu Lys Gln Xaa
50 55

55

(2) INFORMATION FOR SEQ ID NO: 322:

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 59 amino acids

529

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

5 Asp Phe Val Pro Val Leu Val Phe Val Leu Ile Lys Ala Asn Pro Pro
 1 5 10 15
 Cys Leu Leu Ser Thr Val Gln Tyr Ile Ser Ser Phe Tyr Ala Ser Cys
 20 25 30
 10 Leu Ser Gly Glu Glu Ser Tyr Trp Trp Met Gln Phe Thr Ala Ala Val
 35 40 45
 15 Glu Phe Ile Lys Thr Ile Asp Asp Arg Lys Xaa
 50 55

(2) INFORMATION FOR SEQ ID NO: 323:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

20 Met His Pro Ala Arg Lys Leu Leu Ser Leu Leu Phe Leu Ile Leu Met
 1 5 10 15
 30 Gly Thr Glu Leu Thr Gln Asp Ser Ala Ala Pro Asp Ser Leu Leu Arg
 20 25 30
 Ser Ser Lys Gly Ser Thr Arg Gly Ser Leu Ala Ala Ile Val Ile Trp
 35 40 45
 35 Arg Gly Lys Ser Glu Ser Arg Ile Ala Lys Thr Pro Gly Ile Phe Arg
 50 55 60
 40 Gly Gly Gly Thr Leu Val Leu Pro Pro Thr His Thr Pro Glu Trp Leu
 65 70 75 80
 Ile Leu Pro Leu Gly Ile Thr Leu Pro Leu Gly Ala Pro Glu Thr Gly
 85 90 95
 45 Gly Gly Asp Cys Ala Ala Glu Thr Trp Lys Gly Ser Gln Arg Ala Gly
 100 105 110
 Gln Leu Cys Ala Leu Leu Ala Xaa
 115 120
 50

(2) INFORMATION FOR SEQ ID NO: 324:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

60

530

Phe Phe Leu Val Val Phe Ser Leu Ser Phe Xaa Pro Ser Val Leu Thr
 1 5 10 15

5 Ser Pro Val His Xaa Pro His Cys Cys Gln Xaa Asp Xaa Ile Leu Phe
 20 25 30

Lys Asn Thr Leu Xaa Xaa Phe Xaa Ala Lys Tyr Xaa
 35 40

10

(2) INFORMATION FOR SEQ ID NO: 325:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

20 Met Phe Ser Arg Thr Ser Asn Phe Trp Thr Phe Phe Phe Gln Phe Leu
 1 5 10 15

Ile Phe Lys Val Phe Leu Val Leu Lys Asn Xaa Phe Thr Ser Gln Lys
 20 25 30

25

Ile Xaa Xaa Ile Xaa Xaa Glu Lys Pro Lys Lys Lys Lys Xaa Arg Gly
 35 40 45

30 Gly Arg Ala Pro Ser Pro Gln Gly Gly Pro Xaa
 50 55

35 (2) INFORMATION FOR SEQ ID NO: 326:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

Met Gly Leu Leu Ile Phe Met Leu Leu Ile Gly Ile His Ser Gln Cys
 1 5 10 15

45 Ser Xaa

50 (2) INFORMATION FOR SEQ ID NO: 327:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids

(B) TYPE: amino acid

55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

Met Val Leu Phe Cys Phe Val Leu Phe Cys Phe Val Phe Glu Met Asp
 1 5 10 15

60

531

Ser Ser Ser Val Thr Gln Ala Gly Val Gln Trp Cys Asp Leu Gly Ser
 20 25 30

5 Leu Gln Ala Pro Pro Pro Gly Phe Ser Pro Phe Ser Cys Leu Ser Leu
 35 40 45

Pro Ser Ser Trp Asp Tyr Arg Arg Pro Pro Pro Arg Pro Ala Asn Phe
 50 55 60

10 Leu Tyr Phe Leu Val Glu Thr Gly Phe His His Val Ser Gln Asp Gly
 65 70 75 80

Leu Asp Leu Leu Thr Ser Xaa
 85

15

(2) INFORMATION FOR SEQ ID NO: 328:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 538 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

25 Met Ser Thr Lys Lys Leu Cys Ile Val Gly Gly Ile Leu Leu Val Phe
 1 5 10 15

30 Gln Ile Ile Ala Phe Leu Val Gly Gly Leu Ile Ala Pro Gly Pro Thr
 20 25 30

Thr Ala Val Ser Tyr Met Ser Val Lys Cys Val Asp Ala Arg Lys Asn
 35 40 45

35 His His Lys Thr Lys Trp Phe Val Pro Trp Gly Pro Asn His Cys Asp
 50 55 60

Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu Ile Glu Ala Asn
 65 70 75 80

40 Asp Ile Val Phe Ser Val His Ile Pro Leu Pro His Met Glu Met Ser
 85 90 95

45 Pro Trp Phe Gln Phe Met Leu Phe Ile Leu Gln Leu Asp Ile Ala Phe
 100 105 110

Lys Leu Asn Asn Gln Ile Arg Glu Asn Ala Glu Val Ser Met Asp Val
 115 120 125

50 Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp Thr Glu Met Ala
 130 135 140

His Glu Arg Val Pro Arg Lys Leu Lys Cys Thr Phe Thr Ser Pro Lys
 145 150 155 160

55 Thr Pro Glu His Glu Gly Arg Tyr Tyr Glu Cys Asp Val Leu Pro Phe
 165 170 175

60 Met Glu Ile Gly Ser Val Ala His Lys Phe Tyr Leu Leu Asn Ile Arg
 180 185 190

532

Leu Pro Val Asn Glu Lys Lys Lys Ile Asn Val Gly Ile Gly Glu Ile
 195 200 205
 5 Lys Asp Ile Arg Leu Val Gly Ile His Gln Asn Gly Gly Phe Thr Lys
 210 215 220
 Val Trp Phe Ala Met Lys Thr Phe Leu Thr Pro Ser Ile Phe Ile Ile
 225 230 235 240
 10 Met Val Trp Tyr Trp Arg Arg Ile Thr Met Met Ser Arg Pro Pro Val
 245 250 255
 Leu Leu Glu Lys Val Ile Phe Ala Leu Gly Ile Ser Met Thr Phe Ile
 15 260 265 270
 Asn Ile Pro Val Glu Trp Phe Ser Ile Gly Phe Asp Trp Thr Trp Met
 275 280 285
 20 Leu Leu Phe Gly Asp Ile Arg Gln Gly Ile Phe Tyr Ala Met Leu Leu
 290 295 300
 Ser Phe Trp Ile Ile Phe Cys Gly Glu His Met Met Asp Gln His Glu
 305 310 315 320
 25 Arg Asn His Ile Ala Gly Tyr Trp Lys Gln Val Gly Pro Ile Ala Val
 325 330 335
 Gly Ser Phe Cys Leu Phe Ile Phe Asp Met Cys Glu Arg Gly Val Gln
 30 340 345 350
 Leu Thr Asn Pro Phe Tyr Ser Ile Trp Thr Thr Asp Ile Gly Thr Glu
 355 360 365
 35 Leu Ala Met Ala Phe Ile Ile Val Ala Gly Ile Cys Leu Cys Leu Tyr
 370 375 380
 Phe Leu Phe Leu Cys Phe Met Val Phe Gln Val Phe Arg Asn Ile Ser
 385 390 395 400
 40 Gly Lys Gln Ser Ser Leu Pro Ala Met Ser Lys Val Arg Arg Leu His
 405 410 415
 Tyr Glu Gly Leu Ile Phe Arg Phe Lys Phe Leu Met Leu Ile Thr Leu
 45 420 425 430
 Ala Cys Ala Ala Met Thr Val Ile Phe Phe Ile Val Ser Gln Val Thr
 435 440 445
 50 Glu Gly His Trp Lys Trp Gly Gly Val Thr Val Gln Val Asn Ser Ala
 450 455 460
 Phe Phe Thr Gly Ile Tyr Gly Met Trp Asn Leu Tyr Val Phe Ala Leu
 465 470 475 480
 55 Met Phe Leu Tyr Ala Pro Ser His Lys Asn Tyr Gly Glu Asp Gln Ser
 485 490 495
 60 Asn Gly Met Gln Leu Pro Cys Lys Ser Arg Glu Asp Cys Ala Leu Phe
 500 505 510

533

Val Ser Glu Leu Tyr Gln Glu Leu Phe Ser Ala Ser Lys Tyr Ser Phe
515 520 525

5 Ile Asn Asp Asn Ala Ala Ser Gly Ile Xaa
530 535

10 (2) INFORMATION FOR SEQ ID NO: 329:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 202 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

Met Gly Ile Ala Leu Ala Val Leu Gly Trp Leu Ala Val Met Leu Cys
1 5 10 15
20 Cys Ala Leu Pro Met Trp Arg Val Thr Ala Phe Ile Gly Ser Asn Ile
20 25 30
25 Val Thr Ser Gln Thr Ile Trp Glu Gly Leu Trp Met Asn Cys Val Val
35 40 45
Gln Ser Thr Gly Gln Met Gln Cys Lys Val Tyr Asp Ser Leu Leu Ala
50 55 60
30 Leu Pro Gln Asp Leu Gln Ala Ala Arg Ala Leu Val Ile Ile Ser Ile
65 70 75 80
Ile Val Ala Ala Leu Gly Val Leu Leu Ser Val Val Gly Gly Lys Cys
85 90 95
35 Thr Asn Cys Leu Glu Asp Glu Ser Ala Lys Ala Lys Thr Met Ile Val
100 105 110
40 Ala Gly Val Val Phe Leu Leu Ala Gly Leu Met Val Ile Val Pro Val
115 120 125
Ser Trp Thr Ala His Asn Ile Ile Gln Asp Phe Tyr Asn Pro Leu Val
130 135 140
45 Ala Ser Gly Gln Lys Arg Glu Met Gly Ala Ser Leu Tyr Val Gly Trp
145 150 155 160
Ala Ala Ser Gly Leu Leu Leu Leu Gly Gly Gly Leu Leu Cys Cys Asn
165 170 175
50 Cys Pro Pro Arg Thr Asp Lys Pro Tyr Ser Ala Lys Tyr Ser Ala Ala
180 185 190
55 Arg Ser Ala Ala Ala Ser Asn Tyr Val Xaa
195 200

60 (2) INFORMATION FOR SEQ ID NO: 330:

534

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 263 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

Met Ala Thr Val Thr Ala Thr Thr Lys Val Pro Glu Ile Arg Asp Val
 1 5 10 15

10 Thr Arg Ile Glu Arg Ile Gly Ala His Ser His Ile Arg Gly Leu Gly
 20 25 30

Leu Asp Asp Ala Leu Glu Pro Arg Gln Ala Ser Gln Gly Met Val Gly
 35 40 45

15 Gln Leu Ala Ala Arg Arg Ala Ala Gly Val Val Leu Glu Met Ile Arg
 50 55 60

20 Glu Gly Lys Ile Ala Gly Arg Ala Val Leu Ile Ala Gly Gln Pro Gly
 65 70 75 80

Thr Gly Lys Thr Ala Ile Ala Met Gly Met Ala Gln Ala Leu Gly Pro
 85 90 95

25 Asp Thr Pro Phe Thr Ala Ile Ala Gly Ser Glu Ile Phe Ser Leu Glu
 100 105 110

Met Ser Lys Thr Glu Ala Leu Thr Gln Ala Phe Arg Arg Ser Ile Gly
 115 120 125

30 Val Arg Ile Lys Glu Glu Thr Glu Ile Ile Glu Gly Glu Val Val Glu
 130 135 140

Ile Gln Ile Asp Arg Pro Ala Thr Gly Thr Gly Ser Lys Val Gly Lys
 145 150 155 160

Leu Thr Leu Lys Thr Thr Glu Met Glu Thr Ile Tyr Asp Leu Gly Thr
 165 170 175

40 Lys Met Ile Xaa Ser Leu Thr Lys Asp Lys Val Gln Ala Gly Asp Val
 180 185 190

Ile Thr Ile Asp Lys Ala Thr Gly Lys Ile Ser Lys Leu Gly Arg Ser
 195 200 205

45 Phe Thr Arg Ala Arg Glu Leu Arg Arg Tyr Gly Leu Pro Asp Gln Val
 210 215 220

Arg Ala Val Pro Arg Trp Gly Ala Pro Glu Thr Gln Gly Gly Gly Ala
 225 230 235 240

His Arg Val Pro Ala Arg Asp Arg Arg His Gln Leu Ser His Pro Gly
 245 250 255

55 Leu Pro Gly Ala Leu Leu Arg
 260

60 (2) INFORMATION FOR SEQ ID NO: 331:

535

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 260 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

5 Met Leu Ala Leu Leu Gly Leu Ser Gln Ala Leu Asn Ile Leu Leu Gly
 1 5 10 15
 10 Leu Lys Gly Leu Ala Pro Ala Glu Ile Ser Ala Val Cys Glu Lys Gly
 20 25 30
 15 Asn Phe Asn Val Ala His Gly Leu Ala Trp Ser Tyr Tyr Ile Gly Tyr
 35 40 45
 Leu Arg Leu Ile Leu Pro Glu Leu Gln Ala Arg Ile Arg Thr Tyr Asn
 50 55 60
 20 Gln His Tyr Asn Asn Leu Leu Arg Gly Ala Val Ser Gln Arg Leu Tyr
 65 70 75 80
 Ile Leu Leu Pro Leu Asp Cys Gly Val Pro Asp Asn Leu Ser Met Ala
 85 90 95
 25 Asp Pro Asn Ile Arg Phe Leu Asp Lys Leu Pro Gln Gln Thr Gly Asp
 100 105 110
 30 Arg Ala Gly Ile Lys Asp Arg Val Tyr Ser Asn Ser Ile Tyr Glu Leu
 115 120 125
 Leu Glu Asn Gly Gln Arg Ala Gly Thr Cys Val Leu Glu Tyr Ala Thr
 130 135 140
 35 Pro Leu Gln Thr Leu Phe Ala Met Ser Gln Tyr Ser Gln Ala Gly Phe
 145 150 155 160
 Ser Gly Glu Asp Arg Leu Glu Gln Ala Lys Leu Phe Cys Arg Thr Leu
 165 170 175
 40 Glu Asp Ile Leu Ala Asp Ala Pro Glu Ser Gln Asn Asn Cys Arg Leu
 180 185 190
 45 Ile Ala Tyr Gln Glu Pro Ala Asp Asp Ser Ser Phe Ser Leu Ser Gln
 195 200 205
 Glu Val Leu Arg His Leu Arg Gln Glu Glu Lys Glu Glu Val Thr Val
 210 215 220
 50 Gly Ser Leu Lys Thr Ser Ala Val Pro Ser Thr Ser Thr Met Ser Gln
 225 230 235 240
 Glu Pro Glu Leu Leu Ile Ser Gly Met Glu Lys Pro Leu Pro Leu Arg
 245 250 255
 55 Thr Asp Phe Ser
 260

60

(2) INFORMATION FOR SEQ ID NO: 332:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

5
10 Met Thr Pro Gln Lys Pro Ala Leu Ala Val Leu Leu Leu Glu Val Pro
1 5 10 15
Leu Leu Leu Thr Leu Ser Val Leu Lys Lys Arg Cys Leu Val Thr Cys
20 25 30
15 Glu Pro Thr Ser Arg Phe Val Ser Cys Asp Leu Pro Leu Ser Val Xaa
35 40 45

20

(2) INFORMATION FOR SEQ ID NO: 333:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 334 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

25
30 Met Ala Ala Ala Ala Trp Leu Gln Val Leu Pro Val Ile Leu Leu Leu
1 5 10 15
35 Leu Gly Ala His Pro Ser Pro Leu Ser Phe Phe Ser Ala Gly Pro Ala
20 25 30
Thr Val Ala Ala Ala Asp Arg Ser Lys Trp His Ile Pro Ile Pro Ser
35 40 45
40 Gly Lys Asn Tyr Phe Ser Phe Gly Lys Ile Leu Phe Arg Asn Thr Thr
50 55 60
Ile Phe Leu Lys Phe Asp Gly Glu Pro Cys Asp Leu Ser Leu Asn Ile
65 70 75 80
45 Thr Trp Tyr Leu Lys Ser Ala Asp Cys Tyr Asn Glu Ile Tyr Asn Phe
85 90 95
50 Lys Ala Glu Glu Val Glu Leu Tyr Leu Glu Lys Leu Lys Glu Lys Arg
100 105 110
Gly Leu Ser Gly Lys Tyr Gln Thr Ser Ser Lys Leu Phe Gln Asn Cys
115 120 125
55 Ser Glu Leu Phe Lys Thr Gln Thr Phe Ser Gly Asp Phe Met His Arg
130 135 140
Leu Pro Leu Leu Gly Glu Lys Gln Glu Ala Lys Glu Asn Gly Thr Asn
145 150 155 160
60

537

Leu Thr Phe Ile Gly Asp Lys Thr Ala Met His Glu Pro Leu Gln Thr
 165 170 175
 5 Trp Gln Asp Ala Pro Tyr Ile Phe Ile Val His Ile Gly Ile Ser Ser
 180 185 190
 Ser Lys Glu Ser Ser Lys Glu Asn Ser Leu Ser Asn Leu Phe Thr Met
 195 200 205
 10 Thr Val Glu Val Lys Gly Pro Tyr Glu Tyr Leu Thr Leu Glu Asp Tyr
 210 215 220
 Pro Leu Met Ile Phe Phe Met Val Met Cys Ile Val Tyr Val Leu Phe
 225 230 235 240
 15 Gly Val Leu Trp Leu Ala Trp Ser Ala Cys Tyr Trp Arg Asp Leu Leu
 245 250 255
 Arg Ile Gln Phe Trp Ile Gly Ala Val Ile Phe Leu Gly Met Leu Glu
 260 265 270
 Lys Ala Val Phe Tyr Ala Glu Phe Gln Asn Ile Arg Tyr Lys Gly Xaa
 275 280 285
 25 Ser Val Gln Gly Ala Leu Ile Leu Ala Glu Leu Leu Ser Ala Val Lys
 290 295 300
 Arg Ser Leu Ala Arg Thr Leu Val Ile Ile Val Ser Leu Gly Tyr Gly
 305 310 315 320
 30 Ile Val Lys Pro Arg Leu Glu Ser Leu Phe Ile Arg Leu Xaa
 325 330

35

(2) INFORMATION FOR SEQ ID NO: 334:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 200 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

45 Met Val Leu Xaa Val Val Thr Leu Gly Leu Ala Leu Phe Thr Leu Cys
 1 5 10 15
 Gly Lys Phe Lys Arg Trp Lys Leu Asn Gly Ala Phe Leu Leu Ile Thr
 20 25 30
 50 Ala Phe Leu Ser Val Leu Ile Trp Val Ala Trp Met Thr Met Tyr Leu
 35 40 45
 Phe Gly Asn Val Lys Leu Gln Gln Gly Asp Ala Trp Asn Asp Pro Thr
 50 55 60
 55 Leu Ala Ile Thr Leu Ala Ala Ser Ala Gly Ser Ser Ser Ser Thr
 65 70 75 80
 60 Pro Ser Leu Arg Ser Thr Ala Pro Phe Cys Gln Pro Cys Arg Arg Thr
 85 90 95

538

Arg Pro Thr Thr Ser Thr Arg Arg Ser Pro Gly Cys Gly Arg Arg Pro
 100 105 110

5 Ser Arg Arg Thr Cys Ser Cys Arg Gly Pro Ile Trp Arg Thr Arg Pro
 115 120 125

Ser Pro Trp Met Asn Thr Met Gln Leu Ser Glu Gln Gln Asp Phe Pro
 130 135 140

10 Thr Ala Ala Trp Glu Lys Asp Pro Val Ala Ala Trp Gly Lys Asp Pro
 145 150 155 160

15 Ala Leu Arg Leu Glu Ala Thr Cys Ile Ser Gln Leu Arg Trp Pro Ser
 165 170 175

Cys Ser Thr Val Gly Pro Ser Gln Leu Leu Arg Gln Val Thr Gln Glu
 180 185 190

20 Xaa Thr Phe Gly Glu Arg Leu Xaa
 195 200

25 (2) INFORMATION FOR SEQ ID NO: 335:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

Met Leu Leu His His Gln Leu Leu Ile Val Thr Leu His Leu Val Leu
 1 5 10 15

35 Leu Leu Ala Thr Leu Leu Val Xaa
 20

40 (2) INFORMATION FOR SEQ ID NO: 336:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 143 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

Met Thr Lys Ala Leu Leu Ile Tyr Leu Val Ser Ser Phe Leu Ala Leu
 1 5 10 15

Asn Gln Ala Ser Leu Ile Ser Arg Cys Asp Leu Ala Gln Val Leu Gln
 20 25 30

55 Leu Glu Asp Leu Asp Gly Phe Glu Gly Tyr Ser Leu Ser Asp Trp Leu
 35 40 45

Cys Leu Ala Phe Val Glu Ser Lys Phe Asn Ile Ser Lys Ile Asn Glu
 50 55 60

60

539

Asn Ala Asp Gly Ser Phe Asp Tyr Gly Leu Phe Gln Ile Asn Ser His
 65 70 75 80
 Tyr Trp Cys Asn Xaa Tyr Lys Ser Tyr Ser Glu Asn Leu Cys His Val
 5 85 90 95
 Asp Cys Gln Asp Leu Leu Asn Pro Asn Leu Leu Ala Gly Ile His Cys
 100 105 110
 Ala Lys Arg Ile Val Ser Gly Ala Arg Gly Met Asn Asn Trp Val Arg
 115 120 125
 Met Glu Xaa Cys Thr Val Gln Ala Gly His Ser Ser Thr Gly Xaa
 130 135 140
 15

(2) INFORMATION FOR SEQ ID NO: 337:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 95 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:
 25 Met Leu Val Ile Ala Gly Gly Ile Leu Ala Ala Leu Leu Leu Leu Ile
 1 5 10 15
 Val Val Val Leu Cys Leu Tyr Phe Lys Ile His Asn Ala Leu Lys Ala
 30 20 25 30
 Ala Lys Glu Pro Glu Ala Val Ala Val Lys Asn His Asn Pro Asp Lys
 35 35 40 45
 Val Trp Trp Ala Lys Asn Ser Gln Ala Lys Thr Ile Ala Thr Glu Ser
 50 55 60
 Cys Pro Ala Leu Gln Cys Cys Glu Gly Tyr Arg Met Cys Ala Ser Phe
 65 70 75 80
 Asp Ser Leu Pro Pro Cys Cys Cys Asp Ile Asn Glu Gly Leu Xaa
 85 90 95
 45

(2) INFORMATION FOR SEQ ID NO: 338:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 38 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:
 50 Met Leu Leu Lys Ser Asn Ile Leu Met Leu Asn Leu Phe Ala Ala Asn
 55 1 5 10 15
 Val Gly Ala Asn Phe Ala Leu Thr Val Glu Lys Ile Gly Met Ile Leu
 20 25 30
 60 Leu Asn Val Ser Gly Xaa

35

5 (2) INFORMATION FOR SEQ ID NO: 339:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

Met Leu Val Val Ala Phe Gly Leu Leu Val Leu Tyr Ile Leu Leu Ala
 1 5 10 15

15 Ser Ser Trp Lys Arg Pro Glu Pro Gly Ile Leu Thr Asp Arg Gln Pro
 20 25 30

20 Leu Leu His Asp Gly Glu Xaa
 35

25 (2) INFORMATION FOR SEQ ID NO: 340:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

Ser Asp Pro Leu Ala Ser Ala Ser Gln Asn Ala Gly Ile Val Ser Val
 1 5 10 15

35 Gly Leu Cys Thr Arg Pro Gly Pro Gln Phe Lys Asn Ala Gln Pro Pro
 20 25 30

Phe Pro Xaa Gln Lys Ala Pro Arg Cys Leu Trp Glu Asn Gln Pro Pro
 35 40 45

40 Pro Trp Arg Lys Ala Trp Asp Leu Pro Ser His Leu Gly Arg Arg Gly
 50 55 60

45 Ile Cys Gly Lys Ser Phe Xaa
 65 70

50 (2) INFORMATION FOR SEQ ID NO: 341:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 85 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

Tyr Val Met Ile Phe Lys Lys Glu Phe Ala Pro Ser Asp Glu Glu Leu
 1 5 10 15

60 Asp Ser Tyr Arg Arg Gly Glu Glu Trp Asp Pro Gln Lys Ala Glu Glu

541

20 25 30

Lys Arg Asn Xaa Lys Glu Leu Ala Gln Arg Gln Xaa Gly Gly Gly Ser
35 40 45

5 Pro Ala Gly Ala Cys Gly Gly Glu Pro Cys Gln Arg Leu Gln Gly Gln
50 55 60

10 Val Gln Pro Pro His Arg Gln Gly Ser Ser Gln Arg Arg Ser Pro His
65 70 75 80

Ala Thr Gly Gln Xaa
85

15

(2) INFORMATION FOR SEQ ID NO: 342:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

25 Met Trp Asp Trp Asp Trp Ser Ala Pro Trp Ser Trp Pro Leu Trp Leu
1 5 10 15

Ser Leu Ala Leu Val Cys Leu Ser Ala Gly Ala Lys Gly His Arg Ala
20 25 30

30 Ser Glu Ala Gly His Ala Arg Ala Leu Thr Cys Glu Met Gly Ser Glu
35 40 45

35 Phe Xaa Thr Ala Xaa Gly Leu Val Leu Gly Xaa Xaa Xaa Trp Thr Xaa
50 55 60

Xaa Asn Gly Ser Ala Gly Pro Glu Arg Arg Gly Trp Arg Pro Ala Ala
65 70 75 80

40 Phe Leu Ala Val Phe Leu Leu Gly Asp Xaa
85 90

45 (2) INFORMATION FOR SEQ ID NO: 343:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

55 Met Phe Gly Pro Thr Phe His Ser Leu Val Leu Val Pro Pro Trp Pro
1 5 10 15

Asn Leu Ser Leu Leu His Phe Thr Ser Pro Val Gly Gln His Ser Ser
20 25 30

60 Phe Leu Pro Thr Ser Leu Arg Leu Xaa Lys Lys Lys Lys Lys Lys Lys
35 40 45

5

(2) INFORMATION FOR SEQ ID NO: 344:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

15

Met Cys Ser Lys Asn Gly Phe Leu Leu Ala Trp Ser Trp Asn Ser Pro
 1 5 10 15

20

Trp Leu Pro Gln Ala Ser Leu Ala His Gly Cys Trp Gly Arg Trp Met
 20 25 30

Ser Asp Leu Val Gly Cys Ser Arg Glu Asn Lys Cys Ala Leu Arg Asp
 35 40 45

25

His Ser Glu Arg Val Gln Gly Xaa
 50 55

30

(2) INFORMATION FOR SEQ ID NO: 345:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 222 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

Ser Pro Leu Xaa Phe Cys Val Val Leu Leu Leu Gln Ala Ala Arg Gly
 1 5 10 15

40

Tyr Val Val Arg Lys Pro Ala Gln Ser Arg Leu Asp Asp Asp Pro Pro
 20 25 30

Pro Ser Thr Leu Leu Lys Asp Tyr Gln Asn Val Pro Gly Ile Glu Lys
 35 40 45

45

Val Asp Asp Val Val Lys Arg Leu Leu Ser Leu Glu Met Ala Asn Lys
 50 55 60

50

Lys Glu Met Leu Lys Ile Lys Gln Glu Gln Phe Met Lys Lys Ile Val
 65 70 75 80

Ala Asn Pro Glu Asp Thr Arg Ser Leu Glu Ala Arg Ile Ile Ala Leu
 85 90 95

55

Ser Val Lys Ile Arg Ser Tyr Glu Glu His Leu Glu Lys His Arg Lys
 100 105 110

Asp Lys Ala His Lys Arg Tyr Leu Leu Met Ser Ile Asp Gln Arg Lys
 115 120 125

60

543

Lys Met Leu Lys Asn Leu Arg Asn Thr Asn Tyr Asp Val Phe Glu Lys
 130 135 140
 5 Ile Cys Trp Gly Leu Gly Ile Glu Tyr Thr Phe Pro Pro Leu Tyr Tyr
 145 150 155 160
 Arg Arg Ala His Arg Arg Phe Val Thr Lys Lys Ala Leu Cys Ile Arg
 165 170 175
 10 Val Phe Gln Glu Thr Gln Lys Leu Lys Lys Arg Arg Arg Ala Leu Lys
 180 185 190
 Ala Ala Ala Ala Ala Gln Lys Gln Ala Lys Arg Arg Asn Pro Asp Ser
 195 200 205
 15 Pro Ala Lys Ala Ile Pro Lys Thr Leu Lys Asp Ser Gln Xaa
 210 215 220

20

(2) INFORMATION FOR SEQ ID NO: 346:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

30 Met Gly Ala Pro Ala Ala Ser Leu Leu Leu Leu Leu Leu Phe Ala
 1 5 10 15
 Cys Cys Trp Ala Pro Gly Gly Ala Asn Leu Ser Gln Asp Asp Ser Gln
 20 25 30
 35 Pro Trp Thr Ser Asp Glu Thr Val Val Ala Gly Gly Thr Val Val Leu
 35 40 45
 Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp Ser Xaa
 50 55 60

40

45

(2) INFORMATION FOR SEQ ID NO: 347:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 154 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

55 Met Val Ala Pro Val Trp Tyr Leu Val Ala Ala Ala Leu Leu Val Gly
 1 5 10 15
 Phe Ile Leu Phe Leu Thr Arg Ser Arg Gly Arg Ala Ala Ser Ala Gly
 20 25 30
 60 Gln Glu Pro Leu His Asn Glu Glu Leu Ala Gly Ala Gly Arg Val Ala

544

35 40 45

Gln Pro Gly Pro Leu Glu Pro Glu Glu Pro Arg Ala Gly Gly Arg Pro
50 55 60

5 Arg Arg Arg Arg Asp Leu Gly Ser Arg Leu Gln Ala Gln Arg Arg Ala
65 70 75 80

Gln Arg Val Ala Trp Ala Glu Ala Asp Glu Asn Glu Glu Glu Ala Val
10 85 90 95

Ile Leu Ala Gln Glu Glu Glu Gly Val Glu Lys Pro Ala Glu Xaa His
100 105 110

15 Leu Ser Gly Lys Ile Gly Ala Lys Lys Leu Arg Xaa Xaa Glu Glu Lys
115 120 125

Gln Ala Arg Lys Ala Gln Xaa Glu Ala Glu Glu Ala Glu Arg Glu Xaa
20 130 135 140

Arg Lys Arg Leu Glu Ser Gln Arg Glu Xaa
145 150

25

(2) INFORMATION FOR SEQ ID NO: 348:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

35 Met Gln Lys Cys Met Leu Ser Ala Leu Val Phe His Ile Gln Trp Ser
1 5 10 15

Xaa

40

(2) INFORMATION FOR SEQ ID NO: 349:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

50 Met Leu Val Cys Ser Phe Leu Phe Leu Xaa
1 5 10

55

(2) INFORMATION FOR SEQ ID NO: 350:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

60

545

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

Val Ile Glu Leu Cys Val Ser Leu Arg Ser Leu Asn Phe Xaa
 1 5 10

5

(2) INFORMATION FOR SEQ ID NO: 351:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

15

Met Cys Glu Phe Xaa Xaa Xaa Ile Met Xaa Leu Ala Gly Tyr Phe Ala
 1 5 10 15

Cys Xaa

20

(2) INFORMATION FOR SEQ ID NO: 352:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

30

Met Val Gly Gly Tyr Val Ser Ser Phe Ser Phe Pro Pro Val Ser Ser
 1 5 10 15

35

Ser Leu Leu Leu Pro Ala Ser Phe Ala Phe Pro Phe Leu Pro Gly Thr
 20 25 30

Pro Cys Pro Phe Leu Tyr Phe Leu Pro Ser Pro Phe Ser Pro Leu Pro
 35 40 45

40

Leu Ser Leu Thr Arg Ser Asn Ser Phe Leu Leu Asn Gly Xaa
 50 55 60

45

(2) INFORMATION FOR SEQ ID NO: 353:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

50

Glu Lys Lys Ser Met Ser Val Ser Asp Ile Tyr Ala Leu Glu Ser Leu
 1 5 10 15

55

Gly Arg Ser Leu Phe Thr Leu Asn Ser Met Cys Leu Pro Leu Ser Phe
 20 25 30

60

Xaa

5 (2) INFORMATION FOR SEQ ID NO: 354:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 245 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

Met Gly Gly Ala Ser Arg Arg Val Glu Ser Gly Ala Trp Ala Tyr Leu
 1 5 10 15

Ser Pro Leu Val Leu Arg Lys Glu Leu Glu Ser Leu Val Glu Asn Glu
 20 25 30

Gly Ser Glu Val Leu Ala Leu Pro Glu Leu Pro Ser Ala His Pro Ile
 35 40 45

Ile Phe Trp Asn Leu Leu Trp Tyr Phe Gln Arg Leu Arg Leu Pro Ser
 50 55 60

Ile Leu Pro Gly Leu Val Leu Ala Ser Cys Asp Gly Pro Ser Xaa Ser
 65 70 75 80

Gln Ala Pro Ser Pro Trp Leu Thr Pro Asp Pro Ala Ser Val Gln Val
 85 90 95

Arg Leu Leu Trp Asp Val Leu Thr Pro Asp Pro Asn Ser Cys Pro Pro
 100 105 110

Leu Tyr Val Leu Trp Arg Val His Ser Gln Ile Pro Gln Arg Val Val
 115 120 125

Trp Pro Gly Pro Val Pro Ala Ser Leu Ser Leu Ala Leu Leu Glu Ser
 130 135 140

Val Leu Arg His Val Gly Leu Asn Glu Val His Lys Ala Val Gly Leu
 145 150 155 160

Leu Leu Glu Thr Leu Gly Pro Pro Pro Thr Gly Leu His Leu Gln Arg
 165 170 175

Gly Ile Tyr Arg Glu Ile Leu Phe Leu Thr Met Ala Ala Leu Gly Lys
 180 185 190

Asp His Val Asp Ile Val Ala Phe Asp Lys Lys Tyr Lys Ser Ala Phe
 195 200 205

Asn Lys Leu Ala Ser Ser Met Gly Lys Glu Glu Leu Arg His Arg Arg
 210 215 220

Ala Gln Met Pro Thr Pro Lys Ala Ile Asp Cys Arg Lys Cys Phe Gly
 225 230 235 240

Ala Pro Pro Glu Cys
 245

60

(2) INFORMATION FOR SEQ ID NO: 355:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

Met Lys Phe Ser Leu Leu Phe Leu Pro Met Leu Leu Ile Leu Lys Pro
 1 5 10 15

15

Asp Leu Phe His Ile Ser Ile Cys Thr Leu Ala Ala Cys Gly Leu Thr
 20 25 30

Phe Pro Xaa
 35

20

(2) INFORMATION FOR SEQ ID NO: 356:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

30

Met Leu Phe Phe Phe Ile Leu His Leu Leu Ser Ile Met Ser Phe Leu
 1 5 10 15

Ser Pro Asp Ile Met Xaa
 20

35

(2) INFORMATION FOR SEQ ID NO: 357:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 98 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

Met Phe Gly Leu Leu Val Glu Ser Gln Thr Leu Leu Glu Glu Asn Ala
 1 5 10 15

50

Val Gln Gly Thr Glu Arg Thr Leu Gly Leu Asn Ile Ala Pro Phe Ile
 20 25 30

Asn Gln Phe Gln Val Pro Ile Arg Val Phe Leu Asp Leu Ser Ser Leu
 35 40 45

55

Pro Cys Ile Pro Leu Ser Lys Pro Val Glu Leu Leu Arg Leu Asp Leu
 50 55 60

60

Met Thr Pro Tyr Leu Asn Thr Ser Asn Arg Glu Val Lys Val Tyr Val
 65 70 75 80

548

Cys Xaa Ile Trp Glu Asp Leu Thr Ala Ile Pro Phe Trp Val Ser Tyr
 85 90 95

Val Pro

5

(2) INFORMATION FOR SEQ ID NO: 358:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

Met Phe Gly Ala His Arg Xaa Trp Gln Gly Ser Val Leu Leu Phe Leu
 1 5 10 15

20

Ser Phe Ala Trp Gly Asn Gly Gly Ser Val Thr Phe Ser Asp Val Pro
 20 25 30

Arg Val Met Pro Leu Ala Gly Gly Pro Xaa Xaa Gln Val Ser Ser Thr
 35 40 45

25

Pro Arg Pro Pro Pro His Gln Val Thr Ser Ser Pro Gly Leu Glu Ser
 50 55 60

30

Ala His Ile Val Cys Pro Glu Arg Lys Lys Lys Lys Lys Lys
 65 70 75

(2) INFORMATION FOR SEQ ID NO: 359:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

Thr Leu Leu Xaa Phe Leu Xaa Leu Leu Thr Thr Glu Gly Gly Arg Glu
 1 5 10 15

45

Asn Ile Phe Xaa Gly Arg Ile Leu Xaa Leu Gln Xaa Ser Pro Xaa
 20 25 30

(2) INFORMATION FOR SEQ ID NO: 360:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

Met Leu Ser Phe Phe Ile Cys Leu Leu Ile Phe Val His Leu Leu Leu
 1 5 10 15

60

Leu Ser Phe Leu Ile Ser Asp Trp Pro Pro Thr Gly Ser Ala Xaa
 20 25 30

5 His Lys Ile Leu Arg Leu Met Val Val Gln Arg Leu Ser Leu Leu Asp
 35 40 45

Gln Arg Lys Arg Trp Ser Glu Ala Xaa
 50 55

10

(2) INFORMATION FOR SEQ ID NO: 361:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

20 Lys Tyr Xaa
 1

25 (2) INFORMATION FOR SEQ ID NO: 362:

 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

30 Trp Ser Ser Ala Ser Ser Ser Trp Val Thr Thr Pro Glu Arg Ile Arg
 1 5 10 15

35 Pro Arg Met Asp Thr Leu Pro Val Lys Gly His Phe Leu Ser Met Xaa
 20 25 30

40

45 (2) INFORMATION FOR SEQ ID NO: 363:

 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

50 Asp Ile Phe Val Phe Leu Leu Ser Thr Arg Ala Gly Gly Leu Gly Ile
 1 5 10 15

55 Asn Leu Thr Ala Xaa Asp Thr Val His Phe Leu Xaa
 20 25

60 (2) INFORMATION FOR SEQ ID NO: 364:

550

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

Thr Leu Thr Ser Phe Leu Glu Leu Pro Leu Ala Pro Glu Pro Xaa
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 365:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

Met His Arg Tyr Ile Thr Phe Phe Lys Cys Phe Arg Ser Val Ile Leu
 1 5 10 15

Asp Leu Leu Phe Ile Leu Ser Pro Leu Ser Gln Gly Cys Phe Ile Leu
 20 25 30

Phe Xaa

(2) INFORMATION FOR SEQ ID NO: 366:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

Met Phe Gly Phe Ile Phe Leu Leu Leu Ile Phe Cys Ile Xaa Leu Cys
 1 5 10 15

Ser Arg Thr Leu Ser Thr Phe Ile Pro Lys Leu Val Gly Phe Leu Tyr
 20 25 30

Trp Lys Phe Ser Ile Asn Leu Ser Leu Leu Leu Thr Leu Ile Lys Lys
 35 40 45

Lys Lys Lys Lys Lys Lys Thr Pro Arg Gly Gly Pro Gly Xaa Gln Ser
 50 55 60

Pro Pro
 65

(2) INFORMATION FOR SEQ ID NO: 367:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 317 amino acids

551

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

5 Met Pro Gly Leu Gly Arg Pro Arg Gln Ala Arg Trp Thr Leu Met Leu
 1 5 10 15
 Leu Leu Ser Thr Ala Met Tyr Gly Ala His Ala Pro Leu Leu Ala Leu
 20 25 30
 10 Cys His Val Asp Gly Arg Val Pro Phe Arg Pro Ser Ser Ala Val Leu
 35 40 45
 Leu Thr Glu Leu Thr Lys Leu Leu Cys Ala Phe Ser Leu Leu Val
 15 50 55 60
 Gly Trp Gln Ala Trp Pro Gln Gly Pro Pro Pro Trp Arg Gln Ala Ala
 65 70 75 80
 20 Pro Phe Ala Leu Ser Ala Leu Leu Tyr Gly Ala Asn Asn Asn Leu Val
 85 90 95
 Ile Tyr Leu Gln Arg Tyr Met Asp Pro Ser Thr Tyr Gln Val Leu Ser
 100 105 110
 25 Asn Leu Lys Ile Gly Ser Thr Ala Val Leu Tyr Cys Leu Cys Leu Arg
 115 120 125
 His Arg Leu Ser Val Arg Gln Gly Leu Ala Leu Leu Leu Met Ala
 130 135 140
 Ala Gly Ala Cys Tyr Ala Ala Gly Gly Leu Gln Val Pro Gly Asn Thr
 145 150 155 160
 35 Leu Pro Ser Pro Pro Pro Ala Ala Ala Ala Ser Pro Met Pro Leu His
 165 170 175
 Ile Thr Pro Leu Gly Leu Leu Leu Leu Ile Leu Tyr Cys Leu Ile Ser
 180 185 190
 40 Gly Leu Ser Ser Val Tyr Thr Glu Leu Leu Met Lys Arg Gln Xaa Leu
 195 200 205
 Pro Leu Ala Leu Gln Asn Leu Phe Leu Tyr Thr Phe Gly Val Leu Leu
 210 215 220
 Asn Leu Gly Leu His Ala Gly Gly Gly Ser Gly Pro Gly Leu Leu Glu
 225 230 235 240
 50 Gly Phe Ser Gly Trp Ala Ala Leu Val Val Leu Ser Gln Ala Leu Asn
 245 250 255
 Gly Leu Leu Met Ser Ala Val Met Lys His Gly Ser Ser Ile Thr Arg
 260 265 270
 55 Leu Phe Val Val Ser Cys Ser Leu Val Val Asn Ala Val Leu Ser Ala
 275 280 285
 Val Leu Leu Arg Leu Gln Leu Thr Ala Ala Phe Phe Leu Ala Thr Leu
 290 295 300
 60

552

Leu Ile Gly Leu Ala Met Arg Leu Tyr Tyr Gly Ser Arg
 305 310 315

5

(2) INFORMATION FOR SEQ ID NO: 368:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

15

Met Gly Glu Gln Pro His Phe Ser Leu Cys Val Leu Leu Ala Ala Val
 1 5 10 15

Arg Glu Asp Xaa Asp Pro Xaa Val Phe Pro Cys Cys Phe Leu Xaa
 20 25 30

20

(2) INFORMATION FOR SEQ ID NO: 369:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

30

Met Ser Phe Ile Ala Leu His Pro Leu Leu Pro Glu Ala Ala Leu Gly
 1 5 10 15

35

Val Pro Gly Gln Ser Pro His Arg Pro Leu Trp Gln Thr Gln Cys Cys
 20 25 30

Val Ala Pro Pro Gln Pro Arg Ala Glu Phe Xaa
 35 40

40

(2) INFORMATION FOR SEQ ID NO: 370:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 255 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

50

Met Val Thr Ala Leu Thr Leu Leu Ala Phe Pro Leu Leu Leu Leu His
 1 5 10 15

Ala Glu Arg Ile Ser Leu Val Phe Leu Leu Leu Phe Leu Gln Ser Phe
 20 25 30

55

Leu Leu Leu His Leu Leu Ala Ala Gly Ile Pro Val Thr Thr Pro Gly
 35 40 45

60

Pro Phe Thr Val Pro Trp Gln Ala Val Ser Ala Trp Ala Leu Met Ala
 50 55 60

553

Thr Gln Thr Phe Tyr Ser Thr Gly His Gln Pro Val Phe Pro Ala Ile
 65 70 75 80
 5 His Trp His Ala Ala Phe Val Gly Phe Pro Glu Gly His Gly Ser Cys
 85 90 95
 Thr Trp Leu Pro Ala Leu Leu Val Gly Ala Asn Thr Phe Ala Ser His
 100 105 110
 10 Leu Leu Phe Ala Val Gly Cys Pro Leu Leu Leu Trp Pro Phe Leu
 115 120 125
 Cys Glu Ser Gln Gly Leu Arg Lys Arg Gln Gln Pro Pro Gly Asn Glu
 115 130 135 140
 15 Ala Asp Ala Arg Val Arg Pro Glu Glu Glu Glu Glu Pro Leu Met Glu
 145 150 155 160
 20 Met Arg Leu Arg Asp Ala Pro Gln His Phe Tyr Ala Ala Leu Leu Gln
 165 170 175
 Leu Gly Leu Lys Tyr Leu Phe Ile Leu Gly Ile Gln Ile Leu Ala Cys
 180 185 190
 25 Ala Leu Ala Ala Ser Ile Leu Arg Arg His Leu Met Val Trp Lys Val
 195 200 205
 Phe Ala Pro Lys Phe Ile Phe Glu Ala Val Gly Phe Ile Val Ser Ser
 210 215 220
 Val Gly Leu Leu Leu Gly Ile Ala Leu Val Met Arg Val Asp Gly Ala
 225 230 235 240
 35 Val Ser Ser Trp Phe Arg Gln Leu Phe Leu Ala Gln Gln Arg Xaa
 245 250 255

40 (2) INFORMATION FOR SEQ ID NO: 371:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

Met Xaa Gly Pro Trp Gly Glu Glu Ala Leu Ile Arg Leu Pro Thr Pro
 1 5 10 15
 50 Ser Gly Leu Xaa
 20

55

(2) INFORMATION FOR SEQ ID NO: 372:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

60

554

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

5 Met Ala Thr Leu Glu Xaa Asn Gln Arg Glu Val Asp Arg Glu Ile Arg
 1 5 10 15
 Ser Leu Leu Leu Trp Phe Leu Leu Cys Glu Ile Val Ser Gly Trp Leu
 20 25 30
 10 Cys Pro Glu Gly Pro Trp Phe Ser Gln Gly Cys Gln Ile Tyr Lys Asn
 35 40 45
 Leu Ser Ser Ser Ser Ser Tyr Asn Leu Ser Phe Leu Leu Ser Leu Xaa
 50 55 60
 15

20

(2) INFORMATION FOR SEQ ID NO: 373:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 40 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

30 Met Ile His Ser Gly Cys Thr Ser Gln Cys Leu Glu Gly Phe Phe Leu
 1 5 10 15
 Ile Phe Leu Leu Asp Phe Asn Pro Val Leu Ala Leu Asp Leu Ile Gly
 20 25 30
 35 Ile Met Arg Lys Ala Ser His Xaa
 35 40

40

(2) INFORMATION FOR SEQ ID NO: 374:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

50 Met Val Phe Ser Ala Arg Val Ser Leu Tyr Thr Arg Phe Lys Val Ile
 1 5 10 15
 Leu Leu Ser Leu Leu Ile Met Ile Leu His Val Cys Trp Val Trp Val
 20 25 30
 55 Ile Leu Xaa
 35

60

(2) INFORMATION FOR SEQ ID NO: 375:

555

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

Gly Leu Leu Tyr Ile Met Tyr Cys Asn Ile Xaa
1 5 10

10

(2) INFORMATION FOR SEQ ID NO: 376:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

20 Met Asn Asn Gly Leu Leu Gln Gln Pro Ser Ala Leu Met Leu Leu Pro
1 5 10 15

Cys Arg Pro Val Leu Thr Ser Val Ala Leu Asn Ala Asn Phe Val Ser
20 25 30

25 Trp Lys Ser Arg Thr Lys Tyr Thr Ile Thr Pro Val Lys Met Arg Lys
35 40 45

30 Ser Gly Gly Arg Asp His Thr Gly Gly Asn Lys Asp Arg Gly Ile Xaa
50 55 60

35

(2) INFORMATION FOR SEQ ID NO: 377:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

45 Met Arg Lys Gln Arg Leu Val Pro Met Tyr Leu Gly Leu Ile Tyr Ile
1 5 10 15

Leu Leu Xaa

50

(2) INFORMATION FOR SEQ ID NO: 378:

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

Met Arg Gln His Xaa
1 5

5

(2) INFORMATION FOR SEQ ID NO: 379:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

15 Leu Leu Leu Pro Val Leu Ala Ser Ser Val Pro Ser His Ser Ala Thr
1 5 10 15

Xaa

20

(2) INFORMATION FOR SEQ ID NO: 380:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

30 Met Leu Pro Leu Leu Leu Phe Thr Tyr Leu Asn Ser Phe Leu His Gln
1 5 10 15

Arg Ile Pro Gln Ser Val Arg Ile Leu Gly Ser Leu Val Ala Ile Leu
20 25 30

35

Leu Val Phe Leu Ile Thr Ala Ile Leu Val Lys Val Gln Leu Asp Ala
35 40 45

40 Leu Pro Phe Phe Val Ile Thr Met Ile Lys Ile Val Leu Ile Asn Ser
50 55 60

Phe Gly Ala Ile Leu Gln Gly Ser Leu Phe Gly Leu Ala Gly Leu Leu
65 70 75 80

45

Pro Ala Ser Xaa

50

(2) INFORMATION FOR SEQ ID NO: 381:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

60 Met Lys Leu Ser Leu Phe Leu Ile Leu Ser Asp Val Phe Tyr Leu Gly
1 5 10 15

Ser Pro Xaa Thr Xaa
20

5

(2) INFORMATION FOR SEQ ID NO: 382:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

10

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

15 Met Gly Thr Arg Arg Lys Gly Val Ala Trp Leu Ser Leu Ala Pro Leu
1 5 10 15

Ile Thr Gly Leu Ala Pro Ala His Ile Thr Ala Val Xaa
20 25

20

(2) INFORMATION FOR SEQ ID NO: 383:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

30 Met Lys Asp Leu Leu Gln Arg Asn Pro Trp Lys Asn Ser Leu Leu Leu
1 5 10 15

Leu Gln Val Cys Gln Ala Phe Leu Val Cys Ser Leu Thr Gln Leu Ala
20 25 30

35

Val Xaa

40

(2) INFORMATION FOR SEQ ID NO: 384:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

50 Met Ser Glu Ser His Lys Ile Trp Trp Cys Tyr Arg His Leu Ala Phe
1 5 10 15

Pro Leu Leu Thr Leu Ile Leu Tyr Pro Ala Thr Leu Gly Arg Ser Val
20 25 30

55

Phe Cys His Asp Cys Lys Phe Pro Glu Ala Ser Pro Ala Met Xaa
35 40 45

60

(2) INFORMATION FOR SEQ ID NO: 385:

558

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

Met Leu Asn Arg Ile Met Val Ala Ser Phe Gly Ala Val Leu Val Gln
 1 5 10 15

Val Cys Arg Gly Xaa Gly Gln Gly Xaa
 20 25

(2) INFORMATION FOR SEQ ID NO: 386:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

Met Gln Leu Leu Leu Leu Gly Leu Ile Arg Ser Gln Pro Ser Pro Pro
 1 5 10 15

Pro Ser Leu Cys Leu Met Leu Cys Pro Cys Leu Pro Cys Leu Arg Tyr
 20 25 30

Ser Pro Phe Val Pro Gln His Pro Cys Pro Leu Pro Leu Asp Leu Cys
 35 40 45

Leu Ala Gly Cys Ser Ser Leu Ser Val Gln Asp Lys Cys Ser Trp Pro
 50 55 60

Tyr Pro Ile Xaa
 65

(2) INFORMATION FOR SEQ ID NO: 387:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

Lys Glu Phe Phe Val Phe Leu Phe Val Cys Leu Phe Trp Leu Leu Ser
 1 5 10 15

Asn Thr Pro Leu Thr Phe Ile Ser Ile Ile Leu Gln Arg Lys Glu Thr
 20 25 30

Asn Xaa

(2) INFORMATION FOR SEQ ID NO: 388:

559

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

Ser Phe Leu Met Val Leu Val Ile Leu Ala Ala Ser Pro Xaa
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 389:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

1 5 10

(2) INFORMATION FOR SEQ ID NO: 390:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 154 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

Met Thr Lys Ala Arg Leu Phe Arg Leu Trp Leu Val Leu Gly Ser Val
 1 5 10 15

Phe Met Ile Leu Leu Ile Ile Val Tyr Trp Asp Ser Ala Gly Ala Ala
 20 25 30

His Phe Tyr Leu His Thr Ser Phe Ser Arg Pro His Thr Gly Pro Pro
 35 40 45

Leu Pro Thr Pro Gly Pro Asp Arg Asp Arg Glu Leu Thr Ala Asp Ser
 50 55 60

Asp Val Asp Xaa Phe Leu Asp Xaa Phe Leu Ser Ala Gly Val Lys Gln
 65 70 75 80

Ser Asp Xaa Pro Arg Lys Glu Thr Glu Gln Pro Pro Ala Pro Gly Ser
 85 90 95

Met Glu Glu Ser Val Arg Xaa Tyr Asp Trp Ser Pro Arg Xaa Ala Arg
 100 105 110

Arg Thr Gln Thr Arg Ala Gly Ser Xaa Arg Xaa Gly Gly Xaa Cys Cys
 115 120 125

Gly Ala Ser Ala Pro Xaa Pro Ala Trp Pro Ser Pro Pro Arg Ser Ala
 130 135 140

560

His Ser Thr Thr Ser Pro Thr Arg Ser Xaa
145 150

5

(2) INFORMATION FOR SEQ ID NO: 391:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

10

15

Met Val Leu Leu Gly Leu Leu Ser Xaa
1 5

20

(2) INFORMATION FOR SEQ ID NO: 392:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

25

Met Cys Ile His Val Phe Met Xaa Val Leu Trp Val Leu Phe Leu Leu
1 5 10 15

30

Asn Pro Leu Cys Thr Gly Leu Trp Pro Leu Xaa Asn Cys Phe Ser Val
20 25 30

35

Leu Arg His Ala Asp Trp Val Leu Gly Ala Asp Tyr Lys Gly Glu Glu
35 40 45

Leu Asn Arg His Gln Gly Pro Met Lys Pro Lys Asp Xaa
50 55 60

40

(2) INFORMATION FOR SEQ ID NO: 393:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 447 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

45

50

Met Leu Leu Gly Leu Leu Met Ala Ala Cys Phe Thr Phe Cys Leu Ser
1 5 10 15

His Gln Asn Leu Lys Glu Phe Ala Leu Thr Asn Pro Glu Lys Ser Ser
20 25 30

55

Thr Lys Glu Thr Glu Arg Lys Glu Thr Lys Ala Glu Glu Glu Leu Asp
35 40 45

Ala Glu Val Leu Glu Val Phe His Pro Thr His Glu Trp Gln Ala Leu
50 55 60

60

561

Gln Pro Gly Gln Ala Val Pro Ala Gly Ser His Val Arg Leu Asn Leu
 65 70 75 80
 5 Gln Thr Gly Glu Arg Glu Ala Lys Leu Gln Tyr Glu Asp Lys Phe Arg
 85 90 95
 Asn Asn Leu Lys Gly Lys Arg Leu Asp Ile Asn Thr Asn Thr Tyr Thr
 100 105 110
 10 Ser Gln Asp Leu Lys Ser Ala Leu Ala Lys Phe Lys Glu Gly Ala Glu
 115 120 125
 Met Glu Ser Ser Lys Glu Asp Lys Ala Arg Gln Ala Glu Val Lys Arg
 130 135 140
 15 Leu Phe Arg Pro Ile Glu Glu Leu Lys Lys Asp Phe Asp Glu Leu Asn
 145 150 155 160
 Val Val Ile Glu Thr Asp Met Gln Ile Met Val Arg Leu Ile Asn Lys
 165 170 175
 Phe Asn Ser Ser Ser Ser Ser Leu Glu Glu Lys Ile Ala Ala Leu Phe
 180 185 190
 25 Asp Leu Glu Tyr Tyr Val His Gln Met Asp Asn Ala Gln Asp Leu Leu
 195 200 205
 Ser Phe Gly Gly Leu Gln Val Val Ile Asn Gly Leu Asn Ser Thr Glu
 210 215 220
 30 Pro Leu Val Lys Glu Tyr Ala Ala Phe Val Leu Gly Ala Ala Phe Ser
 225 230 235 240
 Ser Asn Pro Lys Val Gln Val Glu Ala Ile Glu Gly Gly Ala Leu Gln
 245 250 255
 Lys Leu Leu Val Ile Leu Ala Thr Glu Gln Pro Leu Thr Ala Lys Lys
 260 265 270
 40 Lys Val Leu Phe Ala Leu Cys Ser Leu Leu Arg His Phe Pro Tyr Ala
 275 280 285
 Gln Arg Gln Phe Leu Lys Leu Gly Gly Leu Gln Val Leu Arg Thr Leu
 290 295 300
 45 Val Gln Glu Lys Gly Thr Glu Val Leu Ala Val Arg Val Val Thr Leu
 305 310 315 320
 Leu Tyr Asp Leu Val Thr Glu Lys Met Phe Ala Glu Glu Glu Ala Glu
 325 330 335
 50 Leu Thr Gln Glu Met Ser Pro Glu Lys Leu Gln Gln Tyr Arg Gln Val
 340 345 350
 55 His Leu Leu Pro Gly Leu Trp Glu Gln Gly Trp Cys Glu Ile Thr Ala
 355 360 365
 His Leu Leu Ala Leu Pro Glu His Asp Ala Arg Glu Lys Val Leu Gln
 370 375 380
 60

562

Thr Leu Gly Val Leu Leu Thr Thr Cys Arg Asp Arg Tyr Arg Gln Asp
385 390 395 400

5 Pro Gln Leu Gly Arg Thr Leu Ala Ser Leu Gln Ala Glu Tyr Gln Val
405 410 415

Leu Ala Ser Leu Glu Leu Gln Asp Gly Glu Asp Glu Gly Tyr Phe Gln
420 425 430

10 Glu Leu Leu Gly Ser Val Asn Ser Leu Leu Lys Glu Leu Arg Xaa
435 440 445

15 (2) INFORMATION FOR SEQ ID NO: 394:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

Met Val Ile Ser Tyr Val Thr Phe Thr Pro Val Ser Ala Asp Cys Phe
1 5 10 15

25 Phe Asn Val Leu Val Cys Phe Xaa
20

30 (2) INFORMATION FOR SEQ ID NO: 395:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

35 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

Glu Leu Leu Phe Leu Leu Ile Ile Ile Leu Gly Glu Ser Leu Ser Asp
1 5 10 15

40 Val Ile Leu Leu Ile Cys Phe Xaa
20

45 (2) INFORMATION FOR SEQ ID NO: 396:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

50 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

55 Met Phe Tyr Trp Gly Gly Leu Ser Phe Tyr Phe Leu Leu Ser Ser Gly
1 5 10 15

Val Gly Phe Tyr Cys Phe Leu Phe Gly Phe Gly Met Glu Ile Trp Ile
20 25 30

60

Ala Ala Xaa
35

5

(2) INFORMATION FOR SEQ ID NO: 397:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

Gly Arg Xaa
15 1

20

(2) INFORMATION FOR SEQ ID NO: 398:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

Met Lys Leu Ser Leu Leu Ile Leu Thr Leu Met Gln Arg Tyr Phe Arg
 1 5 10 15
 Thr Ile Thr Asn Ser Leu Cys Lys Xaa
 20 25

35

(2) INFORMATION FOR SEQ ID NO: 399:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 79 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

Met Pro Ala Val Ser Gly Pro Gly Pro Leu Phe Cys Leu Leu Leu Leu
 1 5 10 15
 Leu Leu Asp Pro His Ser Pro Glu Thr Gly Cys Pro Pro Leu Arg Arg
 20 25 30
 Phe Glu Tyr Lys Leu Ser Phe Lys Gly Pro Arg Leu Ala Leu Pro Gly
 35 40 45
 Ala Gly Ile Pro Phe Trp Ser His His Gly Gly Glu Gly Gln Gly Trp
 50 55 60
 Gly Pro Leu Cys Pro Gly Ser Leu Lys Val Leu Glu Gly Leu Xaa
 65 70 75

60

(2) INFORMATION FOR SEQ ID NO: 400:

564

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

Met Lys Val Phe Leu Ser Met Pro Phe Leu Val Leu Phe Gln Ser Leu
 1 5 10 15
 Ile Gln Glu Asp Xaa
 20

(2) INFORMATION FOR SEQ ID NO: 401:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 257 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

Met Ala Ala Leu Thr Ser His Leu Gln Asn Gln Ser Asn Asn Ser Asn
 1 5 10 15
 Trp Asn Leu Arg Thr Arg Ser Lys Cys Lys Lys Asp Val Phe Met Pro
 20 25 30
 Pro Ser Ser Ser Ser Glu Leu Gln Glu Ser Arg Gly Leu Ser Asn Phe
 35 40 45
 Thr Ser Thr His Leu Leu Leu Lys Glu Asp Glu Gly Val Asp Asp Val
 50 55 60
 Asn Phe Arg Lys Val Arg Lys Pro Lys Gly Lys Val Thr Ile Leu Lys
 65 70 75 80
 Gly Ile Pro Ile Lys Lys Thr Lys Lys Gly Cys Arg Lys Ser Cys Ser
 85 90 95
 Gly Phe Val Xaa Ser Asp Ser Lys Arg Glu Ser Val Cys Asn Lys Ala
 100 105 110
 Asp Ala Glu Ser Glu Pro Val Ala Gln Lys Ser Gln Leu Asp Arg Thr
 115 120 125
 Val Cys Ile Ser Asp Ala Gly Ala Cys Gly Glu Thr Leu Ser Val Thr
 130 135 140
 Ser Glu Glu Asn Ser Leu Val Lys Lys Lys Glu Arg Ser Leu Ser Ser
 145 150 155 160
 Gly Ser Asn Phe Cys Ser Glu Gln Lys Thr Ser Gly Ile Ile Asn Lys
 165 170 175
 Phe Cys Ser Ala Lys Asp Ser Glu His Asn Glu Lys Tyr Glu Asp Thr
 180 185 190
 Phe Leu Glu Ser Glu Glu Ile Gly Thr Lys Val Glu Val Val Glu Arg

565

195 200 205
 Lys Glu His Leu His Thr Asp Ile Leu Lys Arg Gly Ser Glu Met Asp
 210 215 220
 5
 Asn Asn Cys Ser Pro Thr Arg Lys Asp Phe Thr Glu Asp Thr Ile Pro
 225 230 235 240
 10 Arg Asn Thr Asp Arg Lys Lys Glu Asn Lys Pro Val Phe Phe Gln Gln
 245 250 255
 Ile
 15
 (2) INFORMATION FOR SEQ ID NO: 402:
 (i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 424 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:
 25 Met Glu Lys Gln Cys Cys Ser His Pro Val Ile Cys Ser Leu Ser Thr
 1 5 10 15
 Met Tyr Thr Phe Leu Leu Gly Ala Ile Phe Ile Ala Leu Ser Ser Ser
 20 25 30
 30 Arg Ile Leu Leu Val Lys Tyr Ser Ala Asn Glu Glu Asn Lys Tyr Asp
 35 40 45
 35 Tyr Leu Pro Thr Thr Val Asn Val Cys Ser Glu Leu Val Lys Leu Val
 50 55 60
 Phe Cys Val Leu Val Ser Phe Cys Val Ile Lys Lys Asp His Gln Ser
 65 70 75 80
 40 Arg Asn Leu Lys Tyr Ala Ser Trp Lys Glu Phe Ser Asp Phe Met Lys
 85 90 95
 Trp Ser Ile Pro Ala Phe Leu Tyr Phe Leu Asp Asn Leu Ile Val Phe
 100 105 110
 45 Tyr Val Leu Ser Tyr Leu Gln Pro Ala Met Ala Val Ile Phe Ser Asn
 115 120 125
 50 Phe Ser Ile Ile Thr Thr Ala Leu Leu Phe Arg Ile Val Leu Lys Xaa
 130 135 140
 Arg Leu Asn Trp Ile Gln Trp Ala Ser Leu Leu Thr Leu Phe Leu Ser
 145 150 155 160
 55 Ile Val Ala Leu Thr Ala Gly Thr Lys Thr Leu Gln His Asn Leu Ala
 165 170 175
 Gly Arg Gly Phe His His Asp Ala Phe Phe Ser Pro Ser Asn Ser Cys
 180 185 190
 60

566

Leu Leu Phe Arg Asn Glu Cys Pro Arg Lys Asp Asn Cys Thr Ala Lys
 195 200 205
 5 Glu Trp Thr Phe Pro Glu Ala Lys Trp Asn Thr Thr Ala Arg Val Phe
 210 215 220
 Ser His Ile Arg Leu Gly Met Gly His Val Leu Ile Ile Val Gln Cys
 225 230 235 240
 10 Phe Ile Ser Ser Met Ala Asn Ile Tyr Asn Glu Lys Ile Leu Lys Glu
 245 250 255
 Gly Asn Gln Leu Thr Glu Xaa Ile Phe Ile Gln Asn Ser Lys Leu Tyr
 260 265 270
 15 Phe Phe Gly Ile Leu Phe Asn Gly Leu Thr Leu Gly Leu Gln Arg Ser
 275 280 285
 Asn Arg Asp Gln Ile Lys Asn Cys Gly Phe Phe Tyr Gly His Ser Ala
 290 295 300
 Phe Ser Val Ala Leu Ile Phe Val Thr Ala Phe Gln Gly Leu Ser Val
 305 310 315 320
 25 Ala Phe Ile Leu Lys Phe Leu Asp Asn Met Phe His Val Leu Met Ala
 325 330 335
 Gln Val Thr Thr Val Ile Ile Thr Thr Val Ser Val Leu Val Phe Asp
 340 345 350
 30 Phe Arg Pro Ser Leu Glu Phe Phe Leu Glu Ala Pro Ser Val Leu Leu
 355 360 365
 Ser Ile Phe Ile Tyr Asn Ala Ser Lys Pro Gln Val Pro Glu Tyr Ala
 370 375 380
 Pro Arg Gln Glu Arg Ile Arg Asp Leu Ser Gly Asn Leu Trp Glu Arg
 385 390 395 400
 40 Ser Ser Gly Asp Gly Glu Glu Leu Glu Arg Leu Thr Lys Pro Lys Ser
 405 410 415
 Asp Glu Ser Asp Glu Asp Thr Phe
 420
 45

(2) INFORMATION FOR SEQ ID NO: 403:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

60

Met Trp Gly Gln Gly Ser Gln Lys Ser His Phe Ser Asp Leu Val Phe
 1 5 10 15
 Gly Val Arg Glu Leu Cys Ala Gln Pro Ser Asp Pro Gly Ser Pro His
 20 25 30

567

Xaa

5

(2) INFORMATION FOR SEQ ID NO: 404:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

15

Met Val Gln His Ile Gln Pro Ala Ala Leu Ser Leu Leu Ala Gln Trp
 1 5 10 15

20

Ser Thr Leu Val Gln Glu Leu Glu Ala Ala Leu Gln Leu Ala Phe Tyr
 20 25 30

Pro Asp Ala Val Glu Glu Trp Leu Glu Glu Asn Val His Pro Ser Leu
 35 40 45

25

Gln Arg Leu Gln Xaa Leu Leu Gln Asp Leu Ser Glu Val Ser Ala Pro
 50 55 60

Pro Leu Pro Pro Thr Ser Pro Gly Arg Asp Val Ala Gln Asp Pro Xaa
 65 70 75 80

30

35

(2) INFORMATION FOR SEQ ID NO: 405:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

45

Met Leu Asn Gln Gly Tyr Ile Arg Lys Ile Ile Leu Ile Ile Leu
 1 5 10 15

Gly Ser Phe Ser Ser Pro Lys Lys Ala Ile Leu Met Gly Phe Gln Asn
 20 25 30

50

Gln Lys Lys Ala Leu Asn Glu Glu Gln Thr Thr Gly Val Pro Met Ser
 35 40 45

Ile Ser Gly Lys Leu Arg Pro Ser Arg Ser Leu Asp Phe Val Gln Pro
 50 55 60

55

Pro Arg Phe Gln Ser Gln Gln Pro Ser Ala Val Val Asp Arg Arg Gly
 65 70 75 80

Phe Xaa Xaa Lys Ala Ala Arg Gly Gln Glu Phe Ser Glu Ser Xaa
 85 90 95

60

(2) INFORMATION FOR SEQ ID NO: 406:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 257 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

Met Arg Gly Pro Ala Gln Ala Lys Leu Leu Pro Gly Ser Ala Ile Gln
 1 5 10 15

Ala Leu Val Gly Leu Ala Arg Pro Leu Val Leu Ala Leu Leu Leu Val
 15 20 25 30

Ser Ala Ala Leu Ser Ser Val Val Ser Arg Thr Asp Ser Pro Ser Pro
 35 40 45

20 Thr Val Leu Asn Ser His Ile Ser Thr Pro Asn Val Asn Ala Leu Thr
 50 55 60

His Glu Asn Gln Thr Lys Pro Ser Ile Ser Gln Ile Ser Thr Thr Leu
 65 70 75 80

25 Pro Pro Thr Thr Ser Thr Lys Lys Ser Gly Gly Ala Ser Val Val Pro
 85 90 95

His Pro Ser Pro Thr Pro Leu Ser Gln Glu Glu Ala Asp Asn Asn Glu
 30 100 105 110

Asp Pro Ser Ile Glu Glu Glu Asp Leu Leu Met Leu Asn Ser Ser Pro
 115 120 125

35 Ser Thr Ala Lys Asp Thr Leu Asp Asn Gly Asp Tyr Gly Glu Pro Asp
 130 135 140

Tyr Asp Trp Thr Thr Gly Pro Arg Asp Asp Asp Glu Ser Asp Asp Thr
 40 145 150 155 160

Leu Glu Glu Asn Arg Gly Tyr Met Glu Ile Glu Gln Ser Val Lys Ser
 165 170 175

45 Phe Lys Met Pro Ser Ser Asn Ile Glu Glu Glu Asp Ser His Phe Phe
 180 185 190

Phe His Leu Ile Ile Phe Ala Phe Cys Ile Ala Val Val Tyr Ile Thr
 195 200 205

50 Tyr His Asn Lys Arg Lys Ile Phe Leu Leu Val Gln Ser Arg Lys Trp
 210 215 220

Arg Asp Gly Leu Cys Ser Lys Thr Val Glu Tyr His Arg Leu Asp Gln
 225 230 235 240

55 Asn Val Asn Glu Ala Met Pro Ser Leu Lys Ile Thr Asn Asp Tyr Ile
 245 250 255

60 Phe

(2) INFORMATION FOR SEQ ID NO: 407:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 623 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

Met Phe Met Arg Ile Ala Lys Ala Tyr Ala Ala Leu Thr Asp Glu Glu
 1 5 10 15
 Ser Arg Lys Asn Trp Glu Glu Phe Gly Asn Pro Asp Gly Pro Gln Ala
 20 25 30
 Thr Ser Phe Gly Ile Ala Leu Pro Ala Trp Ile Val Asp Gln Lys Asn
 35 40 45
 Ser Ile Leu Val Leu Leu Val Tyr Gly Leu Ala Phe Met Val Ile Leu
 50 55 60
 Pro Val Val Val Gly Ser Trp Trp Tyr Arg Ser Ile Arg Tyr Ser Gly
 65 70 75 80
 Asp Gln Ile Leu Ile Arg Thr Thr Gln Ile Tyr Thr Tyr Phe Val Tyr
 85 90 95
 Lys Thr Arg Asn Met Asp Met Lys Arg Leu Ile Met Val Leu Xaa Gly
 100 105 110
 Ala Ser Glu Phe Asp Pro Gln Tyr Asn Lys Asp Ala Thr Ser Arg Pro
 115 120 125
 Thr Asp Asn Ile Leu Ile Pro Gln Leu Ile Arg Glu Ile Gly Ser Ile
 130 135 140
 Asn Leu Lys Lys Asn Glu Pro Pro Leu Thr Cys Pro Tyr Ser Leu Lys
 145 150 155 160
 Ala Arg Val Leu Leu Leu Ser His Leu Ala Arg Met Lys Ile Pro Glu
 165 170 175
 Thr Leu Glu Glu Asp Gln Gln Phe Met Leu Lys Lys Cys Pro Ala Leu
 180 185 190
 Leu Gln Glu Met Val Asn Val Ile Cys Gln Leu Ile Val Met Ala Arg
 195 200 205
 Asn Arg Glu Glu Arg Glu Phe Arg Ala Pro Thr Leu Ala Ser Leu Glu
 210 215 220
 Asn Cys Met Lys Leu Ser Gln Met Ala Val Gln Gly Leu Gln Gln Phe
 225 230 235 240
 Lys Ser Pro Leu Leu Gln Leu Pro His Ile Glu Glu Asp Asn Leu Arg
 245 250 255
 Arg Val Ser Asn His Lys Lys Tyr Lys Ile Lys Thr Ile Gln Asp Leu

570

	260	265	270
	Val Ser Leu Lys Glu Ser Asp Arg His Thr Leu Leu His Phe Leu Glu		
	275	280	285
5	Asp Glu Lys Tyr Glu Glu Val Met Ala Val Leu Gly Ser Phe Pro Tyr		
	290	295	300
10	Val Thr Met Asp Ile Lys Ser Gln Val Leu Asp Asp Glu Asp Ser Asn		
	305	310	315 320
	Asn Ile Thr Val Gly Ser Leu Val Thr Val Leu Val Lys Leu Thr Arg		
	325	330	335
15	Gln Thr Met Ala Glu Val Phe Glu Lys Glu Gln Ser Ile Cys Ala Ala		
	340	345	350
	Glu Glu Gln Pro Ala Glu Asp Gly Gln Gly Glu Thr Asn Lys Asn Arg		
	355	360	365
20	Thr Lys Gly Gly Trp Gln Gln Lys Ser Lys Gly Pro Lys Lys Thr Ala		
	370	375	380
25	Lys Ser Lys Lys Lys Lys Pro Leu Lys Lys Lys Pro Thr Pro Val Leu		
	385	390	395 400
	Leu Pro Gln Ser Lys Gln Gln Lys Gln Lys Gln Ala Asn Gly Val Val		
	405	410	415
30	Gly Asn Glu Ala Ala Val Lys Glu Asp Glu Glu Glu Val Ser Asp Lys		
	420	425	430
	Gly Ser Asp Ser Glu Glu Glu Glu Thr Asn Arg Asp Ser Gln Ser Glu		
	435	440	445
35	Lys Asp Asp Gly Ser Asp Arg Asp Ser Asp Arg Glu Gln Asp Glu Lys		
	450	455	460
40	Gln Asn Lys Asp Asp Glu Ala Glu Trp Gln Glu Leu Gln Gln Ser Ile		
	465	470	475 480
	Gln Arg Lys Glu Arg Ala Leu Leu Glu Thr Lys Ser Lys Ile Thr His		
	485	490	495
45	Pro Val Tyr Ser Leu Tyr Phe Pro Glu Glu Lys Gln Glu Trp Trp Trp		
	500	505	510
	Leu Tyr Ile Ala Asp Arg Lys Glu Gln Thr Leu Ile Ser Met Pro Tyr		
	515	520	525
50	His Val Cys Thr Leu Lys Asp Thr Glu Glu Val Glu Leu Lys Phe Pro		
	530	535	540
55	Ala Pro Gly Lys Pro Gly Asn Tyr Gln Tyr Thr Val Phe Leu Arg Ser		
	545	550	555 560
	Asp Ser Tyr Met Gly Leu Asp Gln Ile Lys Pro Leu Glu Val Xaa Lys		
	565	570	575
60	Phe Met Arg Leu Lys Pro Val Pro Glu Asn His Pro Gln Trp Asp Thr		

571

580 585 590

Ala Ile Glu Gly Asp Glu Asp Gln Glu Asp Ser Glu Gly Phe Glu Asp
595 600 605

5 Ser Phe Glu Gly Gly Arg Gly Arg Glu Glu Gly Arg Trp Trp Thr
610 615 620

10 (2) INFORMATION FOR SEQ ID NO: 408:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 190 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

20 Met Lys Ala Ser Gln Cys Cys Cys Cys Leu Ser His Leu Leu Ala Ser
1 5 10 15

Val Leu Leu Leu Leu Leu Pro Glu Leu Ser Gly Xaa Leu Xaa Val
20 25 30

25 Leu Leu Gln Ala Ala Glu Ala Ala Pro Gly Leu Gly Pro Pro Asp Pro
35 40 45

Arg Pro Arg Thr Leu Pro Pro Leu Pro Pro Gly Pro Thr Pro Ala Gln
50 55 60

30 Gln Pro Gly Arg Gly Leu Ala Glu Ala Ala Gly Pro Arg Gly Ser Glu
65 70 75 80

Gly Gly Asn Gly Ser Asn Pro Val Ala Gly Leu Glu Thr Asp Asp His
85 90 95

Gly Gly Lys Ala Gly Glu Gly Ser Val Gly Gly Gly Leu Ala Val Ser
100 105 110

40 Pro Asn Pro Gly Asp Lys Pro Met Thr Gln Arg Ala Leu Thr Val Leu
115 120 125

Met Val Val Ser Gly Ala Val Leu Val Tyr Phe Val Val Arg Thr Val
130 135 140

45 Arg Met Arg Arg Arg Asn Arg Lys Thr Arg Arg Tyr Gly Val Leu Asp
145 150 155 160

Thr Asn Ile Glu Asn Met Glu Leu Thr Pro Leu Glu Gln Asp Asp Glu
165 170 175

50 Asp Asp Asp Asn Thr Leu Phe Asp Ala Asn His Pro Arg Arg
180 185 190

55

(2) INFORMATION FOR SEQ ID NO: 409:

60 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 179 amino acids

572

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

5 Met Ser Pro Ser Gly Arg Leu Cys Leu Leu Thr Ile Val Gly Leu Ile
 1 5 10 15
 Leu Pro Thr Arg Gly Gln Thr Leu Lys Asp Thr Thr Ser Ser Ser Ser
 20 25 30
 10 Ala Asp Ser Thr Ile Met Asp Ile Gln Val Pro Thr Arg Ala Pro Asp
 35 40 45
 Ala Val Tyr Thr Gln Leu Gln Pro Thr Ser Pro Thr Pro Thr Trp Pro
 15 50 55 60
 Ala Asp Glu Thr Pro Gln Pro Gln Thr Gln Thr Gln Gln Leu Glu Gly
 65 70 75 80
 20 Thr Asp Gly Pro Leu Val Thr Asp Pro Glu Thr His Lys Ser Thr Lys
 85 90 95
 Ala Ala His Pro Thr Asp Asp Thr Thr Thr Leu Ser Glu Arg Pro Ser
 100 105 110
 25 Pro Ser Thr Asp Val Gln Thr Asp Pro Gln Thr Leu Lys Pro Ser Gly
 115 120 125
 Phe His Glu Asp Asp Pro Phe Phe Tyr Asp Glu His Thr Leu Arg Lys
 30 130 135 140
 Arg Gly Leu Leu Val Ala Ala Val Leu Phe Ile Thr Gly Ile Ile Ile
 145 150 155 160
 35 Leu Thr Ser Gly Lys Cys Arg Gln Leu Ser Arg Leu Cys Arg Asn His
 165 170 175
 Cys Arg Xaa

40

(2) INFORMATION FOR SEQ ID NO: 410:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

50

Met Phe Lys Cys Leu Gln Thr Thr Phe Leu Phe Ile Xaa Xaa
 1 5 10

55

(2) INFORMATION FOR SEQ ID NO: 411:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 232 amino acids

(B) TYPE: amino acid

60

573

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

5 Met Leu Ala Gly Lys Leu Ile Pro Val His Gln Val Arg Gly Leu Lys
 1 5 10 15
 Glu Lys Ile Val Arg Ser Phe Glu Val Ser Pro Asp Gly Ser Phe Leu
 20 25 30
 10 Leu Ile Asn Gly Ile Ala Gly Tyr Leu His Leu Leu Ala Met Lys Thr
 35 40 45
 Lys Glu Leu Ile Gly Ser Met Lys Ile Asn Gly Arg Val Ala Ala Ser
 50 55 60
 15 Thr Phe Ser Ser Asp Ser Lys Lys Val Tyr Ala Ser Ser Gly Asp Gly
 65 70 75 80
 20 Glu Val Tyr Val Trp Asp Val Asn Ser Arg Lys Cys Leu Asn Arg Phe
 85 90 95
 Val Asp Glu Gly Ser Leu Tyr Gly Leu Ser Ile Ala Thr Ser Arg Asn
 100 105 110
 25 Gly Gln Tyr Val Ala Cys Gly Ser Asn Cys Gly Val Val Asn Ile Tyr
 115 120 125
 Asn Gln Asp Ser Cys Leu Gln Glu Thr Asn Pro Lys Pro Ile Lys Ala
 130 135 140
 30 Ile Met Asn Leu Val Thr Gly Val Thr Ser Leu Thr Phe Asn Pro Thr
 145 150 155 160
 35 Thr Glu Ile Leu Ala Ile Ala Ser Glu Lys Met Lys Glu Ala Val Arg
 165 170 175
 Leu Val His Leu Pro Ser Cys Thr Val Phe Ser Asn Phe Pro Val Ile
 180 185 190
 40 Lys Asn Lys Asn Ile Ser His Val His Thr Met Asp Phe Ser Pro Arg
 195 200 205
 Ser Gly Tyr Phe Ala Leu Gly Asn Glu Lys Gly Lys Ala Leu Met Tyr
 210 215 220
 45 Arg Leu His His Tyr Ser Asp Phe
 225 230

50

(2) INFORMATION FOR SEQ ID NO: 412:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

60 Ile Leu Leu Cys Ser Trp Pro Thr Gly Leu Val Gly Gly Arg Asp Pro
 1 5 10 15

574

Gly Ser Ser Arg Gly Ser Ser Ala Ser Leu Thr Pro Ser Pro Gly Arg
 20 25 30
 5 Gln Pro Cys Ser Arg Arg Arg Gly Tyr Ser Val Gly Arg Arg Ser Ser
 35 40 45
 Pro Pro Asp Gly Ser Xaa
 50

10

(2) INFORMATION FOR SEQ ID NO: 413:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

20

Met Ser Leu Gln Ser Asn Ala Trp Ser Lys Xaa Leu Phe Ile Val Phe
 1 5 10 15

25

Leu Phe Leu Arg Val Leu Phe Lys Thr Gly Val Ser Ser Glu Glu Ser
 20 25 30

Xaa

30

(2) INFORMATION FOR SEQ ID NO: 414:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

40

Met Ala Val Val Leu Leu Ala Asn Leu Ala Gln Gly Asp Ser Leu Ala
 1 5 10 15

Ala Arg Ala Ile Ala Val Gln Lys Gly Ser Ile Gly Asn Leu Leu Gly
 20 25 30

45

Phe Leu Glu Asp Ser Leu Ala Ala Thr Gln Phe Gln Gln Ser Gln Ala
 35 40 45

50

Ser Leu Leu His Met Gln Asn Pro Pro Phe Glu Pro Xaa Ser Val Asp
 50 55 60

Met Met Arg Arg Ala Ala Arg Ala Leu Leu Ala Leu Ala Lys Val Asp
 65 70 75 80

55

Glu Asn His Ser Glu Phe Thr Leu Tyr Glu Ser Arg Leu Leu Asp Ile
 85 90 95

Ser Val Ser Pro Leu Met Asn Ser Xaa Val Ser Gln Val Ile Cys Asp
 100 105 110

60

--

575

Val Leu Phe Leu Xaa Trp Pro Val Met Thr Ala Val Gly His Leu Pro
 115 120 125

5 Pro Pro Cys Val Cys Ala Cys Val Glu Asn Leu Glu Thr Asp Cys Cys
 130 135 140

Pro Leu Phe Met Gln Asn His Leu Arg Ile Gln Phe Thr Leu Cys Cys
 145 150 155 160

10 Pro Ala Ser Pro Leu Gly Lys Ser Leu Ser Cys Phe Ser Leu Leu Leu
 165 170 175

Pro Pro Pro Leu Pro Pro Ser Pro His Ala Phe Leu Phe Leu Val Leu
 180 185 190

15 Thr Leu Leu Pro Ser Gly Pro Tyr Pro Thr Leu Phe Glu Lys Thr Lys
 195 200 205

20 Leu Cys Leu His Arg Arg Leu Phe Leu Phe Xaa
 210 215

25 (2) INFORMATION FOR SEQ ID NO: 415:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

Met Leu Pro Asp Glu Ser Phe Gly Leu Leu Leu Ser Ile Pro Ser Leu
 1 5 10 15

35 Thr Pro Ser Ala Ala Ala Pro Ser Phe Cys Val His Leu Met Gln Ala
 20 25 30

Ser Arg Ser Ser Lys Arg Ala Ser His Val Pro Val His Leu Leu Trp
 35 40 45

40 Gly Asp Xaa
 50

45 (2) INFORMATION FOR SEQ ID NO: 416:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

Met Arg Pro Gly Ser Phe Ser Phe Ile Ala Phe Leu Ala Thr Glu Val
 1 5 10 15

Ser Ser Cys Phe Pro Gly Arg Pro Asp Cys Xaa Thr Gly Met Trp Leu
 20 25 30

60 Leu Gln Leu Gln Lys Lys Gln Arg Thr Leu Leu Ala Met Ala Pro Arg

576

35 40 45

Arg Xaa
50

5

(2) INFORMATION FOR SEQ ID NO: 417:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

Asp Arg Pro Cys Pro Ser Ser Leu Trp Lys Val Phe Pro Leu Leu Leu
1 5 10 15

Leu Leu Met Arg Leu Phe Pro Leu Pro Val Pro Gly Asn Gln Arg Ala
20 25 30

Xaa Leu Pro His Pro Phe Xaa Ala Pro Arg Leu Pro Cys Leu Leu Cys
35 40 45

25 Leu Cys Thr Gln Gln Phe Xaa Val Cys Ser His Tyr Leu Pro Ala Gly
50 55 60

Tyr Arg Val Asn Ser Xaa
65 70

30

(2) INFORMATION FOR SEQ ID NO: 418:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

Met His Glu Lys Ala Trp Asn Leu Ile Leu Leu Trp Trp Leu Ser Leu
1 5 10 15

45 Asp Leu Leu Gly Val Ala Lys Thr Ala Met Trp Ala Gln Trp Cys Gly
20 25 30

Leu Asn Asp His Lys Gly Lys Xaa
35 40

50

(2) INFORMATION FOR SEQ ID NO: 419:

55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

60 Met Ala Phe Val Leu Leu Xaa Cys Phe Val Xaa Leu Gln Ser Ser Xaa

1 5 10 15
Gly Arg Ala Val Gln Xaa
 20

5

(2) INFORMATION FOR SEQ ID NO: 42:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420;

Met Phe Ser Leu Leu Trp Leu Val Cys Val Pro Ser Asn Ser Ser Val
1 5 10 15

20

Ala Asn Val Thr Ala Ser Arg Gly Gly Val Phe Lys Arg Ser Leu Gly
20 25 30

His Glu Gly Phe Ser Xaa
35

25

(2) INFORMATION FOR SEQ ID NO: 42:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

35

Lys Trp Leu Leu Phe Ile Phe Leu Leu Cys Leu Gln Leu Val Asn Ala
1 5 10 15

40

Leu Leu Ser Leu Phe Gln Glu Arg Phe Val His Cys Pro Ala Arg Phe
20 25 30

Val Ser Xaa
35

45

(2) INFORMATION FOR SEQ ID NO: 422:

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

55

Met Leu Leu Phe Leu Ser Ile Thr Asn Ser Leu Ser Phe Ile Ser Val
1 5 10 15

Asp Lys Pro Phe Gly Gln Ser Glu Asp Val Cys Pro Val Ile Ser Xaa
20 25 30

60

5 (2) INFORMATION FOR SEQ ID NO: 423:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:

Met Glu Phe Leu Phe Asn Lys Thr Gly Trp Ala Phe Ala Ala Leu Cys
 1 5 10 15
 Phe Val Leu Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg Gly
 20 25 30
 Pro Pro Tyr Ala His Lys Asn Pro His Thr Gly His Val Asn Tyr Ile
 35 40 45
 His Gly Ser Ser Gln Ala Gln Phe Val Ala Glu Thr His Ile Val Leu
 50 55 60
 Leu Phe Asn Gly Gly Val Thr Leu Gly Met Val Leu Leu Cys Glu Ala
 65 70 75 80
 Ala Thr Ser Asp Met Asp Ile Gly Lys Arg Lys Ile Met Cys Val Ala
 85 90 95
 Gly Ile Gly Leu Val Val Leu Phe Phe Ser Trp Met Leu Ser Ile Phe
 100 105 110
 Arg Ser Lys Tyr His Gly Tyr Pro Tyr Ser Phe Leu Met Ser Xaa
 115 120 125

40 (2) INFORMATION FOR SEQ ID NO: 424:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid

45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424:

Met Thr Trp His Ser Arg Glu Ser Phe Xaa Leu Leu Arg Val Val Ala
 1 5 10 15
 Pro Ser Gln Ala Pro Gly Met Gln Val Ser Pro Ser Gln Arg Ala Trp
 20 25 30
 Arg Arg Pro Leu His Arg Cys His Val Ala Ala Pro Arg Pro His His
 35 40 45
 Phe Ala Phe Phe Arg Asn Pro Phe Ser Trp Ser Phe Ile Lys Leu Leu
 50 55 60
 Tyr Arg Tyr Leu Xaa
 65

5 (2) INFORMATION FOR SEQ ID NO: 425:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

Met Gly Leu Lys Leu Asn Gly Arg Tyr Ile Ser Leu Ile Leu Ala Val
 1 5 10 15
 Gln Ile Ala Tyr Leu Val Gln Ala Val Arg Ala Ala Gly Lys Cys Asp
 20 25 30
 Ala Val Phe Lys Gly Phe Ser Asp Cys Leu Leu Lys Leu Gly Asp Thr
 35 40 45
 Trp Pro Thr Thr Arg Ser Leu Gly Arg Gln Asp Glu His Gln Asp Arg
 50 55 60
 Val His Ile Leu Gly Gly Phe Pro Gln Leu His Gly His Ser Pro Tyr
 65 70 75 80
 Gly Leu Pro Gly Arg Gly Glu Arg Tyr Val Gly Xaa
 85 90

30

(2) INFORMATION FOR SEQ ID NO: 426:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 380 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

40 Met Ala Arg Arg Ser Ala Phe Pro Ala Ala Ala Leu Trp Leu Trp Ser
 1 5 10 15
 Ile Leu Leu Cys Leu Leu Ala Leu Arg Ala Glu Ala Gly Pro Pro Gln
 20 25 30
 Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu
 35 40 45
 Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
 50 55 60
 Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile
 65 70 75 80
 55 Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln
 85 90 95
 Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly
 100 105 110

60

580

Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro
 115 120 125
 5 His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln
 130 135 140
 Asp Gly Val Ala Ala Phe Glu Val Asp Val Ile Val Met Asn Ser Glu
 145 150 155 160
 10 Gly Asn Thr Ile Leu Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr
 165 170 175
 Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys
 180 185 190
 15 Asn Glu Arg Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His
 195 200 205
 20 Cys Glu Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys
 210 215 220
 Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn
 225 230 235 240
 25 Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys
 245 250 255
 Phe Tyr Pro Gly Lys Cys Ile Xaa Pro Pro Gly Leu Glu Gly Glu Gln
 260 265 270
 30 Cys Glu Ile Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys
 275 280 285
 35 Ile Gly Lys Ser Lys Cys Lys Xaa Ser Lys Gly Tyr Gln Gly Asp Leu
 290 295 300
 Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys
 305 310 315 320
 40 His Glu Pro Asn Lys Cys Gln Cys Gln Glu Gly Trp His Gly Arg His
 325 330 335
 Cys Asn Lys Arg Tyr Glu Ala Ser Leu Ile His Ala Leu Arg Pro Ala
 340 345 350
 45 Gly Ala Gln Leu Arg Gln His Thr Pro Ser Leu Lys Lys Ala Glu Glu
 355 360 365
 50 Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp Xaa
 370 375 380

- 55 (2) INFORMATION FOR SEQ ID NO: 427:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

Met Thr Ser Asn Leu Leu Leu Leu Thr Leu Leu Leu Lys Asp Thr Leu
 1 5 10 15

5 Xaa Leu Ala Lys Xaa Asn Xaa Xaa
 20

10 (2) INFORMATION FOR SEQ ID NO: 428:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

Met Arg His His Thr Gln Leu Asn Phe Ile Phe Leu Val Glu Met Val
 1 5 10 15

20 Phe Leu His Val Gly Gln Ala Gly Leu Lys Leu Pro Thr Ser Gly Asp
 20 25 30

25 Xaa Ala Cys Phe Gly Leu Pro Lys Val Leu Gly Leu Gln Ala Xaa
 35 40 45

30 (2) INFORMATION FOR SEQ ID NO: 429:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

Met Cys Ser Asp Xaa
 1 5

40

(2) INFORMATION FOR SEQ ID NO: 430:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 144 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

50 Leu Leu Ser Ile Leu Leu Cys Leu Leu Ala Ser Gly Leu Val Val Phe
 1 5 10 15

Phe Leu Phe Pro His Ser Val Leu Val Asp Asp Asp Gly Ile Lys Val
 20 25 30

55

Val Lys Val Thr Phe Asn Lys Gln Asp Ser Leu Val Ile Leu Thr Ile
 35 40 45

60 Met Ala Thr Leu Lys Ile Arg Asn Ser Asn Phe Tyr Thr Val Ala Val
 50 55 60

582

Thr Ser Leu Ser Ser Gln Ile Gln Tyr Met Asn Thr Val Val Asn Phe
 65 70 75 80
 5 Thr Gly Lys Ala Glu Met Gly Gly Pro Phe Ser Tyr Val Tyr Phe Phe
 85 90 95
 Cys Thr Val Pro Glu Ile Leu Val His Asn Ile Val Ile Phe Met Arg
 100 105 110
 10 Thr Ser Val Lys Ile Ser Tyr Ile Gly Leu Met Thr Gln Ser Ser Leu
 115 120 125
 15 Glu Thr His His Tyr Val Asp Cys Gly Gly Asn Ser Thr Ala Ile Xaa
 130 135 140

20

(2) INFORMATION FOR SEQ ID NO: 431:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

30 Met Phe Phe Phe Leu Tyr Val Tyr Ser Val Leu Cys Gly Leu Leu Val
 1 5 10 15
 Tyr Pro Ser Leu Pro Ser His Ser Val Ser Leu Val Thr Ser Leu Val
 20 25 30
 35 Ala Ser Ala Leu Xaa
 35

40

(2) INFORMATION FOR SEQ ID NO: 432:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:

50 Met Ala Ser Ile Asn Ala Val Tyr Ile His Val Phe Leu Gly Val Cys
 1 5 10 15
 Val Gln Ala Thr Ala Ala Cys Pro Trp Cys Ser Gln Cys Arg Xaa Gly
 20 25 30
 55 Ser Val Pro Ser Xaa
 35

60 (2) INFORMATION FOR SEQ ID NO: 433:

583

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433:

5 Met Met Ala Ala Met Val Leu Thr Ser Leu Ser Cys Ser Pro Val Val
 1 5 10 15
 10 Gln Ser Pro Pro Gly Thr Glu Ala Asn Phe Ser Ala Ser Arg Ala Ala
 20 25 30
 15 Cys Asp Pro Trp Lys Glu Ser Gly Asp Ile Ser Asp Ser Gly Xaa Ser
 35 40 45
 Thr Thr Ser Gly His Trp Ser Gly Ser Ser Gly Val Ser Thr Pro Ser
 50 55 60
 20 Pro Pro His Pro Gln Ala Ser Pro Lys Tyr Leu Gly Asp Ala Phe Gly
 65 70 75 80
 Ser Pro Gln Thr Asp His Gly Phe Glu Thr Asp Pro Asp Pro Phe Leu
 85 90 95
 25 Leu Asp Glu Pro Ala Pro Arg Lys Arg Lys Asn Ser Val Lys Val Met
 100 105 110
 Tyr Lys Cys Leu Trp Pro Asn Cys Gly Lys Val Leu Arg Ser Ile Val
 115 120 125
 Gly Ile Lys Arg His Val Lys Ala Leu His Leu Gly Asp Thr Val Asp
 130 135 140
 35 Ser Asp Gln Phe Lys Arg Glu Glu Asp Phe Tyr Tyr Thr Glu Val Gln
 145 150 155 160
 Leu Lys Glu Glu Ser Ala Ala Ala Ala Ala Ala Ala Ala Asp Pro
 165 170 175
 40 Gln Ser Leu Gly Leu Pro Pro Pro Ser Gln Leu Pro Pro Pro Ala Xaa
 180 185 190

45

(2) INFORMATION FOR SEQ ID NO: 434:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

55

Met Ser Thr Asn Tyr Leu Thr Asp Val Cys Ser Leu Phe Ser Tyr Leu
 1 5 10 15

60

Asn Tyr Leu Tyr Phe His His His Leu Pro Val Pro Asn Thr Xaa

584

20

25

30

5 (2) INFORMATION FOR SEQ ID NO: 435:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

Met Gly Phe Phe Phe Val Leu Phe Phe Leu Tyr Leu Ala Leu Ser Arg
 1 5 10 15
 Asp Trp Ser Ile Asn Phe Leu Lys Asp His Arg Ile Asn Phe Phe Val
 20 25 30
 Ala Thr Ser Tyr Phe Ser Val Tyr Val Arg Gly Xaa Pro Xaa Val Pro
 35 40 45
 Ala Asp Thr Pro Leu Gly Pro Leu Leu Ser Leu Trp Leu His His Asn
 50 55 60
 Ala Phe Phe Ser Ile Leu Pro Lys Phe Pro Glu Asn Xaa Xaa Phe Leu
 65 70 75 80
 Ile Leu Lys Lys Leu Val Val Glu Met Gly Trp Asp Leu Phe Ile Ser
 85 90 95
 Pro Glu Asn Lys Xaa
 100

35

(2) INFORMATION FOR SEQ ID NO: 436:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

Met Ala Arg Tyr Phe Ile Phe Phe Ile Leu Val Phe Met Lys Val Ser
 1 5 10 15
 Leu Asn Thr Thr Trp Pro Ala Pro Arg Pro Ala Thr Leu Arg Thr Ala
 20 25 30
 Asn Lys Ser Lys Xaa
 35

55

(2) INFORMATION FOR SEQ ID NO: 437:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

5 Phe Ser Thr Ile Arg Ser Gly Leu Thr Asp Arg Ser Val Asn Phe Leu
 1 5 10 15
 Phe Leu Phe Leu Asp Val Pro Asp Cys Arg Leu Val Asn Ile Glu Leu
 20 25 30
 10 Met Ala Asn Ser Thr Val Thr His Ala Xaa
 35 40

(2) INFORMATION FOR SEQ ID NO: 438:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

Leu
 1

25

(2) INFORMATION FOR SEQ ID NO: 439:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:

35 Met Pro Trp Arg Arg Ala Gly Leu Met Met Leu Pro Ile Ile Thr Gly
 1 5 10 15
 Cys Cys Pro Cys Ser Ala Ser Ile Xaa
 20 25
 40

(2) INFORMATION FOR SEQ ID NO: 440:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440:

50

Met Tyr Leu Cys Lys Thr Val Lys Val Leu Ile Cys Tyr Asp Trp Ile
 1 5 10 15

55

Leu Gly Leu Val Ser Ser Gly Gln His Trp Val Val Ser Leu Ser Tyr
 20 25 30

Ser Ile Arg Val Tyr Pro Ala Met His Phe Thr Leu Cys Val His Ile
 35 40 45

60

Tyr Ser Lys Glu Pro Cys

50

5 (2) INFORMATION FOR SEQ ID NO: 441:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441:

Met Thr Ala Leu Val Trp Arg Lys Gly Pro Asp Gly Gly Ser Arg Lys
 1 5 10 15

15

Pro Ile Leu Leu Leu Phe Phe Phe Leu Pro Leu Ile Leu Cys Phe His
 20 25 30

20

Ser Phe Ile His Ser Ser Asn Ile Cys Xaa
 35 40

25

(2) INFORMATION FOR SEQ ID NO: 442:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442:

Met Phe Leu Thr Thr Trp Phe Leu Leu Leu Ser Val Ala Trp Xaa Ala
 1 5 10 15

35

Leu Thr Arg Ser Gly Arg Ser Cys Leu Pro Leu Val Gly Arg Pro Arg
 20 25 30

Glu Gln Ser Pro Arg Thr His Cys Ala Ala Ser Ser Thr Lys Glu Arg
 35 40 45

40

Asn Ser Asp Pro Gln Pro Ser Pro Pro Glu Val Val Gly Pro Leu Trp
 50 55 60

45

Ser Xaa
 65

50

(2) INFORMATION FOR SEQ ID NO: 443:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 156 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443:

Met Lys Ala Ile Gly Ile Glu Pro Ser Leu Ala Thr Tyr His His Ile
 1 5 10 15

60

Ile Arg Leu Phe Asp Gln Pro Gly Asp Pro Leu Lys Arg Ser Ser Phe

587

20 25 30

Ile Ile Tyr Asp Ile Met Asn Glu Leu Met Gly Lys Arg Phe Ser Pro
35 40 45

5 Lys Asp Pro Asp Asp Asp Lys Phe Phe Gln Ser Ala Met Ser Ile Cys
50 55 60

10 Ser Ser Leu Arg Asp Leu Glu Leu Ala Tyr Gln Val His Gly Leu Leu
65 70 75 80

Lys Thr Gly Asp Asn Trp Lys Phe Ile Gly Pro Asp Gln His Arg Asn
85 90 95

15 Phe Tyr Tyr Ser Lys Phe Phe Asp Leu Ile Cys Leu Met Glu Gln Ile
100 105 110

Asp Val Thr Leu Lys Trp Tyr Glu Asp Leu Ile Pro Ser Ala Tyr Phe
115 120 125

20 Pro His Ser Gln Thr Met Ile His Leu Leu Gln Ala Leu Asp Val Ala
130 135 140

Asn Arg Leu Glu Val Ile Pro Lys Ile Trp Glu Arg
25 145 150 155

30 (2) INFORMATION FOR SEQ ID NO: 444:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444:

Met His Phe Leu Phe Arg Phe Ile Val Phe Phe Tyr Leu Trp Gly Leu
1 5 10 15

40 Phe Thr Ala Gln Arg Gln Lys Lys Glu Glu Ser Thr Glu Glu Val Lys
20 25 30

Ile Glu Val Leu His Arg Pro Glu Asn Cys Ser Lys Thr Ser Lys Lys
35 40 45

45 Gly Asp Leu Leu Lys Cys Pro Leu Xaa
50 55

50

(2) INFORMATION FOR SEQ ID NO: 445:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 416 amino acids

55

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445:

60 Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro
1 5 10 15

588

Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala Ala Ser Lys
 20 25 30

5 Thr Leu Leu Glu Lys Ser Gln Phe Ser Asp Lys Pro Val Gln Asp Arg
 35 40 45

Gly Leu Val Val Thr Asp Leu Lys Ala Glu Ser Val Val Leu Glu His
 50 55 60

10 Arg Ser Tyr Cys Ser Ala Lys Ala Arg Asp Arg His Phe Ala Gly Asp
 65 70 75 80

15 Val Leu Gly Tyr Val Thr Pro Trp Asn Ser His Gly Tyr Asp Val Thr
 85 90 95

Lys Val Phe Gly Ser Lys Phe Thr Gln Ile Ser Pro Val Trp Leu Gln
 100 105 110

20 Leu Lys Arg Arg Gly Arg Glu Met Phe Glu Val Thr Gly Leu His Asp
 115 120 125

Val Asp Gln Gly Trp Met Arg Ala Val Arg Lys His Ala Lys Gly Leu
 130 135 140

25 His Ile Val Pro Arg Leu Leu Phe Glu Asp Trp Thr Tyr Asp Asp Phe
 145 150 155 160

30 Arg Asn Val Leu Asp Ser Glu Asp Glu Ile Glu Glu Leu Ser Lys Thr
 165 170 175

Val Val Gln Val Ala Lys Asn Gln His Phe Asp Gly Phe Val Val Glu
 180 185 190

35 Val Trp Asn Gln Leu Leu Ser Gln Lys Arg Val Gly Leu Ile His Met
 195 200 205

Leu Thr His Leu Ala Glu Ala Leu His Gln Ala Arg Leu Leu Ala Leu
 210 215 220

40 Leu Val Ile Pro Pro Ala Ile Thr Pro Gly Thr Asp Gln Leu Gly Met
 225 230 235 240

Phe Thr His Lys Glu Phe Glu Gln Leu Ala Pro Val Leu Asp Gly Phe
 245 250 255

45 Ser Leu Met Thr Tyr Asp Tyr Ser Thr Ala His Gln Pro Gly Pro Asn
 260 265 270

50 Ala Pro Leu Ser Trp Val Arg Ala Cys Val Gln Val Leu Asp Pro Lys
 275 280 285

Ser Lys Trp Arg Ser Lys Ile Leu Leu Gly Leu Asn Phe Tyr Gly Met
 290 295 300

55 Asp Tyr Ala Thr Ser Lys Asp Ala Arg Glu Pro Val Val Gly Ala Arg
 305 310 315 320

60 Tyr Ile Gln Thr Leu Lys Asp His Arg Pro Arg Met Val Trp Asp Ser
 325 330 335

589

Gln Xaa Ser Glu His Phe Phe Glu Tyr Lys Lys Ser Arg Ser Gly Arg
 340 345 350

5 His Val Val Phe Tyr Pro Thr Leu Lys Ser Leu Gln Val Arg Leu Glu
 355 360 365

Leu Ala Arg Glu Leu Gly Val Gly Val Ser Ile Trp Glu Leu Ala Arg
 370 375 380

10 Ala Trp Thr Thr Ser Thr Thr Cys Ser Arg Trp Ala Leu Arg Pro Pro
 385 390 395 400

15 Arg Trp Thr Cys Ser Phe Leu Ser His Gly Val Ser Glu Gln Val Xaa
 405 410 415

20

(2) INFORMATION FOR SEQ ID NO: 446:

(i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 64 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

30 Met Ala Pro Gly Pro Leu Ser Ala Thr Gln Ala Val Val Ile His Thr
 1 5 10 15

Thr His Cys Leu Gln Leu Pro Val Trp Cys Leu Ser Leu Val Ser Glu
 20 25 30

35 Leu Leu Gly Arg Ala Pro Pro His Asn Lys Asp Ala Leu Arg Pro Ser
 35 40 45

40 Lys Lys Lys Lys Lys Lys Leu Xaa Gly Gly Pro Val Pro Ile Pro Pro
 50 55 60

45

(2) INFORMATION FOR SEQ ID NO: 447:

(i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 206 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447:

55 Met Leu Gly Ala Lys Pro His Trp Leu Pro Gly Pro Leu His Ser Pro
 1 5 10 15

Gly Leu Pro Leu Val Leu Val Leu Leu Ala Leu Gly Ala Gly Trp Ala
 20 25 30

60

590

Gln Glu Gly Ser Glu Pro Val Leu Leu Glu Gly Glu Cys Leu Val Val
 35 40 45
 Cys Glu Pro Gly Arg Ala Ala Ala Gly Gly Pro Gly Gly Ala Ala Leu
 5 50 55 60
 Gly Glu Ala Pro Pro Gly Arg Val Ala Phe Ala Ala Val Arg Ser Xaa
 65 70 75 80
 10 His His Glu Pro Ala Gly Glu Thr Gly Asn Gly Thr Xaa Gly Ala Ile
 85 90 95
 Tyr Phe Asp Gln Val Leu Val Asn Glu Gly Gly Gly Phe Asp Arg Ala
 100 105 110
 15 Ser Gly Ser Phe Val Ala Pro Val Arg Gly Val Tyr Ser Phe Arg Phe
 115 120 125
 His Val Val Lys Val Tyr Asn Arg Gln Thr Val Gln Val Ser Leu Met
 20 130 135 140
 Leu Asn Thr Trp Pro Val Ile Ser Ala Phe Ala Asn Asp Pro Asp Val
 145 150 155 160
 25 Thr Arg Glu Ala Ala Thr Ser Ser Val Leu Leu Pro Leu Asp Pro Gly
 165 170 175
 Asp Arg Val Ser Leu Arg Leu Arg Arg Gly Asn Leu Leu Gly Gly Trp
 180 185 190
 30 Lys Tyr Ser Ser Phe Ser Gly Phe Leu Ile Phe Pro Leu Xaa
 195 200 205

35

(2) INFORMATION FOR SEQ ID NO: 448:

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 62 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448:

45

Met Ser Ser Leu Leu Ser Ala Gly Leu Gln Ala Ser Leu Cys Gly Lys
 1 5 10 15

Xaa Leu Trp Ala Ser Thr Trp Tyr Leu Val Cys Cys Leu Leu Pro Phe
 20 25 30

50

Phe His Gln Gly Cys Cys Asp His Lys Ser Lys Gln Gln Tyr Ile Pro
 35 40 45

Asn Leu Lys Ser Tyr Cys Gly Leu Ser Thr Ile Glu Ile Xaa
 50 55 60

55

(2) INFORMATION FOR SEQ ID NO: 449:

60

(i) SEQUENCE CHARACTERISTICS:

591

(A) LENGTH: 316 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449:

5

Met Ser Thr Lys Lys Leu Cys Ile Val Gly Gly Ile Leu Leu Val Phe
 1 5 10 15

10

Gln Ile Ile Ala Phe Leu Val Gly Gly Leu Ile Ala Pro Gly Pro Thr
 20 25 30

Thr Ala Val Ser Tyr Met Ser Val Lys Cys Val Asp Ala Arg Lys Asn
 35 40 45

15

His His Lys Thr Lys Trp Phe Val Pro Trp Gly Pro Asn His Cys Asp
 50 55 60

Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu Ile Glu Ala Asn
 65 70 75 80

20

Asp Ile Val Phe Ser Val His Ile Pro Leu Pro His Met Glu Met Ser
 85 90 95

25

Pro Trp Phe Gln Phe Met Xaa Phe Ile Leu Gln Leu Asp Ile Ala Phe
 100 105 110

Lys Leu Asn Asn Gln Ile Arg Glu Asn Ala Glu Val Ser Met Asp Val
 115 120 125

30

Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp Thr Glu Met Ala
 130 135 140

His Glu Arg Val Pro Arg Lys Leu Lys Cys Thr Phe Thr Ser Pro Lys
 145 150 155 160

35

Thr Pro Glu His Gly Gly Pro Val Thr Met Asn Val Met Ser Phe Leu
 165 170 175

40

Ser Trp Lys Leu Gly Leu Trp Pro Met Lys Phe Tyr Leu Leu Asn Ile
 180 185 190

Arg Leu Pro Val Asn Glu Lys Lys Lys Ile Asn Val Gly Ile Gly Glu
 195 200 205

45

Ile Lys Asp Ile Arg Leu Val Gly Ile His Gln Asn Gly Gly Phe Thr
 210 215 220

Lys Val Trp Phe Ala Met Lys Thr Phe Leu Thr Pro Ser Ile Phe Ile
 225 230 235 240

50

Ile Met Val Trp Tyr Trp Arg Arg Ile Thr Met Met Ser Arg Pro Pro
 245 250 255

55

Val Leu Leu Glu Lys Val Ile Phe Ala Leu Gly Ile Ser Met Thr Phe
 260 265 270

Ile Asn Ile Pro Val Glu Trp Phe Ser Ile Gly Phe Asp Trp Thr Trp
 275 280 285

60

Met Leu Leu Phe Gly Asp Ile Arg Gln Ala Ser Ser Met Xaa Cys Phe

290 295 300

Xaa Pro Ser Gly Ser Ser Ser Val Ala Ser Thr Xaa
305 310 315

5

(2) INFORMATION FOR SEQ ID NO: 450:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450:

15 Met Leu Ala Leu Leu Gly Leu Leu Ala Gly Thr Glu His Pro Pro Gly
1 5 10 15

Pro Gln Gly Pro Gly Pro Ser Xaa
20 20

(2) INFORMATION FOR SEQ ID NO: 451:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451:

30 Met Pro Ser Gly Ala Cys Cys Ser Pro Xaa
1 5 10

35 (2) INFORMATION FOR SEQ ID NO: 452:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452:

45 Met Leu Pro Ala Leu Ser Thr Val Leu Leu Pro Thr Pro Ser Leu Cys
1 5 10 15

Ser Gly Asn Pro Arg Glu Gly Trp Ala Xaa
20 25

50 (2) INFORMATION FOR SEQ ID NO: 453:

55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 172 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 453:

60

593

Met Tyr Ser Leu His Ser Trp Val Gly Leu Ile Ala Val Ile Cys Tyr
 1 5 10 15

Leu Leu Gln Leu Leu Ser Gly Phe Ser Val Phe Leu Leu Pro Trp Ala
 5 20 25 30

Pro Leu Ser Leu Arg Ala Phe Leu Met Pro Ile His Val Tyr Ser Gly
 35 40 45

Ile Val Ile Phe Gly Thr Val Ile Ala Thr Ala Leu Met Gly Leu Thr
 10 50 55 60

Glu Lys Leu Ile Phe Ser Leu Arg Asp Pro Ala Tyr Ser Thr Phe Pro
 65 70 75 80

Pro Glu Gly Val Phe Val Asn Thr Leu Gly Leu Leu Ile Leu Val Phe
 15 85 90 95

Gly Ala Leu Ile Phe Trp Ile Val Thr Arg Pro Gln Trp Lys Arg Pro
 20 100 105 110

Lys Glu Pro Asn Ser Thr Ile Leu His Pro Asn Gly Gly Thr Glu Gln
 115 120 125

Gly Ala Arg Gly Ser Met Pro Ala Tyr Ser Gly Asn Asn Met Asp Lys
 25 130 135 140

Ser Asp Ser Glu Leu Asn Xaa Glu Val Ala Ala Arg Lys Arg Asn Leu
 145 150 155 160

Ala Leu Asp Glu Ala Gly Gln Arg Ser Thr Met Xaa
 30 165 170

35

(2) INFORMATION FOR SEQ ID NO: 454:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

40

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 454:

Met Phe His Val Leu Met Ala Gln Val Thr Xaa Val Ile Ile Thr Thr
 45 1 5 10 15

Val Ser Val Leu Val Phe Asp Phe Arg Pro Ser Leu Glu Phe Phe Leu
 20 25 30

Glu Ala Xaa Ser Val Xaa Leu Ser Ile Phe Ile Tyr Asn Ala Ser Lys
 35 40 45

Pro Gln Val Pro Glu Tyr Ala Pro Arg Gln Glu Arg Ile Arg Asp Leu
 50 55 60

Ser Gly Asn Leu Trp Glu Arg Ser Ser Gly Asp Gly Glu Glu Leu Glu
 55 65 70 75 80

Arg Leu Thr Lys Pro Lys Ser Asp Glu Ser Asp Glu Asp Thr Phe Xaa
 60 85 90 95

5

(2) INFORMATION FOR SEQ ID NO: 455:

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 455:

15 Met Arg Gly Pro Ala Gln Ala Lys Leu Leu Pro Gly Ser Ala Ile Gln
1 5 10 15

Ala Leu Val Gly Leu Ala Arg Pro Leu Val Leu Ala Leu Leu Val
20 25 30

Ser Ala Ala Leu Ser Ser Val Val Ser Arg Thr Asp Ser Pro Ser Pro
35 40 45

Thr Val Leu Asn Ser His Ile Ser Thr Pro Asn Val Asn Ala Leu Thr
25 50 55 60

His Glu Asn Gln Thr Lys Pro Ser Ile Ser Gln Ile Ser Thr Thr Leu
65 70 75 80

30 Pro Pro Thr Thr Ser Thr Lys Lys Ser Gly Gly Ala Ser Val Val Pro
85 90 95

His Pro Ser Pro Thr Pro Leu Ser Gln Glu Glu Ala Asp Asn Asn Glu
100 105 110

35 Asp Pro Ser Ile Glu Glu Glu Asp Leu Leu Met Leu Asn Ser Ser Pro
115 120 125

Ser Thr Ala Lys Asp Thr Leu Asp Asn Gly Asp Tyr Gly Glu Pro Asp
40 130 135 140

Tyr Asp Trp Thr Thr Gly Pro Arg Asp Asp Asp Glu Ser Asp Xaa His
145 150 155 160

45 Leu Gly Arg Lys Gln Gly Leu His Gly Asn Xaa
165 170

50 (2) INFORMATION FOR SEQ ID NO: 456:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 456:

55 Met Lys Ala Ser Gln Cys Cys Cys Cys Leu Ser His Leu Leu Ala Ser.
1 5 10 15

60

595

Val Leu Leu Leu Leu Leu Leu Pro Glu Leu Ser Gly Xaa Leu Xaa Val
 20 25 30

5 Leu Leu Gln Ala Ala Glu Ala Ala Pro Gly Xaa Gly Pro Pro Asp Pro
 35 40 45

Arg Pro Gly His Tyr Arg Arg Cys His Arg Ala Leu Thr Pro Ala Gln
 50 55 60

10 Gln Pro Gly Arg Gly Leu Ala Glu Ala Ala Gly Ala Ala Gly Leu Arg
 65 70 75 80

Gly Arg Gln Trp Gln Gln Pro Cys Gly Arg Ala Xaa
 85 90

15

(2) INFORMATION FOR SEQ ID NO: 457:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 206 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 457:

Ile Ser Val Leu Xaa Tyr Pro His Cys Val Val His Glu Leu Pro Glu
 1 5 10 15

30 Leu Thr Ala Glu Ser Leu Glu Ala Gly Asp Ser Asn Gln Phe Cys Trp
 20 25 30

Arg Asn Leu Phe Ser Cys Ile Asn Leu Leu Arg Ile Leu Asn Lys Leu
 35 40 45

35 Thr Lys Trp Lys His Ser Arg Thr Met Met Leu Val Val Phe Lys Ser
 50 55 60

Ala Pro Ile Leu Lys Arg Ala Leu Lys Val Lys Gln Ala Met Met Gln
 65 70 75 80

40 Leu Tyr Val Leu Lys Leu Leu Lys Val Gln Thr Lys Tyr Leu Gly Arg
 85 90 95

Gln Trp Arg Lys Ser Asn Met Lys Thr Met Ser Ala Ile Tyr Gln Lys
 100 105 110

45 Val Arg His Arg Leu Asn Asp Asp Trp Ala Tyr Gly Asn Asp Leu Asp
 115 120 125

50 Ala Arg Pro Trp Asp Phe Gln Ala Glu Glu Cys Ala Leu Arg Ala Asn
 130 135 140

Ile Glu Arg Phe Asn Ala Arg Arg Tyr Asp Arg Ala His Ser Asn Pro
 145 150 155 160

55 Asp Phe Leu Pro Val Asp Asn Cys Leu Gln Ser Val Leu Gly Gln Arg
 165 170 175

60 Val Asp Leu Pro Glu Asp Phe Gln Met Asn Tyr Asp Leu Trp Leu Glu
 180 185 190

596

Arg Glu Val Phe Ser Lys Pro Ile Ser Trp Glu Glu Leu Leu
 195 200 205

5

(2) INFORMATION FOR SEQ ID NO: 458:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 317 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 458:

15 Met Ala Pro Pro Ala Pro Gly Pro Ala Ser Gly Gly Ser Gly Glu Val
 1 5 10 15

Asp Glu Leu Phe Asp Val Lys Asn Ala Phe Tyr Ile Gly Ser Tyr Gln
 20 25 30

20 Gln Cys Ile Asn Glu Ala Xaa Xaa Val Lys Leu Ser Ser Pro Glu Arg
 35 40 45

25 Asp Val Glu Arg Asp Val Phe Leu Tyr Arg Ala Tyr Leu Ala Gln Arg
 50 55 60

Lys Phe Gly Val Val Leu Asp Glu Ile Lys Pro Ser Ser Ala Pro Glu
 65 70 75 80

30 Leu Gln Ala Val Arg Met Phe Ala Asp Tyr Leu Ala His Glu Ser Arg
 85 90 95

Arg Asp Ser Ile Val Ala Glu Leu Asp Arg Glu Met Ser Arg Ser Xaa
 100 105 110

35 Asp Val Thr Asn Thr Thr Phe Leu Leu Met Ala Ala Ser Ile Tyr Leu
 115 120 125

His Asp Gln Asn Pro Asp Ala Ala Leu Arg Ala Leu His Gln Gly Asp
 130 135 140

Ser Leu Glu Cys Thr Ala Met Thr Val Gln Ile Leu Leu Lys Leu Asp
 145 150 155 160

45 Arg Leu Asp Leu Ala Arg Lys Glu Leu Lys Arg Met Gln Asp Leu Asp
 165 170 175

Glu Asp Ala Thr Leu Thr Gln Leu Ala Thr Ala Trp Val Ser Leu Ala
 180 185 190

50 Thr Gly Gly Glu Lys Leu Gln Asp Ala Tyr Tyr Ile Phe Gln Glu Met
 195 200 205

Ala Asp Lys Cys Ser Pro Thr Leu Leu Leu Leu Asn Gly Gln Ala Ala
 210 215 220

55 Cys His Met Ala Gln Gly Arg Trp Glu Ala Ala Glu Gly Leu Leu Gln
 225 230 235 240

60 Glu Ala Leu Asp Lys Asp Ser Gly Tyr Pro Glu Thr Leu Val Asn Leu

597

245 250 255
 Ile Val Leu Ser Gln His Leu Gly Lys Pro Pro Glu Val Thr Asn Arg
 260 265 270
 5 Tyr Leu Ser Gln Leu Lys Asp Ala His Arg Ser His Pro Phe Ile Lys
 275 280 285
 10 Glu Tyr Gln Ala Lys Glu Asn Asp Phe Asp Arg Leu Val Leu Gln Tyr
 290 295 300
 Ala Pro Ser Ala Glu Ala Gly Pro Glu Leu Ser Gly Pro
 305 310 315
 15
 (2) INFORMATION FOR SEQ ID NO: 459:
 (i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 261 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459:
 25 Arg Asp Val Glu Arg Asp Val Phe Leu Tyr Arg Ala Tyr Leu Ala Gln
 1 5 10 15
 Arg Lys Phe Gly Val Val Leu Asp Glu Ile Lys Pro Ser Ser Ala Pro
 20 25 30
 30 Glu Leu Gln Ala Val Arg Met Phe Ala Asp Tyr Leu Ala His Glu Ser
 35 40 45
 Arg Arg Asp Ser Ile Val Ala Glu Leu Asp Arg Glu Met Ser Arg Ser
 35 50 55 60
 Xaa Asp Val Thr Asn Thr Thr Phe Leu Leu Met Ala Ala Ser Ile Tyr
 65 70 75 80
 40 Leu His Asp Gln Asn Pro Asp Ala Ala Leu Arg Ala Leu His Gln Gly
 85 90 95
 Asp Ser Leu Glu Cys Thr Ala Met Thr Val Gln Ile Leu Leu Lys Leu
 100 105 110
 45 Asp Arg Leu Asp Leu Ala Arg Lys Glu Leu Lys Arg Met Gln Asp Leu
 115 120 125
 Asp Glu Asp Ala Thr Leu Thr Gln Leu Ala Thr Ala Trp Val Ser Leu
 50 130 135 140
 Ala Thr Gly Gly Glu Lys Leu Gln Asp Ala Tyr Tyr Ile Phe Gln Glu
 145 150 155 160
 55 Met Ala Asp Lys Cys Ser Pro Thr Leu Leu Leu Leu Asn Gly Gln Ala
 165 170 175
 Ala Cys His Met Ala Gln Gly Arg Trp Glu Ala Ala Glu Gly Leu Leu
 180 185 190
 60

598

Gln Glu Ala Leu Asp Lys Asp Ser Gly Tyr Pro Glu Thr Leu Val Asn
 195 200 205

Leu Ile Val Leu Ser Gln His Leu Gly Lys Pro Pro Glu Val Thr Asn
 5 210 215 220

Arg Tyr Leu Ser Gln Leu Lys Asp Ala His Arg Ser His Pro Phe Ile
 225 230 235 240

10 Lys Glu Tyr Gln Ala Lys Glu Asn Asp Phe Asp Arg Leu Val Leu Gln
 245 250 255

Tyr Ala Pro Ser Ala
 15 260

(2) INFORMATION FOR SEQ ID NO: 460:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 156 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 460:

25 Met Lys Ala Ile Gly Ile Glu Pro Ser Leu Ala Thr Tyr His His Ile
 1 5 10 15

Ile Arg Leu Phe Asp Gln Pro Gly Asp Pro Leu Lys Arg Ser Ser Phe
 30 20 25 30

Ile Ile Tyr Asp Ile Met Asn Glu Leu Met Gly Lys Arg Phe Ser Pro
 35 35 40 45

35 Lys Asp Pro Asp Asp Asp Lys Phe Phe Gln Ser Ala Met Ser Ile Cys
 50 55 60

Ser Ser Leu Arg Asp Leu Glu Leu Ala Tyr Gln Val His Gly Leu Leu
 40 65 70 75 80

Lys Thr Gly Asp Asn Trp Lys Phe Ile Gly Pro Asp Gln His Arg Asn
 85 90 95

Phe Tyr Tyr Ser Lys Phe Phe Asp Leu Ile Cys Leu Met Glu Gln Ile
 45 100 105 110

Asp Val Thr Leu Lys Trp Tyr Glu Asp Leu Ile Pro Ser Ala Tyr Phe
 115 120 125

50 Pro His Ser Gln Thr Met Ile His Leu Leu Gln Ala Leu Asp Val Ala
 130 135 140

Asn Arg Leu Glu Val Ile Pro Lys Ile Trp Glu Arg
 145 150 155

55

(2) INFORMATION FOR SEQ ID NO: 461:

60 (i) SEQUENCE CHARACTERISTICS:

599

(A) LENGTH: 176 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 461:

5
 Lys Asp Ser Lys Glu Tyr Gly His Thr Phe Arg Ser Asp Leu Arg Glu
 1 5 10 15
 10
 Glu Ile Leu Met Leu Met Ala Arg Asp Lys His Pro Pro Glu Leu Gln
 20 25 30
 Val Ala Phe Ala Asp Cys Ala Ala Asp Ile Lys Ser Ala Tyr Glu Ser
 35 40 45
 15
 Gln Pro Ile Arg Gln Thr Ala Gln Asp Trp Pro Ala Thr Ser Leu Asn
 50 55 60
 Cys Ile Ala Ile Leu Phe Leu Arg Ala Gly Arg Thr Gln Glu Ala Trp
 65 70 75 80
 20
 Lys Met Leu Gly Leu Phe Arg Lys His Asn Lys Ile Pro Arg Ser Glu
 85 90 95
 Leu Leu Asn Glu Leu Met Asp Ser Ala Lys Val Ser Asn Ser Pro Ser
 100 105 110
 25
 Gln Ala Ile Glu Val Val Glu Leu Ala Ser Ala Phe Ser Leu Pro Ile
 115 120 125
 30
 Cys Glu Gly Leu Thr Gln Arg Val Met Ser Asp Phe Ala Ile Asn Gln
 130 135 140
 Glu Gln Lys Glu Ala Leu Ser Asn Leu Thr Ala Leu Thr Ser Asp Ser
 145 150 155 160
 35
 Asp Thr Asp Ser Ser Ser Asp Ser Asp Ser Asp Thr Ser Glu Gly Lys
 165 170 175

40

(2) INFORMATION FOR SEQ ID NO: 462:

45

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 324 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 462:

Met Ser Ser Asp Asn Glu Ser Asp Ile Glu Asp Glu Asp Leu Lys Leu
 1 5 10 15
 55
 Glu Leu Arg Arg Leu Arg Asp Lys His Leu Lys Glu Ile Gln Asp Leu
 20 25 30
 Gln Ser Arg Gln Lys His Glu Ile Glu Ser Leu Tyr Thr Lys Leu Gly
 35 40 45
 60

600

Lys Val Pro Pro Ala Val Ile Ile Pro Pro Ala Ala Pro Leu Ser Gly
 50 55 60
 5 Arg Arg Arg Arg Pro Thr Lys Ser Lys Gly Ser Lys Ser Ser Arg Ser
 65 70 75 80
 Ser Ser Leu Gly Asn Lys Ser Pro Gln Leu Ser Gly Asn Leu Ser Gly
 85 90 95
 10 Gln Ser Ala Ala Ser Val Leu His Pro Gln Gln Thr Leu His Pro Pro
 100 105 110
 Gly Asn Ile Pro Glu Ser Gly Gln Asn Gln Leu Leu Gln Pro Leu Lys
 115 120 125
 15 Pro Ser Pro Ser Ser Asp Asn Leu Tyr Ser Ala Phe Thr Ser Asp Gly
 130 135 140
 20 Ala Ile Ser Val Pro Ser Leu Ser Ala Pro Gly Gln Gly Thr Ser Ser
 145 150 155 160
 Thr Asn Thr Val Gly Ala Thr Val Asn Ser Gln Ala Ala Gln Ala Gln
 165 170 175
 25 Pro Pro Ala Met Thr Ser Ser Arg Lys Gly Thr Phe Thr Asp Asp Leu
 180 185 190
 His Lys Leu Val Asp Asn Trp Ala Arg Asp Ala Met Asn Leu Ser Gly
 195 200 205
 30 Arg Arg Gly Ser Lys Gly His Met Asn Tyr Glu Gly Pro Gly Met Ala
 210 215 220
 35 Arg Lys Phe Ser Ala Pro Gly Gln Leu Cys Ile Ser Met Thr Ser Asn
 225 230 235 240
 Leu Gly Gly Ser Ala Pro Ile Ser Ala Ala Ser Ala Thr Ser Leu Gly
 245 250 255
 40 His Phe Thr Lys Ser Met Cys Pro Pro Gln Gln Tyr Gly Phe Pro Ala
 260 265 270
 Thr Pro Phe Gly Ala Gln Trp Ser Gly Thr Gly Gly Pro Ala Pro Gln
 275 280 285
 45 Pro Leu Gly Gln Phe Gln Pro Val Gly Thr Ala Ser Leu Gln Asn Phe
 290 295 300
 50 Asn Ile Ser Asn Leu Gln Lys Ser Ile Ser Asn Pro Pro Gly Ser Asn
 305 310 315 320
 Leu Arg Thr Thr

55

(2) INFORMATION FOR SEQ ID NO: 463:

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 133 amino acids

601

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463:

5 Ile Gln Asp Leu Gln Ser Arg Gln Lys His Glu Ile Glu Ser Leu Tyr
 1 5 10 15
 Thr Lys Leu Gly Lys Val Pro Pro Ala Val Ile Ile Pro Pro Ala Ala
 20 25 30
 10 Pro Leu Ser Gly Arg Arg Arg Arg Pro Thr Lys Ser Lys Gly Ser Lys
 35 40 45
 Ser Ser Arg Ser Ser Ser Leu Gly Asn Lys Ser Pro Gln Leu Ser Gly
 15 50 55 60
 Asn Leu Ser Gly Gln Ser Ala Ala Ser Val Leu His Pro Gln Gln Thr
 65 70 75 80
 20 Leu His Pro Pro Gly Asn Ile Pro Glu Ser Gly Gln Asn Gln Leu Leu
 85 90 95
 Gln Pro Leu Lys Pro Ser Pro Ser Ser Asp Asn Leu Tyr Ser Ala Phe
 100 105 110
 25 Thr Ser Asp Gly Ala Ile Ser Val Pro Ser Leu Ser Ala Pro Gly Gln
 115 120 125
 Gly Thr Ser Ser Thr
 30 130

(2) INFORMATION FOR SEQ ID NO: 464:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464:

Thr Ser Asp Gly Ala Ile Ser Val Pro Ser Leu Ser Ala Pro Gly Gln
 1 5 10 15
 45 Gly Thr Ser Ser Thr Asn Thr Val Gly Ala Thr Val Asn Ser Gln Ala
 20 25 30
 Ala Gln Ala Gln Pro Pro Ala Met Thr Ser Ser Arg Lys Gly Thr Phe
 35 40 45
 50 Thr Asp Asp Leu His
 50

55

(2) INFORMATION FOR SEQ ID NO: 465:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 amino acids

60

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 465:

5 Lys Gly His Met Asn Tyr Glu Gly Pro Gly Met Ala Arg Lys Phe Ser
1 5 10 15

Ala Pro Gly Gln Leu Cys Ile Ser Met Thr Ser Asn Leu Gly Gly Ser
20 25 30

10 Ala Pro Ile Ser Ala Ala Ser Ala Thr Ser Leu Gly His Phe Thr Lys
35 40 45

15

(2) INFORMATION FOR SEQ ID NO: 466:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466:

25 Gln Pro Leu Lys Pro Ser Pro Ser Ser Asp Asn Leu Tyr Ser Ala Phe
 1 5 10 15

30 Thr Ser Asp Gly Ala Ile Ser Val Pro Ser Leu Ser Ala Pro Gly
 20 25 30

(2) INFORMATION FOR SEQ ID NO: 467:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 467:

Val Arg Val Ala Ala Glu Ser Met Xaa Leu Leu Leu Glu Cys Ala
1 5 10 15

45 Xaa Val Arg Gly Pro Glu Tyr Leu Thr Gln Met Trp His Phe Met Cys
20 25 30

Asp Ala Leu Ile Lys Ala Ile Gly Thr Glu Pro Asp Ser Asp Val Leu
35 40 45

50 Ser Glu Ile Met His Ser Phe Ala Lys
50 55

55

(2) INFORMATION FOR SEQ ID NO: 468:

60 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid

603

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 468:

5 Met Glu Ile Asn Asn Gln Asn Cys Phe Ile Val Ile Asp Leu Val Arg
1 5 10 15

Thr Val Met Glu Asn Gly Val Glu Gly Leu Leu Ile Phe Gly Ala Phe
20 25 30

10 Leu Pro Glu Ser Trp Leu Ile Gly Val Arg Cys Ser Ser Glu Pro Pro
35 40 45

Lys Ala Leu Leu Leu Ile Leu Ala His Ser Gln Lys Arg Arg Leu Asp
50 55 60

15 Gly Trp Ser Phe Ile Arg His Leu Arg Val His Tyr Cys Val Ser Leu
65 70 75 80

20 Thr Ile His Phe Ser
85

(2) INFORMATION FOR SEQ ID NO: 469:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469:

Gln Asp Lys His Ala Glu Glu Val Arg Lys Asn Lys Glu Leu Lys Glu
1 5 10 15

35 Glu Ala Ser Arg
20

40 (2) INFORMATION FOR SEQ ID NO: 470:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470:

Gln Gln Asp Leu Ser Pro Trp Ala Ala Pro Val Gly Cys Pro Leu Xaa
1 5 10 15

50 Xaa Ala Ser Xaa Thr Cys His Xaa Leu Pro Leu Ser Gly Cys Leu Arg
20 25 30

Arg Gln Ser Xaa Ser Leu Pro Val Val Ala Xaa Leu Cys Phe Trp Phe
35 40 45

55 Ser Cys Pro Leu Ala Ser Leu Phe Val Pro Gly Gln Pro Cys Val Thr
50 55 60

60 Cys Pro Phe Pro Ser Leu Pro Phe Gln Asp Lys His Ala Glu Glu Val

604

65 70 75 80
 Arg Lys Asn Lys Glu Leu Lys Glu Glu Ala Ser Arg
 35 90

5

(2) INFORMATION FOR SEQ ID NO: 471:

10

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 471:

15

Pro Thr Arg Cys Cys Thr Thr Gln Pro Cys Arg Ser Ser Ala Arg Arg
 1 5 10 15

20

Pro Cys Trp Val Pro Met Val Pro Ser Pro Glu Gly Arg Glu Xaa Gln
 20 25 30

Pro Thr Cys Pro Ser
 35

25

(2) INFORMATION FOR SEQ ID NO: 472:

30

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 472:

35

Met Lys Arg Ser Leu Asn Glu Asn Ser Ala Arg Ser Thr Ala Gly Cys
 1 5 10 15

40

Leu Pro Val Pro Leu Phe Asn Gln Lys Lys Arg Asn Arg Gln Pro Leu
 20 25 30

Thr Ser Asn Pro Leu Lys Asp Asp Ser Gly Ile Ser Thr Pro Ser Asp
 35 40 45

45

Asn Tyr Asp Phe Pro Pro Leu Pro Thr Asp Trp Ala Trp Glu Ala Val
 50 55 60

Asn Pro Glu Xaa Ala Pro Val Met Lys Thr Val Asp Thr Gly Gln Ile
 65 70 75 80

50

Pro His Ser Val Ser Arg Pro Leu Arg Ser Gln Asp Ser Val Phe Asn
 85 90 95

Ser Ile Gln Ser Asn Thr Gly Arg Ser Gln Gly Gly Trp Ser Tyr Arg
 100 105 110

55

Asp Gly Asn Lys Asn Thr Ser Leu Lys Thr Trp Xaa Lys Asn Asp Phe
 115 120 125

60

Lys Pro Gln Cys Lys Arg Thr Asn Leu Val Ala Asn Asp Gly Lys Asn
 130 135 140

605

Ser Cys Pro Met Ser Ser Gly Ala Gln Gln Gln Lys Gln Leu Arg Thr
 145 150 155 160

5 Pro Glu Pro Pro Asn Leu Ser Arg Asn Lys Glu Thr Glu Leu Leu Arg
 165 170 175

Gln Thr His Ser Ser Lys Ile Ser Gly Cys Thr Met Arg Gly Leu Asp
 180 185 190

10 Lys Asn Ser Ala Leu Gln Thr Leu Lys Pro Asn Phe Gln Gln Asn Gln
 195 200 205

Tyr Lys Xaa Gln Met Leu Asp Asp Ile Pro Glu Asp Asn Thr Leu Lys
 210 215 220

15 Glu Thr Ser Leu Tyr Gln Leu Gln Phe Lys Glu Lys Ala Ser Ser Leu
 225 230 235 240

20 Arg Ile Ile Ser Ala Val Ile Glu Ser Met Lys Tyr Trp Arg Glu His
 245 250 255

Ala Gln Lys Thr Val Leu Leu Phe Glu Val Leu Ala Val Leu Asp Ser
 260 265 270

25 Ala Val Thr Pro Gly Pro Tyr Tyr Ser Lys Thr Phe Leu Met Arg Asp
 275 280 285

Gly Lys Asn Thr Leu Pro Cys Val Phe Tyr Glu Ile Asp Arg Glu Leu
 290 295 300

30 Pro Arg Leu Ile Arg Gly Arg Val His Arg Cys Val Gly Asn Tyr Asp
 305 310 315 320

35 Gln Lys Lys Asn Ile Phe Gln Cys Val Ser Val Arg Pro Ala Ser Val
 325 330 335

Ser Glu Gln Lys Thr Phe Gln Ala Phe Val Lys Ile Ala Asp Val Glu
 340 345 350

40 Met Gln Tyr Tyr Ile Asn Val Met Asn Glu Thr
 355 360

45 (2) INFORMATION FOR SEQ ID NO: 473:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 45 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473:

Ser Gln Asp Ser Val Phe Asn Ser Ile Gln Ser Asn Thr Gly Arg Ser
 1 5 10 15

Gln Gly Gly Trp Ser Tyr Arg Asp Gly Asn Lys Asn Thr Ser Leu Lys
 20 25 30

60 Thr Trp Xaa Lys Asn Asp Phe Lys Pro Gln Cys Lys Arg

35

40

45

5 (2) INFORMATION FOR SEQ ID NO: 474:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 474:

Asn Lys Glu Thr Glu Leu Leu Arg Gln Thr His Ser Ser Lys Ile Ser
1 5 10 15

15

Gly Cys Thr Met Arg Gly Leu Asp Lys Asn Ser Ala Leu Gln Thr Leu
20 25 30

20

Lys Pro Asn Phe
35

25

(2) INFORMATION FOR SEQ ID NO: 475:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475:

Ser Ser Leu Arg Ile Ile Ser Ala Val Ile Glu Ser Met Lys Tyr Trp
1 5 10 15

35

Arg Glu His Ala Gln Lys Thr Val Leu Leu Phe Glu Val Leu Ala Val
20 25 30

Leu Asp Ser Ala Val Thr Pro Gly Pro Tyr Tyr Ser Lys Thr Phe Leu
35 40 45

40

Met

45

(2) INFORMATION FOR SEQ ID NO: 476:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

50 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476:

Pro Arg Leu Ile Arg Gly Arg Val His Arg Cys Val Gly Asn Tyr Asp
1 5 10 15

55

Gln Lys Lys Asn Ile Phe Gln Cys Val Ser Val Arg Pro Ala Ser Val
20 25 30

60

Ser Glu Gln Lys Thr Phe Gln Ala Phe Val

607

35

40

5 (2) INFORMATION FOR SEQ ID NO: 477:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 370 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 477:

Gly Val Phe Arg Pro Cys Val Cys Gly Arg Pro Ala Ser Leu Thr Cys
 1 5 10 15
 Ser Pro Leu Asp Pro Glu Val Gly Pro Tyr Cys Asp Thr Pro Thr Met
 20 25 30
 Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro Val
 35 40 45
 His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala Ala Ser Lys Thr
 50 55 60
 Leu Leu Glu Lys Ser Gln Phe Ser Asp Lys Pro Val Gln Asp Arg Gly
 65 70 75 80
 Leu Val Val Thr Asp Leu Lys Ala Glu Ser Val Val Leu Glu His Arg
 85 90 95
 Ser Tyr Cys Ser Ala Lys Ala Arg Asp Arg His Phe Ala Gly Asp Val
 100 105 110
 Leu Gly Tyr Val Thr Pro Trp Asn Ser His Gly Tyr Asp Val Thr Lys
 115 120 125
 Val Phe Gly Ser Lys Phe Thr Gln Ile Ser Pro Val Trp Leu Gln Leu
 130 135 140
 Lys Arg Arg Gly Arg Glu Met Phe Glu Val Thr Gly Leu His Asp Val
 145 150 155 160
 Asp Gln Gly Trp Met Arg Ala Val Arg Lys His Ala Lys Gly Leu His
 165 170 175
 Ile Val Pro Arg Leu Leu Phe Glu Asp Trp Thr Tyr Asp Asp Phe Arg
 180 185 190
 Asn Val Leu Asp Ser Glu Asp Glu Ile Glu Glu Leu Ser Lys Thr Val
 195 200 205
 Val Gln Val Ala Lys Asn Gln His Phe Asp Gly Phe Val Val Glu Val
 210 215 220
 Trp Asn Gln Leu Leu Ser Gln Lys Arg Val Gly Leu Ile His Met Leu
 225 230 235 240
 Thr His Leu Ala Glu Ala Leu His Gln Ala Arg Leu Leu Ala Leu Leu
 245 250 255

60

608

Val Ile Pro Pro Ala Ile Thr Pro Gly Thr Asp Gln Leu Gly Met Phe
 260 265 270

5 Thr His Lys Glu Phe Glu Gln Leu Ala Pro Val Leu Asp Gly Phe Ser
 275 280 285

Leu Met Thr Tyr Asp Tyr Ser Thr Ala His Gln Pro Gly Pro Asn Ala
 290 295 300

10 Pro Leu Ser Trp Val Arg Ala Cys Val Gln Val Leu Asp Pro Lys Xaa
 305 310 315 320

Lys Trp Arg Thr Lys Ser Ser Trp Gly Ser Thr Ser Met Xaa Trp Thr
 325 330 335

15 Xaa Arg Xaa Pro Xaa Asp Ala Arg Xaa Pro Val Val Gly Xaa Arg Xaa
 340 345 350

Ile Gln Xaa Leu Lys Asp His Xaa Pro Arg Met Val Leu Asp Ser Lys
 355 360 365

20 Pro Gln
 370

25

(2) INFORMATION FOR SEQ ID NO: 478:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478:

35 Thr Cys Ser Pro Leu Asp Pro Glu Val Gly Pro Tyr Cys Asp Thr Pro
 1 5 10 15

Thr Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser
 20 25 30

40 Pro Val His Thr Thr Leu Ser
 35

45

(2) INFORMATION FOR SEQ ID NO: 479:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479:

55 Leu Val Val Thr Asp Leu Lys Ala Glu Ser Val Val Leu Glu His Arg
 1 5 10 15

Ser Tyr Cys Ser Ala Lys Ala Arg Asp Arg His Phe Ala Gly Asp Val
 20 25 30

60 Leu Gly Tyr Val Thr Pro Trp Asn Ser His Gly Tyr Asp Val Thr Lys

35 40 45

Val Phe Gly Ser Lys Phe
50

5

(2) INFORMATION FOR SEQ ID NO: 480:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 480:

15 Arg Glu Met Phe Glu Val Thr Gly Leu His Asp Val Asp Gln Gly Trp
1 5 10 15

20 Met Arg Ala Val Arg Lys His Ala Lys Gly Leu His Ile Val Pro Arg
20 25 30

Leu Leu Phe Glu Asp Trp Thr Tyr Asp Asp Phe Arg Asn Val Leu Asp
35 40 45

25 Ser Glu Asp Glu
50

30 (2) INFORMATION FOR SEQ ID NO: 481:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481:

His Phe Asp Gly Phe Val Val Glu Val Trp Asn Gln Leu Leu Ser Gln
1 5 10 15

40 Lys Arg Val Gly Leu Ile His Met Leu Thr His Leu Ala Glu Ala Leu
20 25 30

His Gln Ala Arg Leu Leu Ala Leu Val Ile Pro Pro Ala Ile Thr
45 35 40 45

Pro Gly Thr Asp Gln Leu Gly Met
50 55

50

(2) INFORMATION FOR SEQ ID NO: 482:

55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 482:

60 Asp Gly Phe Ser Leu Met Thr Tyr Asp Tyr Ser Thr Ala His Gln Pro

610

1 5 10 15
 Gly Pro Asn Ala Pro Leu Ser Trp Val Arg Ala Cys Val Gln Val Leu
 20 25 30
 5 Asp Pro Lys Xaa Lys Trp Arg Thr Lys Ser Ser Trp Gly Ser Thr
 35 40 45

10

(2) INFORMATION FOR SEQ ID NO: 483:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 amino acids

15

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 483:

20 Glu Arg Gly Val Ser Ile Asn Gln Phe Cys Lys Glu Phe Asn Glu Arg
 1 5 10 15
 Thr Lys Asp Ile Lys Glu Gly Ile Pro Leu Pro Thr Lys Ile Leu Val
 20 25 30
 25 Lys Pro Asp Arg Thr Phe Glu Ile Lys Ile Gly Gln Pro Thr Val Ser
 35 40 45
 Tyr Phe Leu Lys Ala Ala Ala Gly Ile Glu Lys Gly Ala Arg Gln Thr
 50 55 60
 30 Gly Lys Glu Val Ala Gly Leu Val Thr Leu Lys His Val Tyr Glu Ile
 65 70 75 80
 Ala Arg Ile Lys Ala Gln Asp Glu Ala Phe Ala Leu Gln Asp Val Pro
 35 85 90 95
 Leu Ser Ser Val Val Arg Ser Ile Ile Gly Ser Ala Arg Ser Leu Gly
 100 105 110
 40 Ile Arg Val Val Lys Asp Leu Ser Ser Glu Glu Leu Ala Ala Phe Gln
 115 120 125
 Lys Glu Arg Ala Ile Phe Leu Ala Ala Gln Lys Glu Ala Asp Leu Ala
 130 135 140
 45 Ala Gln Glu Glu Ala Ala Lys Lys
 145 150

50

(2) INFORMATION FOR SEQ ID NO: 484:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 270 amino acids

55

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 484:

60 Ala Val Tyr Thr Tyr His Glu Lys Lys Lys Asp Thr Ala Ala Ser Gly
 1 5 10 15

611

Tyr Gly Thr Gln Asn Ile Arg Leu Ser Arg Asp Ala Val Lys Asp Phe
 20 25 30
 5 Asp Cys Cys Cys Leu Ser Leu Gln Pro Cys His Asp Pro Val Val Thr
 35 40 45
 Pro Asp Gly Tyr Leu Tyr Glu Arg Glu Ala Ile Leu Glu Tyr Ile Leu
 50 55 60
 10 His Gln Lys Lys Glu Ile Ala Arg Gln Met Lys Ala Tyr Glu Lys Gln
 65 70 75 80
 Arg Gly Thr Arg Arg Glu Glu Gln Lys Glu Leu Gln Arg Ala Ala Ser
 85 90 95
 15 Gln Asp His Val Arg Gly Phe Leu Glu Lys Glu Ser Ala Ile Val Ser
 100 105 110
 20 Arg Pro Leu Asn Pro Phe Thr Ala Lys Ala Leu Ser Gly Thr Ser Pro
 115 120 125
 Asp Asp Val Gln Pro Gly Pro Ser Val Gly Pro Pro Ser Lys Asp Lys
 130 135 140
 25 Asp Lys Val Leu Pro Ser Phe Trp Ile Pro Ser Leu Thr Pro Glu Ala
 145 150 155 160
 Lys Ala Thr Lys Leu Glu Lys Pro Ser Arg Thr Val Thr Cys Pro Met
 165 170 175
 30 Ser Gly Lys Pro Leu Arg Met Ser Asp Leu Thr Pro Val His Phe Thr
 180 185 190
 35 Pro Leu Asp Ser Ser Val Asp Arg Val Gly Leu Ile Thr Arg Ser Glu
 195 200 205
 Arg Tyr Val Cys Ala Val Thr Arg Asp Ser Leu Ser Asn Ala Thr Pro
 210 215 220
 40 Cys Ala Val Leu Arg Pro Ser Gly Ala Val Val Thr Leu Glu Cys Val
 225 230 235 240
 Glu Lys Leu Ile Arg Lys Asp Met Val Asp Pro Val Thr Gly Asp Lys
 245 250 255
 45 Leu Thr Asp Arg Asp Ile Ile Val Leu Gln Arg Gly Gly Thr
 260 265 270
 50

(2) INFORMATION FOR SEQ ID NO: 485:

(i) SEQUENCE CHARACTERISTICS:

55

(A) LENGTH: 54 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 485:

60 Tyr Leu Tyr Glu Arg Glu Ala Ile Leu Glu Tyr Ile Leu His Gln Lys

612

1 5 10 15
 Lys Glu Ile Ala Arg Gln Met Lys Ala Tyr Glu Lys Gln Arg Gly Thr
 20 25 30
 5 Arg Arg Glu Glu Gln Lys Glu Leu Gln Arg Ala Ala Ser Gln Asp His
 35 40 45
 10 Val Arg Gly Phe Leu Glu
 50

15 (2) INFORMATION FOR SEQ ID NO: 486:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 486:

Phe Thr Ala Lys Ala Leu Ser Gly Thr Ser Pro Asp Asp Val Gln Pro
 1 5 10 15
 25 Gly Pro Ser Val Gly Pro Pro Ser Lys Asp Lys Asp Lys Val Leu Pro
 20 25 30
 Ser Phe Trp Ile Pro Ser Leu Thr Pro Glu Ala Lys Ala Thr Lys Leu
 35 40 45
 30 Glu Lys Pro Ser Arg Thr Val Thr Cys Pro Met Ser Gly Lys Pro Leu
 50 55 60

35

(2) INFORMATION FOR SEQ ID NO: 487:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 487:

Val His Phe Thr Pro Leu Asp Ser Ser Val Asp Arg Val Gly Leu Ile
 1 5 10 15
 50 Thr Arg Ser Glu Arg Tyr Val Cys Ala Val Thr Arg Asp Ser Leu Ser
 20 25 30
 Asn Ala Thr Pro Cys Ala Val Leu Arg Pro Ser Gly Ala Val Val Thr
 35 40 45
 55 Leu Glu Cys Val Glu Lys Leu Ile
 50 55

60

(2) INFORMATION FOR SEQ ID NO: 488:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 567 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488:

5 Met Asp Thr Ser Glu Asn Arg Pro Glu Asn Asp Val Pro Glu Pro Pro
 10 1 5 10 15
 Met Pro Ile Ala Asp Gln Val Ser Asn Asp Asp Arg Pro Glu Gly Ser
 20 25 30
 15 Val Glu Asp Glu Glu Lys Lys Glu Ser Ser Leu Pro Lys Ser Phe Lys
 35 40 45
 Arg Lys Ile Ser Val Val Ser Ala Thr Lys Gly Val Pro Ala Gly Asn
 50 55 60
 20 Ser Asp Thr Glu Gly Gly Gln Pro Gly Arg Lys Arg Arg Trp Gly Ala
 65 70 75 80
 Ser Thr Ala Thr Thr Gln Lys Lys Pro Ser Ile Ser Ile Thr Thr Glu
 25 85 90 95
 Ser Leu Lys Ser Leu Ile Pro Asp Ile Lys Pro Leu Ala Gly Gln Glu
 100 105 110
 30 Ala Val Val Asp Leu His Ala Asp Asp Ser Arg Ile Ser Glu Asp Glu
 115 120 125
 Thr Glu Arg Asn Gly Asp Asp Gly Thr His Asp Lys Gly Leu Lys Ile
 130 135 140
 35 Cys Arg Thr Val Thr Gln Val Val Pro Ala Glu Gly Gln Glu Asn Gly
 145 150 155 160
 Gln Arg Glu Glu Glu Glu Glu Lys Glu Pro Glu Ala Glu Pro Pro
 40 165 170 175
 Val Pro Pro Gln Val Ser Val Glu Val Ala Leu Pro Pro Pro Ala Glu
 180 185 190
 45 His Glu Val Lys Lys Val Thr Leu Gly Asp Thr Leu Thr Arg Arg Ser
 195 200 205
 Ile Ser Gln Gln Lys Ser Gly Val Ser Ile Thr Ile Asp Asp Pro Val
 210 215 220
 50 Arg Thr Ala Gln Val Pro Ser Pro Pro Arg Gly Lys Ile Ser Asn Ile
 225 230 235 240
 Val His Ile Ser Asn Leu Val Arg Pro Phe Thr Leu Gly Gln Leu Lys
 245 250 255
 Glu Leu Leu Gly Arg Thr Gly Thr Leu Val Glu Glu Ala Phe Trp Ile
 260 265 270
 60 Asp Lys Ile Lys Ser His Cys Phe Val Thr Tyr Ser Thr Val Glu Glu

614

	275	280	285
	Ala Val Ala Thr Arg Thr	Ala Leu His Gly Val	Lys Trp Pro Gln Ser
	290	295	300
5	Asn Pro Lys Phe Leu Cys Ala Asp Tyr	Ala Glu Gln Asp Glu Leu Asp	
	305	310	315 320
10	Tyr His Arg Gly Leu Leu Val Asp Arg	Pro Ser Glu Thr Lys Thr Glu	
	325	330	335
	Glu Gln Gly Ile Pro Arg Pro Leu His	Pro Pro Pro Pro Pro Pro Val	
	340	345	350
15	Gln Pro Pro Gln His Pro Arg Ala Glu Gln Arg	Glu Gln Glu Arg Ala	
	355	360	365
	Val Arg Glu Gln Trp Ala Glu Arg Glu Arg	Glu Met Glu Arg Arg Glu	
	370	375	380
20	Arg Thr Arg Ser Glu Arg Glu Trp Asp Arg	Asp Lys Val Arg Glu Gly	
	385	390	395 400
25	Pro Arg Ser Arg Ser Arg Ser Arg Xaa	Arg Arg Arg Lys Glu Arg Ala	
	405	410	415
	Lys Ser Lys Glu Lys Lys Ser Glu Lys Lys	Glu Lys Ala Gln Glu Glu	
	420	425	430
30	Pro Pro Ala Lys Leu Leu Asp Asp Leu Phe	Arg Lys Thr Lys Ala Ala	
	435	440	445
	Pro Cys Ile Tyr Trp Leu Pro Leu Thr Asp	Ser Gln Ile Val Gln Lys	
	450	455	460
35	Glu Ala Glu Arg Ala Glu Arg Ala Lys Glu	Arg Glu Lys Arg Arg Lys	
	465	470	475 480
40	Glu Gln Glu Glu Glu Glu Gln Lys Glu	Arg Glu Lys Glu Ala Glu Arg	
	485	490	495
	Glu Arg Asn Arg Gln Leu Glu Arg Glu Lys	Arg Arg Glu His Ser Arg	
	500	505	510
45	Glu Arg Asp Arg Glu Arg Glu Arg Glu Arg	Asp Arg Gly Asp	
	515	520	525
	Arg Asp Arg Asp Arg Glu Arg Asp Arg	Glu Arg Gly Arg Glu Arg Asp	
	530	535	540
50	Arg Arg Asp Thr Lys Arg His Ser Arg Ser	Arg Ser Arg Ser Thr Pro	
	545	550	555 560
55	Val Arg Asp Arg Gly Gly Arg		
	565		

(2) INFORMATION FOR SEQ ID NO: 489:

60

615

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489:

Gly Cys Asp Ser Cys Pro Pro His Leu Pro Arg Glu Ala Phe Ala Gln
 1 5 10 15

10 Asp Thr Gln Ala Glu Gly Glu Cys Ser Ser Arg Ala Glu Arg Ala Asp
 20 25 30

Met Cys Pro Asp Ala Pro Pro Ser Gln Glu Val Pro Glu Gly Pro Gly
 35 40 45

15 Ala Ala Pro
 50

20 (2) INFORMATION FOR SEQ ID NO: 490:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

25 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 490:

30 Pro Gln Leu Pro Ser Cys Gly Arg Pro Trp Pro Gly Thr Ala Ser Val
 1 5 10 15

Phe Gln Ser His Thr Gln Gly Pro Arg Glu Asp Pro Asp Pro Cys Arg
 20 25 30

35 Ala Gln Gly Ser Ala Gly Thr His Cys Pro Ile Ser Leu Ser Pro Pro
 35 40 45

Arg Gln
 50

40

(2) INFORMATION FOR SEQ ID NO: 491:

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491:

50 Pro Gly Phe Arg Gly Pro Ser Gly Ser Leu Gly Cys Ser Phe Phe Pro
 1 5 10 15

55 Arg Ser Leu Gly Arg Val Leu Pro Pro Gly Cys Gln Arg Pro Gly Ala
 20 25 30

His Ala Asp Ser Ser Pro Pro Thr Pro
 35 40

60

(2) INFORMATION FOR SEQ ID NO: 492:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 84 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 492:

10 Glu Asp Leu Lys Lys Pro Asp Pro Ala Ser Leu Arg Ala Ala Ser Cys
1 5 10 15
Gly Glu Gly Lys Lys Arg Lys Ala Cys Lys Asn Cys Thr Cys Gly Leu
20 25 30
15 Ala Glu Glu Leu Glu Lys Glu Lys Ser Arg Glu Gln Met Ser Ser Gln
35 40 45
Pro Lys Ser Ala Cys Gly Asn Cys Tyr Leu Gly Asp Ala Phe Arg Cys
20 50 55 60
Ala Ser Cys Pro Tyr Leu Gly Met Pro Ala Phe Lys Pro Gly Glu Lys
65 70 75 80
25 Val Leu Leu Ser

30 (2) INFORMATION FOR SEQ ID NO: 493:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 90 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 493:

40 Glu Asp Leu Lys Lys Pro Asp Pro Ala Ser Leu Arg Ala Ala Ser Cys
1 5 10 15
Gly Glu Gly Lys Lys Arg Lys Ala Cys Lys Asn Cys Thr Cys Gly Leu
20 25 30
45 Ala Glu Glu Leu Glu Lys Glu Lys Ser Arg Glu Gln Met Ser Ser Gln
35 40 45
Pro Lys Ser Ala Cys Gly Asn Cys Tyr Leu Gly Asp Ala Phe Arg Cys
50 55 60
50 Ala Ser Cys Pro Tyr Leu Gly Met Pro Ala Phe Lys Pro Gly Glu Lys
65 70 75 80
Val Leu Leu Ser Asp Ser Asn Leu His Asp
85 90
55

(2) INFORMATION FOR SEQ ID NO: 494:

60 (i) SEQUENCE CHARACTERISTICS:

617

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 494:

5

Cys Gly Asn Cys Tyr Leu Gly Asp Ala Phe Arg Cys Ala Ser Cys Pro
 1 5 10 15

10

Tyr Leu Gly Met Pro Ala Phe Lys Pro Gly Glu Lys Val Leu Leu Ser
 20 25 30

Asp Ser

15

(2) INFORMATION FOR SEQ ID NO: 495:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 495:

25

Ser Cys Gly Glu Gly Lys Lys Arg Lys Ala Cys Lys Asn Cys Thr Cys
 1 5 10 15

Gly Leu Ala Glu Glu Leu Glu Lys Glu
 20 25

30

(2) INFORMATION FOR SEQ ID NO: 496:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496:

40

Ser Gln Pro Lys Ser Ala Cys Gly Asn Cys Tyr Leu Gly Asp Ala Phe
 1 5 10 15

Arg Cys Ala Ser Cys
 20

45

(2) INFORMATION FOR SEQ ID NO: 497:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 497:

Arg Glu Ala Gly Gln Asn Ser Glu Arg Gln Tyr Val Ser Leu Ser Arg
 1 5 10 15

60

Asp

5 (2) INFORMATION FOR SEQ ID NO: 498:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 498:

Glu Ser Ser Gly Gln Ala Arg Thr Leu Ala Asp Pro Gly Pro Gly Trp
 1 5 10 15

15 Pro Arg Gln Gln Gly Met Cys Phe Gly Ser Leu Thr Gly Leu Ser Thr
 20 25 30

20 Thr Pro His Gly Phe Leu Thr Val Ser Ala Glu Ala Asp Pro Arg Leu
 35 40 45

Ile Glu Ser Leu Ser Gln Met Leu Ser Met Gly Phe Ser Asp Glu Gly
 50 55 60

25 Gly Trp Leu Thr Arg Leu Leu Gln Thr Lys Asn Tyr Asp Ile Gly Ala
 65 70 75 80

Ala Leu Asp Thr Ile Gln Tyr Ser Lys His
 85 90
 30

(2) INFORMATION FOR SEQ ID NO: 499:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 499:

40 Gln Glu Gly Ser Glu Pro Val Leu Leu Glu Gly Glu Cys Leu Val Val
 1 5 10 15

45 Cys Glu Pro Gly Arg Ala Ala Ala Gly Gly Pro Gly Gly Ala Ala Leu
 20 25 30

Gly Glu Ala Pro Pro Gly Arg Val Ala Phe Xaa Ala Val Arg Ser His
 35 40 45

50 His His Glu Pro Ala Gly Glu Thr Gly Asn Gly Thr Ser Gly Ala Ile
 50 55 60

Tyr Phe Asp Gln Val Leu Val Asn Glu Gly Gly Gly Phe Asp Arg Ala
 65 70 75 80

55 Ser Gly Ser Phe Val Ala Pro Val Arg Gly Val Tyr Ser Phe Arg Phe
 85 90 95

60 His Val Val Lys Val Tyr Asn Arg Gln Thr Val Gln Val Ser Leu Met
 100 105 110

619

Leu Asn Thr Trp Pro Val Ile Ser Ala Phe Ala Asn Asp Pro Asp Val
 115 120 125
 5 Thr Arg Glu Ala Ala Thr Ser Ser Val Leu Leu Pro Leu Asp Pro Gly
 130 135 140
 Asp Arg Val Ser Leu Arg Leu Arg Arg Gly Xaa Ser Thr Gly Trp
 145 150 155
 10

(2) INFORMATION FOR SEQ ID NO: 500:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 500:
 20

Pro Arg Ser Arg Pro Ala Leu Arg Pro Gly Arg Gln Arg Pro Pro Ser
 1 5 10 15
 25 His Ser Ala Thr Ser Gly Val Leu Arg Pro Arg Lys Lys Pro Asp Pro
 20 25 30
 30

(2) INFORMATION FOR SEQ ID NO: 501:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501:
 40

Met Thr Leu Ile Thr Pro Ser Xaa Lys Leu Thr Phe Xaa Lys Gly Asn
 1 5 10 15
 Lys Ser Trp Ser Ser Arg Ala Cys Ser Ser Thr Leu Val Asp Pro
 20 25 30
 45

(2) INFORMATION FOR SEQ ID NO: 502:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502:
 55

Gly His Pro Ser Pro Ala Leu Ser Ile Ala Pro Ser Asp Gly Ser Gln
 1 5 10 15
 Leu Pro Cys Asp Glu Val Pro Tyr Gly Glu Ala His Val Thr Arg Tyr
 20 25 30
 60

620

Cys Lys Lys Pro Leu Thr Asn Ser His Leu Glu Thr Glu Ala Gln Ser
 35 40 45

5 Ser Ser Leu
 50

10 (2) INFORMATION FOR SEQ ID NO: 503:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 263 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503:

20 GCTTCGTGTC CAACCTCTTT GCCCTTCGCC TGTGTGCCTG GAGCCAGTCC CACCACGCTC 60
 GCGTTTCCTC CTGTAGTGCT CACAGGTCCC AGCACCGATG GCATTCCCTT TGCCCTGAGT 120
 CTGCAGCGGG TCCCTTTTGT GCTTCCTTCC CCTCAGGTAG CCTCTCTCCC CCTGGGCCAC 180
 25 TCCCGGGGGT GAGGGGGTTA CCCCTTCCCA GTGTTTTTTA TTCCTGTGGG GTCACCCCA 240
 AAGTATTAAA AGTAGCTTTG TAA 263

30

(2) INFORMATION FOR SEQ ID NO: 504:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 263 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 504:

GCTTCGTGTC CAACCTCTTT GCCCTTCGCC TGTGTGCCTG GAGCCAGTCC CACCACGCTC 60
 45 GCGTTTCCTC CTGTAGTGCT CACAGGTCCC AGCACCGATG GCATTCCCTT TGCCCTGAGT 120
 CTGCAGCGGG TCCCTTTTGT GCTTCCTTCC CCTCAGGTAG CCTCTCTCCC CCTGGGCCAC 180
 TCCCGGGGGT GAGGGGGTTA CCCCTTCCCA GTGTTTTTTA TTCCTGTGGG GTCACCCCA 240
 50 AAGTATTAAA AGTAGCTTTG TAA 263

55

(2) INFORMATION FOR SEQ ID NO: 505:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 263 base pairs
 (B) TYPE: nucleic acid

60

621

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 505:

5 GCTTCGTGTC CAACCTCTT GCCCTCGCC TGTGTGCCTG GAGCCAGTCC CACCACGCTC 60
GCGTTTCCTC CTGTAGTGCT CACAGGTCCC AGCACCGATG GCATTCCCTT TGCCCTGAGT 120
10 CTGCAGCGGG TCCCTTTTGT GCTTCCTTCC CCTCAGGTAG CCTCTCTCCC CCTGGGCCAC 180
TCCCGGGGGT GAGGGGGTTA CCCCTTCCCA GTGTTTITTA TTCCTGTGGG GCTCACCCCA 240
AAGTATTAAA AGTAGCTTTG TAA 263
15

(2) INFORMATION FOR SEQ ID NO: 506:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 506:

TGGCTCACTG TCTTACAATC ACTGCTGTGG AATCATGATA CCACTTTTAG CTCTTTGCAT 60
30 CTTCTCTCAG TGTATTTTGT TTTTCAAGA GGAAGTAGAT TTAACTGGA CAACTTTGAG 120
TACTGACATC ATTGATAAAT AACTGGCTT GTGGTTTCAA 160
35

(2) INFORMATION FOR SEQ ID NO: 507:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 292 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 507:

45

Leu Asp Glu Leu Met Ala His Leu Thr Glu Met Gln Ala Lys Val Ala
1 5 10 15

50

Val Arg Ala Asp Ala Gly Lys Lys His Leu Pro Asp Lys Gln Asp His
20 25 30

Lys Ala Ser Leu Asp Ser Met Leu Gly Gly Leu Glu Gln Glu Leu Gln
35 40 45

55

Asp Leu Gly Ile Ala Thr Val Pro Lys Gly His Cys Ala Ser Cys Gln
50 55 60

Lys Pro Ile Ala Gly Lys Val Ile His Ala Leu Gly Gln Ser Trp His
65 70 75 80
60

622

Pro Glu His Phe Val Cys Thr His Cys Lys Glu Glu Ile Gly Ser Ser
 85 90 95

5 Pro Phe Phe Glu Arg Ser Gly Leu Xaa Tyr Cys Pro Asn Asp Tyr His
 100 105 110

 Gln Leu Phe Ser Pro Arg Cys Ala Tyr Cys Ala Ala Pro Ile Leu Asp
 115 120 125

10 Lys Val Leu Thr Ala Met Asn Gln Thr Trp His Pro Glu His Phe Phe
 130 135 140

 Cys Ser His Cys Gly Glu Val Phe Gly Ala Glu Gly Phe His Glu Lys
 145 150 155 160

15 Asp Lys Lys Pro Tyr Cys Arg Lys Asp Phe Leu Ala Met Phe Ser Pro
 165 170 175

 Lys Cys Gly Gly Cys Asn Arg Pro Val Leu Glu Asn Tyr Leu Ser Ala
 180 185 190

20 Met Asp Thr Val Trp His Pro Glu Cys Phe Val Cys Gly Asp Cys Phe
 195 200 205

25 Thr Ser Phe Ser Thr Gly Ser Phe Phe Glu Leu Asp Gly Arg Pro Phe
 210 215 220

 Cys Glu Leu His Tyr His His Arg Arg Gly Thr Leu Cys His Gly Cys
 225 230 235 240

30 Gly Gln Pro Ile Thr Gly Arg Cys Ile Ser Ala Met Gly Tyr Lys Phe
 245 250 255

 His Pro Glu His Phe Val Cys Ala Phe Cys Leu Thr Gln Leu Ser Lys
 260 265 270

35 Gly Ile Phe Arg Glu Gln Asn Asp Lys Thr Tyr Cys Gln Pro Cys Phe
 275 280 285

40 Asn Lys Leu Phe
 290

45 (2) INFORMATION FOR SEQ ID NO: 508:

 (i) SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 43 amino acids

 (B) TYPE: amino acid

50 (D) TOPOLOGY: linear

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 508:

 Lys Ala Ser Leu Asp Ser Met Leu Gly Gly Leu Glu Gln Glu Leu Gln
 1 5 10 15

55 Asp Leu Gly Ile Ala Thr Val Pro Lys Gly His Cys Ala Ser Cys Gln
 20 25 30

 Lys Pro Ile Ala Gly Lys Val Ile His Ala Leu
 35 40

60

(2) INFORMATION FOR SEQ ID NO: 509:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 509:

Cys Pro Asn Asp Tyr His Gln Leu Phe Ser Pro Arg Cys Ala Tyr Cys
 1 5 10 15

15

Ala Ala Pro Ile Leu Asp Lys Val Leu Thr Ala Met Asn Gln Thr Trp
 20 25 30

His Pro Glu His Phe Phe Cys Ser His Cys Gly Glu Val Phe Gly Ala
 35 40 45

20

Glu Gly
 50

25

(2) INFORMATION FOR SEQ ID NO: 510:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 510:

Asp Lys Lys Pro Tyr Cys Arg Lys Asp Phe Leu Ala Met Phe Ser Pro
 1 5 10 15

35

Lys Cys Gly Gly Cys Asn Arg Pro Val Leu Glu Asn Tyr Leu Ser Ala
 20 25 30

40

Met Asp Thr Val Trp His Pro Glu Cys Phe Val Cys Gly Asp Cys Phe
 35 40 45

Thr Ser Phe Ser Thr Gly Ser Phe Phe Glu Leu Asp Gly Arg Pro Phe
 50 55 60

45

Cys Glu Leu
 65

50

(2) INFORMATION FOR SEQ ID NO: 511:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 511:

Cys Gly Gln Pro Ile Thr Gly Arg Cys Ile Ser Ala Met Gly Tyr Lys
 1 5 10 15

60

Phe His Pro Glu His Phe Val Cys Ala Phe Cys Leu Thr Gln Leu Ser
 20 25 30

5 Lys Gly Ile Phe Arg Glu Gln Asn Asp Lys Thr Tyr Cys Gln
 35 40 45

10 (2) INFORMATION FOR SEQ ID NO: 512:

 (i) SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 452 amino acids

 (B) TYPE: amino acid

 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 512:

Met Gly Ser Ser Gln Ser Val Glu Ile Pro Gly Gly Gly Thr Glu Gly
 1 5 10 15

20 Tyr His Val Leu Arg Val Gln Glu Asn Ser Pro Gly His Arg Ala Gly
 20 25 30

25 Leu Glu Pro Phe Phe Asp Phe Ile Val Ser Ile Asn Gly Ser Arg Leu
 35 40 45

Asn Lys Asp Asn Asp Thr Leu Lys Asp Leu Leu Lys Xaa Asn Val Glu
 50 55 60

30 Lys Pro Val Lys Met Leu Ile Tyr Ser Ser Lys Thr Leu Glu Leu Arg
 65 70 75 80

Glu Thr Ser Val Thr Pro Ser Asn Leu Trp Gly Gly Gln Gly Leu Leu
 85 90 95

35 Gly Val Ser Ile Arg Phe Cys Ser Phe Asp Gly Ala Asn Glu Asn Val
 100 105 110

40 Trp His Val Leu Glu Val Glu Ser Asn Ser Pro Ala Ala Leu Ala Gly
 115 120 125

Leu Arg Pro His Ser Asp Tyr Ile Ile Gly Ala Asp Thr Val Met Asn
 130 135 140

45 Glu Ser Glu Asp Leu Phe Ser Leu Ile Glu Thr His Glu Ala Lys Pro
 145 150 155 160

Leu Lys Leu Tyr Val Tyr Asn Thr Asp Thr Asp Asn Cys Arg Glu Val
 165 170 175

50 Ile Ile Thr Pro Asn Ser Ala Trp Gly Gly Glu Gly Ser Leu Gly Cys
 180 185 190

55 Gly Ile Gly Tyr Gly Tyr Leu His Arg Ile Pro Thr Arg Pro Phe Glu
 195 200 205

Glu Gly Lys Lys Ile Ser Leu Pro Gly Gln Met Ala Gly Thr Pro Ile
 210 215 220

60 Thr Pro Leu Lys Asp Gly Phe Thr Glu Val Gln Leu Ser Ser Val Asn

625

225 230 235 240
 Pro Pro Ser Leu Ser Pro Pro Gly Thr Thr Gly Ile Glu Gln Ser Leu
 245 250 255
 5 Thr Gly Leu Ser Ile Ser Ser Thr Pro Pro Ala Val Ser Ser Val Leu
 260 265 270
 10 Ser Thr Gly Val Pro Thr Val Pro Leu Leu Pro Pro Gln Val Asn Gln
 275 280 285
 Ser Leu Thr Ser Val Pro Pro Met Asn Pro Ala Thr Thr Leu Pro Gly
 290 295 300
 15 Leu Met Pro Leu Pro Ala Gly Leu Pro Asn Leu Pro Asn Leu Asn Leu
 305 310 315 320
 Asn Leu Pro Ala Pro His Ile Met Pro Gly Val Gly Leu Pro Glu Leu
 325 330 335
 20 Val Asn Pro Gly Leu Pro Pro Leu Pro Ser Met Pro Pro Arg Asn Leu
 340 345 350
 25 Pro Gly Ile Ala Pro Leu Pro Leu Pro Ser Glu Phe Leu Pro Ser Phe
 355 360 365
 Pro Leu Val Pro Glu Ser Ser Ser Ala Ala Ser Ser Gly Glu Leu Leu
 370 375 380
 30 Ser Ser Leu Pro Pro Thr Ser Asn Ala Pro Ser Asp Pro Ala Thr Thr
 385 390 395 400
 Thr Ala Lys Ala Asp Ala Ala Ser Ser Leu Thr Val Asp Val Thr Pro
 405 410 415
 35 Pro Thr Ala Lys Ala Pro Thr Thr Val Glu Asp Arg Val Gly Asp Ser
 420 425 430
 40 Thr Pro Val Ser Glu Lys Pro Val Ser Ala Ala Val Asp Ala Asn Ala
 435 440 445
 Ser Glu Ser Pro
 450

45

(2) INFORMATION FOR SEQ ID NO: 513:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 513:

55

Ser Val Glu Ile Pro Gly Gly Gly Thr Glu Gly Tyr His Val Leu Arg
 1 5 10 15

Val Gln Glu Asn Ser Pro Gly His Arg Ala Gly Leu Glu Pro Phe Phe
 20 25 30

60

626

Asp Phe Ile Val Ser Ile Asn Gly Ser Arg Leu Asn Lys Asp Asn Asp
 35 40 45
 5 Thr Leu Lys Asp Leu Leu Lys Xaa Asn Val Glu Lys Pro Val Lys Met
 50 55 60
 Leu Ile Tyr Ser Ser Lys Thr Leu Glu Leu Arg Glu Thr Ser Val Thr
 65 70 75 80
 10 Pro Ser Asn Leu Trp Gly Gly Gln Gly Leu Leu Gly Val Ser Ile Arg
 85 90 95
 Phe Cys Ser Phe Asp Gly Ala Asn Glu Asn Val Trp His
 100 105
 15

(2) INFORMATION FOR SEQ ID NO: 514:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 145 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 514:
 26 Glu Ser Asn Ser Pro Ala Ala Leu Ala Gly Leu Arg Pro His Ser Asp
 1 5 10 15
 30 Tyr Ile Ile Gly Ala Asp Thr Val Met Asn Glu Ser Glu Asp Leu Phe
 20 25 30
 Ser Leu Ile Glu Thr His Glu Ala Lys Pro Leu Lys Leu Tyr Val Tyr
 35 40 45
 35 Asn Thr Asp Thr Asp Asn Cys Arg Glu Val Ile Ile Thr Pro Asn Ser
 50 55 60
 Ala Trp Gly Gly Glu Gly Ser Leu Gly Cys Gly Ile Gly Tyr Gly Tyr
 65 70 75 80
 40 Leu His Arg Ile Pro Thr Arg Pro Phe Glu Glu Gly Lys Lys Ile Ser
 85 90 95
 Leu Pro Gly Gln Met Ala Gly Thr Pro Ile Thr Pro Leu Lys Asp Gly
 100 105 110
 45 Phe Thr Glu Val Gln Leu Ser Ser Val Asn Pro Pro Ser Leu Ser Pro
 115 120 125
 50 Pro Gly Thr Thr Gly Ile Glu Gln Ser Leu Thr Gly Leu Ser Ile Ser
 130 135 140
 Ser
 55 145

(2) INFORMATION FOR SEQ ID NO: 515:

60 (i) SEQUENCE CHARACTERISTICS:

627

(A) LENGTH: 145 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 515:

5
 Glu Ser Asn Ser Pro Ala Ala Leu Ala Gly Leu Arg Pro His Ser Asp
 1 5 10 15
 Tyr Ile Ile Gly Ala Asp Thr Val Met Asn Glu Ser Glu Asp Leu Phe
 10 20 25 30
 Ser Leu Ile Glu Thr His Glu Ala Lys Pro Leu Lys Leu Tyr Val Tyr
 35 40 45
 Asn Thr Asp Thr Asp Asn Cys Arg Glu Val Ile Ile Thr Pro Asn Ser
 50 55 60
 Ala Trp Gly Gly Glu Gly Ser Leu Gly Cys Gly Ile Gly Tyr Gly Tyr
 65 70 75 80
 20
 Leu His Arg Ile Pro Thr Arg Pro Phe Glu Glu Gly Lys Lys Ile Ser
 85 90 95
 Leu Pro Gly Gln Met Ala Gly Thr Pro Ile Thr Pro Leu Lys Asp Gly
 25 100 105 110
 Phe Thr Glu Val Gln Leu Ser Ser Val Asn Pro Pro Ser Leu Ser Pro
 115 120 125
 30
 Pro Gly Thr Thr Gly Ile Glu Gln Ser Leu Thr Gly Leu Ser Ile Ser
 130 135 140
 Ser
 145
 35

(2) INFORMATION FOR SEQ ID NO: 516:

40
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 151 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 516:
 45
 Arg Ile Pro Thr Arg Pro Phe Glu Glu Gly Lys Lys Ile Ser Leu Pro
 1 5 10 15
 Gly Gln Met Ala Gly Thr Pro Ile Thr Pro Leu Lys Asp Gly Phe Thr
 50 20 25 30
 Glu Val Gln Leu Ser Ser Val Asn Pro Pro Ser Leu Ser Pro Pro Gly
 35 40 45
 55
 Thr Thr Gly Ile Glu Gln Ser Leu Thr Gly Leu Ser Ile Ser Ser Thr
 50 55 60
 Pro Pro Ala Val Ser Ser Val Leu Ser Thr Gly Val Pro Thr Val Pro
 65 70 75 80
 60

(2) INFORMATION FOR SEQ ID NO: 517:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 517:

Pro Gly Leu Pro Pro Leu Pro Ser Met Pro Pro Arg Asn Leu Pro Gly
1 5 10 15

Ile Ala Pro Leu Pro Leu Pro Ser Glu Phe Leu Pro Ser Phe Pro Leu
20 25 30

Val Pro Glu Ser Ser Ser Ala Ala Ser Ser Gly Glu Leu Leu Ser Ser
35 40 45

Leu Pro Pro Thr Ser Asn Ala Pro Ser Asp Pro Ala Thr Thr Thr Ala
50 55 60

Lys Ala Asp Ala Ala Ser Ser Leu Thr Val Asp Val Thr Pro Pro Thr
65 70 75 80

Ala Lys Ala Pro Thr Val Glu Asp Arg Val Gly Asp Ser Thr Pro
85 90 95

Val Ser Glu Lys Pro Val Ser Ala Ala Val Asp Ala Asn
100 105

(2) INFORMATION FOR SEQ ID NO: 518:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 93 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 518:

Ile Tyr Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser
1 5 10 15
Cys Phe Glu Asn Ile Arg Ser Cys Ala Arg Xaa Xaa Xaa Xaa Xaa Xaa

629

20 25 30
 Xaa Xaa Xaa Xaa Xaa Xaa Trp Ile Phe Gly Val Leu His Val Val His
 35 40 45
 5 Ala Ser Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln
 50 55 60
 10 Gly Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln
 65 70 75 80
 Glu Glu Tyr Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys
 85 90

15

(2) INFORMATION FOR SEQ ID NO: 519:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 519:

25

Trp Ile Phe Gly Val Leu His Val Val His Ala Ser Val Val Thr Ala
 1 5 10 15

30

Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln Gly Met Phe Ile Phe Leu
 20 25 30

Phe Leu Cys Val Leu Ser Arg Lys Ile Gln Glu Glu Tyr Tyr Arg Leu
 35 40 45

35

Phe Lys Asn Val Pro Cys Cys
 50 55

40

(2) INFORMATION FOR SEQ ID NO: 520:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 520:

Ala Leu Thr Arg Ile Pro Pro Gly Asp Trp Val Ile Asn Val Thr Ala
 1 5 10 15

50

Val Ser Phe Ala Gly Lys Thr Thr Ala Arg Phe Phe Xaa His Ser Ser
 20 25 30

Pro Pro Ser Leu Gly Asp Gln Ala Arg Thr Asp Pro Gly His Gln Arg
 35 40 45

55

Arg Asp
 50

60

630

(2) INFORMATION FOR SEQ ID NO: 521:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 521:

5 Leu Gln Glu Val Asn Ile Thr Leu Pro Glu Asn Ser Val Trp Tyr Glu
 10 1 5 10 15
 Arg Tyr Lys Phe Asp Ile Pro Val Phe His Leu
 20 25

15

(2) INFORMATION FOR SEQ ID NO: 522:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 522:

25 Met Gln Gly Ser Gly Ser Gln Phe Arg Ala Cys Leu Leu Cys Leu Cys
 1 5 10 15
 Phe Ser Cys Pro Cys Ser Pro Gly Gly Pro Arg Trp Asn Ser Arg Gln
 20 25 30
 30 Gly Gly Arg Arg Phe Pro Lys Thr Cys Arg Ala Ile Ser Gln Asn Leu
 35 40 45
 Val Phe Lys Tyr Lys Thr Phe Cys Pro Val Arg Tyr Met Gln Pro His
 35 50 55 60
 Arg Ser Ser Leu Cys Leu His Phe Thr Ser Tyr Val Phe Ile Leu Ser
 65 70 75 80
 40 Thr Trp Gly Ser Leu Arg Thr Tyr Ser Thr Asp Leu Lys Lys Lys Lys
 85 90 95
 Lys Asn Ser Arg Gly Gly Pro Val Pro Ile Arg Pro Lys Ser
 100 105 110

45

(2) INFORMATION FOR SEQ ID NO: 523:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 523:

50 TAGCATGTAG CCACTCGAAT AACNTATAAG GACAAAGTGG AGTCCACGCG TGCGGCCGTC 60
 60 TAGACTAGTG GATCCCCCGG CTGCAGGATT CGGCACGAG 99

5 (2) INFORMATION FOR SEQ ID NO: 524:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 524:

Met Gln Gly Ser Gly Ser Gln Phe Arg Ala Cys Leu Leu Cys Leu Cys
 1 5 10 15

15 Phe Ser Cys Pro Cys Ser Pro Gly Gly Pro Arg Trp Asn Ser Arg Gln
 20 25 30

20 Gly Gly Arg Arg Phe Pro Lys Thr Cys Arg Ala Ile Ser Gln Asn Leu
 35 40 45

Val Phe Lys
 50

25

(2) INFORMATION FOR SEQ ID NO: 525:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 525:

35 Pro Val Arg Tyr Met Gln Pro His Arg Ser Ser Leu Cys Leu His Phe
 1 5 10 15

Thr Ser Tyr Val Phe Ile Leu Ser Thr Trp Gly Ser Leu Arg Thr Tyr
 20 25 30

40 Ser Thr Asp Leu Lys Lys Lys Lys Lys Asn Ser Arg Gly Gly Pro Val
 35 40 45

45 Pro Ile Arg Pro Lys Ser
 50

50 (2) INFORMATION FOR SEQ ID NO: 526:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 526:

Gly Glu Glu Gln Arg Asp Cys Ser Leu Gly Trp Arg Gly Val Gly Met
 1 5 10 15

60 Arg Ala Thr His Cys Gln Ala Ala Arg Met Phe Val Leu Phe Ser Leu

632

20 25 30

Pro Lys Tyr Ala Gly Leu
35

5

(2) INFORMATION FOR SEQ ID NO: 527:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 161 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 527:

15 Met Pro Arg Lys Thr Ser Lys Cys Arg Gln Leu Leu Cys Ser Gly Ala
1 5 10 15

20 Ser Arg Asn Ala Asp Thr Ala Ala Arg Gln Ser Thr Cys Ser Ser His
20 25 30

Arg Pro Pro Gly Lys Ile Pro Ser Leu Gly Pro Arg Arg Xaa Pro Gly
35 40 45

25 Cys Xaa Ser Val Pro Ser Ser Arg Gly Glu Gln Ser Thr Gly Ser Pro
50 55 60

Ala Ala Pro Arg Cys Gly Arg Arg Asp Ala His Arg Gly Leu Pro Gly
65 70 75 80

30 Gly Ala Ala Met Thr Pro Gly Asp Thr Trp Ala Ser Phe Asn Pro Arg
85 90 95

35 Ala Gly His Ser Lys Ser Gln Gly Glu Gly Gln Glu Ser Ser Gly Ala
100 105 110

Ser Arg Gln Asp Arg His Pro Val Ser His Trp Val Glu Arg Gln Arg
115 120 125

40 Glu Ala Trp Gly Ala Pro Arg Ser Ser Ser Ala Gly Gly Val Lys Val
130 135 140

Ala Ala Thr Thr Glu Arg Glu Pro Glu Phe Lys Ile Lys Thr Gly Lys
145 150 155 160

45 Ala

50

(2) INFORMATION FOR SEQ ID NO: 528:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 528:

60 Cys Ser Gly Ala Ser Arg Asn Ala Asp Thr Ala Ala Arg Gln Ser Thr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 529:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 529:

Gln Gly Glu Gly Gln Glu Ser Ser Gly Ala Ser Arg Gln Asp Arg His
1 5 10 15

Pro Val Ser His Trp Val Glu Arg Gln Arg Glu Ala Trp Gly Ala Pro
20 25 30

Arg Ser Ser Ser Ala Gly Gly Val Lys Val Ala Ala Thr Thr Glu Arg
35 40 45

Glu Pro Glu Phe Lys Ile Lys Thr Gly Lys Ala
50 55

40 (2) INFORMATION FOR SEQ ID NO: 530:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 235 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 530:

50 Met Ser Pro Arg Tyr Pro Gly Gly Pro Arg Pro Pro Leu Arg Ile Pro
1 5 10 15

Asn Gln Ala Leu Gly Gly Val Pro Gly Ser Gln Pro Leu Leu Pro Ser
20 25 30

55 Gly Met Asp Pro Thr Arg Gln Gln Gly His Pro Asn Met Gly Gly Pro
35 40 45

Met Gln Arg Met Thr Pro Pro Arg Gly Met Val Pro Leu Gly Pro Gln
50 55 60

60

634

Asn Tyr Gly Gly Ala Met Arg Pro Pro Leu Asn Ala Leu Gly Gly Pro
 65 70 75 80
 Gly Met Pro Gly Met Asn Met Gly Pro Gly Gly Gly Arg Pro Trp Pro
 5 85 90 95
 Asn Pro Thr Asn Ala Asn Ser Ile Pro Tyr Ser Ser Ala Ser Pro Gly
 100 105 110
 10 Asn Tyr Val Gly Pro Pro Gly Gly Gly Gly Pro Pro Gly Thr Pro Ile
 115 120 125
 Met Pro Ser Pro Ala Asp Ser Thr Asn Ser Gly Asp Asn Met Tyr Thr
 130 135 140
 15 Leu Met Asn Ala Val Pro Pro Gly Pro Asn Arg Pro Asn Phe Pro Met
 145 150 155 160
 Gly Pro Gly Ser Asp Gly Pro Met Gly Gly Leu Gly Gly Met Glu Ser
 20 165 170 175
 His His Met Asn Gly Ser Leu Gly Ser Gly Asp Met Asp Ser Ile Ser
 180 185 190
 25 Lys Asn Ser Pro Asn Asn Met Ser Leu Ser Asn Gln Pro Gly Thr Pro
 195 200 205
 Arg Asp Asp Gly Glu Met Gly Gly Asn Phe Leu Asn Pro Phe Gln Ser
 210 215 220
 30 Glu Ser Tyr Ser Pro Ser Met Thr Met Ser Val
 225 230 235

35

(2) INFORMATION FOR SEQ ID NO: 531:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 531:

40 Met Ser Pro Arg Tyr Pro Gly Gly Pro Arg Pro Pro Leu Arg Ile Pro
 1 5 10 15
 Asn Gln Ala Leu Gly Gly Val Pro Gly Ser Gln Pro Leu Leu Pro Ser
 20 25 30
 50 Gly Met Asp Pro Thr Arg Gln Gln Gly His Pro Asn Met Gly Gly Pro
 35 40 45
 Met Gln Arg Met Thr Pro Pro Arg Gly Met Val Pro Leu Gly Pro Gln
 50 55 60
 55 Asn Tyr Gly Gly Ala Met Arg Pro Pro Leu Asn Ala Leu Gly Gly Pro
 65 70 75 80
 60 Gly Met Pro Gly Met Asn Met Gly Pro Gly Gly Gly Arg Pro Trp Pro
 85 90 95

635

Asn Pro Thr Asn Ala Asn Ser Ile Pro Tyr Ser Ser Ala Ser Pro Gly
 100 105 110

5 Asn Tyr

10 (2) INFORMATION FOR SEQ ID NO: 532:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 532:

Leu Asn Ala Leu Gly Gly Pro Gly Met Pro Gly Met Asn Met Gly Pro
 1 5 10 15

20 Gly Gly Gly Arg Pro Trp Pro Asn Pro Thr Asn Ala Asn Ser Ile Pro
 20 25 30

25 Tyr Ser Ser Ala Ser Pro Gly Asn Tyr Val Gly Pro Pro Gly Gly Gly
 35 40 45

Gly Pro Pro Gly Thr Pro Ile Met Pro Ser Pro Ala Asp Ser Thr Asn
 50 55 60

30 Ser Gly Asp Asn Met Tyr Thr Leu Met Asn Ala Val Pro Pro Gly Pro
 65 70 75 80

Asn

35

(2) INFORMATION FOR SEQ ID NO: 533:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 533:

Gly Pro Met Gly Gly Leu Gly Gly Met Glu Ser His His Met Asn Gly
 1 5 10 15

50 Ser Leu Gly Ser Gly Asp Met Asp Ser Ile Ser Lys Asn Ser Pro Asn
 20 25 30

Asn Met Ser Leu Ser Asn Gln Pro Gly Thr Pro Arg Asp Asp Gly Glu
 35 40 45

55 Met Gly Gly Asn Phe Leu Asn Pro Phe Gln Ser Glu Ser Tyr Ser Pro
 50 55 60

Ser Met Thr Met Ser Val
 65 70

60

(2) INFORMATION FOR SEQ ID NO: 534:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 534:
- 10 Thr Cys Glu His Ser Ser Glu Ala Lys Ala Phe His Asp Tyr
 1 5 10

15 (2) INFORMATION FOR SEQ ID NO: 535:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 535:
- 25 Gln Ala Phe Val Leu Leu Ser Asp Leu Leu Leu Ile Phe Ser Pro Gln
 1 5 10 15
- Met Ile Val Gly Gly Arg Asp Phe Leu Arg Pro Leu Val Phe Phe Pro
 20 25 30
- 30 Glu Ala Thr Leu Gln Ser Glu Leu Ala Ser Phe Leu Met Asp His Val
 35 40 45
- Phe Ile Gln Pro Gly Asp Leu Gly Ser Gly Ala
 50 55
- 35

(2) INFORMATION FOR SEQ ID NO: 536:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 536:
- 45 Ala Cys Ser Tyr Leu Leu Cys Asn Pro Glu Phe Thr Phe Phe Ser Arg
 1 5 10 15
- Ala Asp Phe Ala Arg Ser Gln Leu Val Asp Leu Leu Thr Asp Arg Phe
 20 25 30
- Gln Gln Glu Leu Glu Glu Leu Leu Gln Val Gly
 35 40
- 55

(2) INFORMATION FOR SEQ ID NO: 537:

- 60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids

637

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 537:

5 Gln Lys Gln Leu Ser Ser Leu Arg Asp Arg Met Val Ala Phe Cys Glu
 1 5 10 15
 Leu Cys Gln Ser Cys Leu Ser Asp Val Asp Thr Glu Ile Gln Glu Gln
 20 25 30
 10 Val Ser Thr
 35

15

(2) INFORMATION FOR SEQ ID NO: 538:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

20

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 538:

25 Gln Val Ile Leu Pro Ala Leu Thr Leu Val Tyr Phe Ser Ile Leu Trp
 1 5 10 15
 Thr Leu Thr His Ile Ser Lys Ser Asp Ala Ser
 20 25

30

(2) INFORMATION FOR SEQ ID NO: 539:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

35

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 539:

40 Ser Thr His Asp Leu Thr Arg Trp Glu Leu Tyr Glu Pro Cys Cys Gln
 1 5 10 15
 Leu Leu Gln Lys Ala Val Asp Thr Gly Xaa Val Pro His Gln Val
 20 25 30
 45

(2) INFORMATION FOR SEQ ID NO: 540:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 540:

55

Leu Ala Val Ser Thr Ser Phe Ile Cys Cys Ala Asp Ile Ser Thr Ala
 1 5 10 15

60

Leu Pro Leu Gly Ser Ser Arg Pro Ala Pro Ala Pro Arg His Arg Glu
 20 25 30

638

His Glu His Gly His Gln Ala Arg Pro Pro Arg Leu Leu Xaa Thr Ser
 35 40 45
 5 Leu Met Pro Leu Ser Thr Pro Ala Ala Ala Gln Leu Leu Trp Thr Gln
 50 55 60
 Leu Thr Pro Met Gly Gly Arg Pro Gly Gly Arg His Ser Pro Pro Thr
 65 70 75 80
 10 Leu His Thr Gly Pro Arg Ala Leu Pro Pro Gly Pro Pro His Pro Ser
 85 90 95
 15 Leu His Val Ala Ala Leu Ser Leu Leu Arg
 100 105

20 (2) INFORMATION FOR SEQ ID NO: 541:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 207 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 541:

Glu Gln Val Leu Ala Leu Leu Trp Pro Arg Phe Glu Leu Ile Leu Glu
 1 5 10 15
 30 Met Asn Val Gln Ser Val Arg Ser Thr Asp Pro Gln Arg Leu Gly Gly
 20 25 30
 Leu Asp Thr Arg Pro His Tyr Ile Thr Arg Arg Tyr Ala Glu Phe Ser
 35 40 45
 35 Ser Ala Leu Val Ser Ile Asn Gln Thr Ile Pro Asn Glu Arg Thr Met
 50 55 60
 40 Gln Leu Leu Gly Gln Leu Gln Val Glu Val Glu Asn Phe Val Leu Arg
 65 70 75 80
 Val Ala Ala Glu Phe Ser Ser Arg Lys Glu Gln Leu Val Phe Leu Ile
 85 90 95
 45 Asn Asn Tyr Asp Met Met Leu Gly Val Leu Met Glu Arg Ala Ala Asp
 100 105 110
 Asp Ser Lys Glu Val Glu Ser Phe Gln Gln Leu Leu Asn Ala Arg Thr
 115 120 125
 50 Gln Glu Phe Ile Glu Glu Leu Leu Ser Pro Pro Phe Gly Gly Leu Val
 130 135 140
 55 Ala Phe Val Lys Glu Ala Glu Ala Leu Ile Glu Arg Gly Gln Ala Glu
 145 150 155 160
 Arg Leu Arg Gly Glu Glu Ala Arg Val Thr Gln Leu Ile Arg Gly Phe
 165 170 175
 60 Gly Ser Ser Trp Lys Ser Ser Val Glu Ser Leu Ser Gln Asp Val Met

639

180 185 190
 Arg Ser Phe Thr Asn Phe Arg Asn Gly Thr Ser Ile Ile Gln Gly
 195 200 205

5

(2) INFORMATION FOR SEQ ID NO: 542:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 542:

15

Ala Leu Leu Lys Tyr Arg Phe Phe Tyr Gln Phe Leu Leu Gly Asn Glu
 1 5 10 15

20

Arg Ala Thr Ala Lys Glu Ile Arg Asp Glu Tyr Val Glu Thr Leu Ser
 20 25 30

Lys Ile Tyr Leu Ser Tyr Tyr Arg Ser Tyr Leu Gly Arg Leu Met Lys
 35 40 45

25

Val Gln Tyr Glu Glu Val Ala Glu Lys Asp Asp Leu Met Gly Val Glu
 50 55 60

Asp Thr Ala Lys Lys Gly Phe Xaa Ser Lys Pro Ser Leu Arg Ser Arg
 65 70 75 80

30

Asn Thr Ile Phe Thr Leu Gly Thr Arg Gly Ser Val Ile Ser Pro Thr
 85 90 95

35

Glu Leu Glu Ala Pro Ile Leu Val Pro His Thr Ala Gln Arg
 100 105 110

(2) INFORMATION FOR SEQ ID NO: 543:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 543:

Glu Gln Arg Tyr Pro Phe Glu Ala Leu Phe Arg Ser Gln His Tyr Xaa
 1 5 10 15

50

Leu Leu Asp Asn Ser Cys Arg Glu Tyr Leu Phe Ile Cys Glu Phe Phe
 20 25 30

Val Val Ser Gly Pro Xaa Ala His Asp Leu Phe His Ala Val Met Gly
 35 40 45

55

Arg Thr Leu Ser Met Thr Leu Lys His Leu Asp Ser Tyr Leu Ala Asp
 50 55 60

60

Cys Tyr Asp Ala Ile Ala Val Phe Leu Cys Ile His Ile Val Leu Arg
 65 70 75 80

640

Phe Arg Asn Ile Ala Ala Lys Arg Asp Val Pro Ala Leu Asp Arg Tyr
 85 90 95

5 Trp

10 (2) INFORMATION FOR SEQ ID NO: 544:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 544:

Gly Gly Leu Asp Thr Arg Pro His Tyr Ile Thr Arg Arg Tyr Ala Glu
 1 5 10 15

20

Phe Ser Ser Ala Leu Val Ser Ile Asn Gln
 20 25

25

(2) INFORMATION FOR SEQ ID NO: 545:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

30 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 545:

Ser Arg Lys Glu Gln Leu Val Phe Leu Ile Asn Asn Tyr Asp Met Met
 1 5 10 15

35

Leu Gly Val Leu
 20

40

(2) INFORMATION FOR SEQ ID NO: 546:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 411 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 546:

50 Ala Leu Leu Lys Tyr Arg Phe Phe Tyr Gln Phe Leu Leu Gly Asn Glu
 1 5 10 15

Arg Ala Thr Ala Lys Glu Ile Arg Asp Glu Tyr Val Glu Thr Leu Ser
 20 25 30

55

Lys Ile Tyr Leu Ser Tyr Tyr Arg Ser Tyr Leu Gly Arg Leu Met Lys
 35 40 45

60

Val Gln Tyr Glu Glu Val Ala Glu Lys Asp Asp Leu Met Gly Val Glu
 50 55 60

641

Asp Thr Ala Lys Lys Gly Phe Xaa Ser Lys Pro Ser Leu Arg Ser Arg
 65 70 75 80

5 Asn Thr Ile Phe Thr Leu Gly Thr Arg Gly Ser Val Ile Ser Pro Thr
 85 90 95

Glu Leu Glu Ala Pro Ile Leu Val Pro His Thr Ala Gln Arg Xaa Glu
 100 105 110

10 Gln Arg Tyr Pro Phe Glu Ala Leu Phe Arg Ser Gln His Tyr Xaa Leu
 115 120 125

Leu Asp Asn Ser Cys Arg Glu Tyr Leu Phe Ile Cys Glu Phe Phe Val
 130 135 140

15 Val Ser Gly Pro Xaa Ala His Asp Leu Phe His Ala Val Met Gly Arg
 145 150 155 160

20 Thr Leu Ser Met Thr Leu Lys His Leu Asp Ser Tyr Leu Ala Asp Cys
 165 170 175

Tyr Asp Ala Ile Ala Val Phe Leu Cys Ile His Ile Val Leu Arg Phe
 180 185 190

25 Arg Asn Ile Ala Ala Lys Arg Asp Val Pro Ala Leu Asp Arg Tyr Trp
 195 200 205

Glu Gln Val Leu Ala Leu Leu Trp Pro Arg Phe Glu Leu Ile Leu Glu
 210 215 220

30 Met Asn Val Gln Ser Val Arg Ser Thr Asp Pro Gln Arg Leu Gly Gly
 225 230 235 240

35 Leu Asp Thr Arg Pro His Tyr Ile Thr Arg Arg Tyr Ala Glu Phe Ser
 245 250 255

Ser Ala Leu Val Ser Ile Asn Gln Thr Ile Pro Asn Gln Arg Thr Met
 260 265 270

40 Gln Leu Leu Gly Gln Leu Gln Val Glu Val Glu Asn Phe Val Leu Arg
 275 280 285

Val Ala Ala Glu Phe Ser Ser Arg Lys Glu Gln Leu Val Phe Leu Ile
 290 295 300

45 Asn Asn Tyr Asp Met Met Leu Gly Val Leu Met Glu Arg Ala Ala Asp
 305 310 315 320

50 Asp Ser Lys Glu Val Glu Ser Phe Gln Gln Leu Leu Asn Ala Arg Thr
 325 330 335

Gln Glu Phe Ile Glu Glu Leu Leu Ser Pro Pro Phe Gly Gly Leu Val
 340 345 350

55 Ala Phe Val Lys Glu Ala Glu Ala Leu Ile Glu Arg Gly Gln Ala Glu
 355 360 365

60 Arg Leu Arg Gly Glu Glu Ala Arg Val Thr Gln Leu Ile Arg Gly Phe
 370 375 380

642

Gly Ser Ser Trp Lys Ser Ser Val Glu Ser Leu Ser Gln Asp Val Met
385 390 395 400

5 Arg Ser Phe Thr Asn Phe Arg Asn Gly Thr Ser
405 410

10 (2) INFORMATION FOR SEQ ID NO: 547:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 303 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 547:

20 Tyr Glu Gly Lys Glu Phe Asp Tyr Val Phe Ser Ile Asp Val Asn Glu
1 5 10 15

Gly Gly Pro Ser Tyr Lys Leu Pro Tyr Asn Thr Ser Asp Asp Pro Trp
20 25 30

25 Leu Thr Ala Tyr Asn Phe Leu Gln Lys Asn Asp Leu Asn Pro Met Phe
35 40 45

Leu Asp Gln Val Ala Lys Phe Ile Ile Asp Asn Thr Lys Gly Gln Met
50 55 60

30 Leu Gly Leu Gly Asn Pro Ser Phe Ser Asp Pro Phe Thr Gly Gly Gly
65 70 75 80

Arg Tyr Val Pro Gly Ser Ser Gly Ser Ser Asn Thr Leu Pro Thr Ala
85 90 95

35 Asp Pro Phe Thr Gly Ala Gly Arg Tyr Val Pro Gly Ser Ala Ser Met
100 105 110

40 Gly Thr Thr Met Ala Gly Val Asp Pro Phe Thr Gly Asn Ser Ala Tyr
115 120 125

Arg Ser Ala Ala Ser Lys Thr Met Asn Ile Tyr Phe Pro Lys Lys Glu
130 135 140

45 Ala Val Thr Phe Asp Gln Ala Asn Pro Thr Gln Ile Leu Gly Lys Leu
145 150 155 160

Lys Glu Leu Asn Gly Thr Ala Pro Glu Glu Lys Lys Leu Thr Glu Asp
165 170 175

50 Asp Leu Ile Leu Leu Glu Lys Ile Leu Ser Leu Ile Cys Asn Ser Ser
180 185 190

55 Ser Glu Lys Pro Thr Val Gln Gln Leu Gln Ile Leu Trp Lys Ala Ile
195 200 205

Asn Cys Pro Glu Asp Ile Val Phe Pro Ala Leu Asp Ile Leu Arg Leu
210 215 220

60 Ser Ile Lys His Pro Ser Val Asn Glu Asn Phe Cys Asn Glu Lys Glu

643

225 230 235 240
 Gly Ala Gln Phe Ser Ser His Leu Ile Asn Leu Leu Asn Pro Lys Gly
 245 250 255
 5 Lys Pro Ala Asn Gln Leu Leu Ala Leu Arg Thr Phe Cys Asn Cys Phe
 260 265 270
 10 Val Gly Gln Ala Gly Gln Lys Leu Met Met Ser Gln Arg Glu Ser Leu
 275 280 285
 Met Ser His Ala Ile Glu Leu Lys Ser Gly Ser Asn Lys Asn Ile
 290 295 300

15

(2) INFORMATION FOR SEQ ID NO: 548:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 548:

25 His Ile Ala Leu Ala Thr Leu Ala Leu Asn Tyr Ser Val Cys Phe His
 1 5 10 15

Lys Asp

30

(2) INFORMATION FOR SEQ ID NO: 549:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 49 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 549:

40

His Asn Ile Glu Gly Lys Ala Gln Cys Leu Ser Leu Ile Ser Thr Ile
 1 5 10 15

45 Leu Glu Val Val Gln Asp Leu Glu Ala Thr Phe Arg Leu Leu Val Ala
 20 25 30

Leu Gly Thr Leu Ile Ser Asp Asp Ser Asn Ala Val Gln Leu Ala Lys
 35 40 45

50 Ser

55 (2) INFORMATION FOR SEQ ID NO: 550:

60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

644

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 550:

Leu Gly Val Asp Ser Gln Ile Lys Lys Tyr Ser Ser Val Ser Glu Pro
 1 5 10 15

Ala Lys Val Ser Glu Cys Cys Arg Phe Ile Leu Asn Leu Leu
 20 25 30

10

(2) INFORMATION FOR SEQ ID NO: 551:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 551:

Tyr Glu Gly Lys Glu Phe Asp Tyr Val Phe Ser Ile Asp Val Asn Glu
 20 1 5 10 15

Gly Gly Pro Ser Tyr Lys Leu Pro Tyr Asn Thr Ser Asp Asp Pro Trp
 20 25 30

Leu Thr Ala Tyr Asn Phe Leu Gln Lys Asn Asp Leu Asn Pro Met Phe
 35 40 45

Leu Asp Gln Val Ala Lys Phe Ile Ile Asp Asn Thr Lys Gly Gln Met
 50 55 60

30

Leu Gly Leu Gly Asn Pro Ser Phe Ser Asp Pro Phe Thr Gly Gly Gly
 65 70 75 80

Arg Tyr Val Pro Gly Ser Ser Gly Ser Ser Asn Thr Leu Pro Thr Ala
 85 90 95

35

Asp Pro Phe Thr Gly Ala Gly Arg Tyr Val Pro Gly Ser Ala Ser Met
 100 105 110

Gly Thr Thr Met Ala Gly Val Asp Pro Phe Thr Gly Asn Ser Ala Tyr
 115 120 125

40

Arg Ser Ala Ala Ser Lys Thr Met Asn Ile Tyr Phe Pro Lys Lys Glu
 130 135 140

45

Ala Val Thr Phe Asp Gln Ala Asn Pro Thr Gln Ile Leu Gly Lys Leu
 145 150 155 160

Lys Glu Leu Asn Gly Thr Ala Pro Glu Glu Lys Lys Leu Thr Glu Asp
 165 170 175

50

Asp Leu Ile Leu Leu Glu Lys Ile Leu Ser Leu Ile Cys Asn Ser Ser
 180 185 190

Ser Glu Lys Pro Thr Val Gln Gln Leu Gln Ile Leu Trp Lys Ala Ile
 195 200 205

55

Asn Cys Pro Glu Asp Ile Val Phe Pro Ala Leu Asp Ile Leu Arg Leu
 210 215 220

60

645

Ser Ile Lys His Pro Ser Val Asn Glu Asn Phe Cys Asn Glu Lys Glu
 225 230 235 240
 Gly Ala Gln Phe Ser Ser His Leu Ile Asn Leu Leu Asn Pro Lys Gly
 5 245 250 255
 Lys Pro Ala Asn Gln Leu Leu Ala Leu Arg Thr Phe Cys Asn Cys Phe
 260 265 270
 10 Val Gly Gln Ala Gly Gln Lys Leu Met Met Ser Gln Arg Glu Ser Leu
 275 280 285
 Met Ser His Ala Ile Glu Leu Lys Ser Gly Ser Asn Lys Asn Ile His
 290 295 300
 15 Ile Ala Leu Ala Thr Leu Ala Leu Asn Tyr Ser Val Cys Phe His Lys
 305 310 315 320
 Asp His Asn Ile Glu Gly Lys Ala Gln Cys Leu Ser Leu Ile Ser Thr
 20 325 330 335
 Ile Leu Glu Val Val Gln Asp Leu Glu Ala Thr Phe Arg Leu Leu Val
 340 345 350
 25 Ala Leu Gly Thr Leu Ile Ser Asp Asp Ser Asn Ala Val Gln Leu Ala
 355 360 365
 Lys Ser Leu Gly Val Asp Ser Gln Ile Lys Lys Tyr Ser Ser Val Ser
 370 375 380
 30 Glu Pro Ala Lys Val Ser Glu Cys Cys Arg Phe Ile Leu Asn Leu Leu
 385 390 395 400

35

- 40 (2) INFORMATION FOR SEQ ID NO: 552:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 139 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 552:

Tyr Pro Asn Gln Asp Gly Asp Ile Leu Arg Asp Gln Val Leu His Glu
 1 5 10 15
 50 His Ile Gln Arg Leu Ser Lys Val Val Thr Ala Asn His Arg Ala Leu
 20 25 30
 Gln Ile Pro Glu Val Tyr Leu Arg Glu Ala Pro Trp Pro Ser Ala Gln
 35 40 45
 55 Ser Glu Ile Arg Thr Ile Ser Ala Tyr Lys Thr Pro Arg Asp Lys Val
 50 55 60
 60 Gln Cys Ile Leu Arg Met Cys Ser Thr Ile Met Asn Leu Leu Ser Leu
 65 70 75 80

646

Ala Asn Glu Asp Ser Val Pro Gly Ala Asp Asp Phe Val Pro Val Leu
85 90 95

5 Val Phe Val Leu Ile Lys Ala Asn Pro Cys Leu Leu Ser Thr Val
100 105 110

Gln Tyr Ile Ser Ser Phe Tyr Ala Ser Cys Leu Ser Gly Glu Glu Ser
115 120 125

10 Tyr Trp Trp Met Gln Phe Thr Ala Ala Val Glu
130 135

15

(2) INFORMATION FOR SEQ ID NO: 553:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 144 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 553:

25 Tyr Pro Asn Gln Asp Gly Asp Ile Leu Arg Asp Gln Val Leu His Glu
1 5 10 15

His Ile Gln Arg Leu Ser Lys Val Val Thr Ala Asn His Arg Ala Leu
20 25 30

30 Gln Ile Pro Glu Val Tyr Leu Arg Glu Ala Pro Trp Pro Ser Ala Gln
35 40 45

Ser Glu Ile Arg Thr Ile Ser Ala Tyr Lys Thr Pro Arg Asp Lys Val
50 55 60

35 Gln Cys Ile Leu Arg Met Cys Ser Thr Ile Met Asn Leu Leu Ser Leu
65 70 75 80

Ala Asn Glu Asp Ser Val Pro Gly Ala Asp Asp Phe Val Pro Val Leu
40 85 90 95

Val Phe Val Leu Ile Lys Ala Asn Pro Pro Cys Leu Leu Ser Thr Val
100 105 110

45 Gln Tyr Ile Ser Ser Phe Tyr Ala Ser Cys Leu Ser Gly Glu Glu Ser
115 120 125

Tyr Trp Trp Met Gln Phe Thr Ala Ala Val Glu Phe Ile Lys Thr Ile
130 135 140

50

55

(2) INFORMATION FOR SEQ ID NO: 554:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid

60

647

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 554:

5 Tyr Pro Asn Gln Asp Gly Asp Ile Leu Arg Asp Gln Val Leu
 1 5 10

10 (2) INFORMATION FOR SEQ ID NO: 555:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 555:

Glu Ala Pro Trp Pro Ser Ala Gln Ser Glu Ile
 1 5 10

20

(2) INFORMATION FOR SEQ ID NO: 556:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 556:

30 Ser Gly Glu Glu Ser Tyr Trp Trp Met Gln Phe Thr Ala Ala Val Glu
 1 5 10 15

Phe Ile Lys Thr Ile
 20

35

(2) INFORMATION FOR SEQ ID NO: 557:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 557:

Ala Asp Asp Phe Val Pro Val Leu Val Phe Val Leu Ile Lys Ala Asn
 1 5 10 15

50 Pro Pro

55 (2) INFORMATION FOR SEQ ID NO: 558:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 558:

648

Tyr Lys Thr Pro Arg Asp Lys Val Gln Cys Ile Leu
 1 5 10

5

(2) INFORMATION FOR SEQ ID NO: 559:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 559:

Gly Ala Asp Asp Phe Val Pro Val Leu Val Phe Val Leu Ile Lys
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 560:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 560:

Pro Val Leu Val Phe Val Leu Ile Lys Ala Asn Pro
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 561:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 561:

Ser Ala Arg Ala Ser Thr Gln Pro Pro Ala Gly Gln His Pro Gly Pro
 1 5 10 15

Cys

(2) INFORMATION FOR SEQ ID NO: 562:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 562:

Met Pro Gly Arg Trp Arg Trp Gln Arg Asp Met His Pro Ala Arg Lys
 1 5 10 15

Leu Leu Ser Leu Leu Phe Leu Ile Leu Met Gly Thr Glu Leu Thr Gln

649

20 25 30

Asp

5

(2) INFORMATION FOR SEQ ID NO: 563:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 563:

15 Ser Ala Ala Pro Asp Ser Leu Leu Arg Ser Ser Lys Gly Ser Thr Arg
1 5 10 15

Gly Ser Leu

20

(2) INFORMATION FOR SEQ ID NO: 564:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 564:

30 Ala Ala Ile Val Ile Trp Arg Gly Lys Ser Glu Ser Arg Ile Ala Lys
1 5 10 15

35 Thr Pro Gly Ile
20

(2) INFORMATION FOR SEQ ID NO: 565:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 565:

45 Pro Leu Gly Ile Thr Leu Pro Leu Gly Ala Pro Glu Thr Gly Gly Gly
1 5 10 15

50 Asp

55

(2) INFORMATION FOR SEQ ID NO: 566:

60 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid

650

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 566:

5 Cys Ala Ala Glu Thr Trp Lys Gly Ser Gln Arg Ala Gly Gln Leu Cys
 1 5 10 15
 Ala Leu Leu Ala
 20

10

(2) INFORMATION FOR SEQ ID NO: 567:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 567:

20 Phe Arg Gly Gly Gly Thr Leu Val Leu Pro Pro Thr His Thr Pro Glu
 1 5 10 15
 Trp Leu Ile Leu
 20

25

(2) INFORMATION FOR SEQ ID NO: 568:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 568:

35 Met Arg Ser Ala Arg Pro Ser Leu Gly Cys Leu Pro Ser Trp Ala Phe
 1 5 10 15
 Ser Gln Ala Leu Asn Ile
 40 20

40

(2) INFORMATION FOR SEQ ID NO: 569:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 569:

50

Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile Ser Ala Val Cys
 1 5 10 15
 Glu Lys Gly Asn Phe Asn
 20

55

60 (2) INFORMATION FOR SEQ ID NO: 570:

651

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 570:

Val Ala His Gly Leu Ala Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu
 1 5 10 15

Ile Leu Pro Glu Leu Gln Ala Arg Ile Arg
 20 25

(2) INFORMATION FOR SEQ ID NO: 571:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 571:

Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly Ala Val Ser Gln
 1 5 10 15

Arg Cys

(2) INFORMATION FOR SEQ ID NO: 572:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 572:

Ile Leu Leu Pro Leu Asp Cys Gly Val Pro Asp Asn Leu Ser Met Ala
 1 5 10 15

Asp Pro Asn Ile Arg Phe Leu Asp Lys Leu Pro Gln Gln Thr Gly Asp
 20 25 30

Arg Ala Gly Ile Lys Asp Arg Val Tyr Ser Asn
 35 40

(2) INFORMATION FOR SEQ ID NO: 573:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 573:

Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr Cys Val
 1 5 10 15

652

Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser Gln Tyr
 20 25 30

5 Ser Gln Ala Gly Phe Ser Gly Glu Asp Arg Leu Glu Gln
 35 40 45

10 (2) INFORMATION FOR SEQ ID NO: 574:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 574:

Ala Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro
 1 5 10 15

20

Glu Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp
 20 25 30

25

Asp Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln
 35 40 45

Glu Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val
 50 55 60

30

Pro Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly
 65 70 75 80

Met Glu Lys Pro Leu Pro Leu Arg Thr Asp Phe Ser
 85 90

35

(2) INFORMATION FOR SEQ ID NO: 575:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 575:

45

Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile Ser Ala Val Cys
 1 5 10 15

50

Glu Lys Gly Asn Phe Asn Val Ala His Gly Leu Ala Trp Ser Tyr Tyr
 20 25 30

Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu
 35 40

55

(2) INFORMATION FOR SEQ ID NO: 576:

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 22 amino acids

653

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 576:

5 Thr Met Lys Leu Leu Lys Leu Arg Arg Asn Ile Val Lys Leu Ser Leu
 1 5 10 15
 Tyr Arg His Phe Thr Asn
 20

10

(2) INFORMATION FOR SEQ ID NO: 577:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 577:

20 Thr Leu Ile Leu Ala Val Ala Ala Ser Ile Val Phe Ile Ile Trp Thr
 1 5 10 15
 Thr Met Lys Phe Arg Ile
 25

25

(2) INFORMATION FOR SEQ ID NO: 578:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 578:

35

Val Thr Cys Gln Ser Asp Trp Arg Glu Leu Trp Val Asp Asp Ala Ile
 1 5 10 15
 Trp Arg Leu Leu Phe Ser Met Ile Leu Phe Val Ile
 20 25

40

45 (2) INFORMATION FOR SEQ ID NO: 579:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 579:

50

Met Val Leu Trp Arg Pro Ser Ala Asn Asn Gln Arg Phe Ala Phe Ser
 1 5 10 15
 Pro Leu Ser Glu Glu Glu Glu Asp Glu Gln
 20 25

55

60

654

(2) INFORMATION FOR SEQ ID NO: 580:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 580:

5
10 Met Val Leu Trp Arg Pro Ser Ala Asn Asn Gln Arg Phe Ala Phe Ser
1 5 10 15
Pro Leu Ser Glu Glu Glu Glu Asp Glu Gln
20 25

15

(2) INFORMATION FOR SEQ ID NO: 581:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 581:

20
25 Lys Glu Pro Met Leu Lys Glu Ser Phe Glu Gly Met Lys Met Arg Ser
1 5 10 15
Thr Lys Gln Glu Pro Asn Gly Asn Ser Lys Val Asn Lys Ala Gln Glu
20 25 30
30 Asp Asp Leu
35

35

(2) INFORMATION FOR SEQ ID NO: 582:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 582:

40
45 Lys Trp Val Glu Glu Asn Val Pro Ser Ser Val Thr Asp Val Ala Leu
1 5 10 15
Pro Ala Leu Leu Asp Ser Asp Glu Glu Arg Met Ile Thr His Phe Glu
20 25 30
50 Arg Ser Lys Met Glu
35

55

(2) INFORMATION FOR SEQ ID NO: 583:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

655

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 833:

Asp Pro Arg Val Arg Leu Asn Ser Leu Thr Cys Lys His Ile Phe Ile
 1 5 10 15
 Ser Leu Thr Gln
 20

(2) INFORMATION FOR SEQ ID NO: 834:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 834:

Tyr Glu Pro Met Asp Phe Xaa Met Ala Leu Ile Tyr Asp
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 835:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 835:

Ile Arg His Glu Leu Thr Val Leu Arg Asp Thr Arg Pro Ala Lys Ala
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 836:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 836:

Met Asp Phe Xaa Met Ala Leu Ile Tyr Asp
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 837:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 837:

656

Met Gln Glu Met Met Arg Asn Gln Asp Arg Ala Leu Ser Asn Leu Glu
 1 5 10 15

5 Ser Ile Pro Gly Gly Tyr Asn Ala
 20

10 (2) INFORMATION FOR SEQ ID NO: 588:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 588:

Leu Arg Arg Met Tyr Thr Asp Ile Gln Glu Pro Met Leu Ser Ala Ala
 1 5 10 15

20 Gln Glu Gln Phe Gly Gly Asn Pro Phe
 20 25

25 (2) INFORMATION FOR SEQ ID NO: 589:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 589:

Ala Ser Leu Val Ser Asn Thr Ser Ser Gly Glu Gly Ser Gln Pro Ser
 1 5 10 15

35 Arg Thr Glu Asn Arg Asp Pro Leu Pro Asn Pro Trp Ala Pro Gln Thr
 20 25 30

40

45 (2) INFORMATION FOR SEQ ID NO: 590:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 71 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 590:

Ser Gln Ser Ser Ser Ala Ser Ser Gly Thr Ala Ser Thr Val Gly Gly
 1 5 10 15

55 Thr Thr Gly Ser Thr Ala Ser Gly Thr Ser Gly Gln Ser Thr Thr Ala
 20 25 30

Pro Asn Leu Val Pro Gly Val Gly Ala Ser Met Phe Asn Thr Pro Gly
 35 40 45

60

657

Met Gln Ser Leu Leu Gln Gln Ile Thr Glu Asn Pro Gln Leu Met Gln
 50 55 60

5 Asn Met Leu Ser Ala Pro Tyr
 65 70

(2) INFORMATION FOR SEQ ID NO: 591:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 591:

Met Arg Ser Met Met Gln Ser Leu Ser Gln Asn Pro Asp Leu Ala Ala
 1 5 10 15

20

Gln Met Met Leu Asn Asn Pro Leu Phe Ala Gly Asn Pro Gln Leu Gln
 20 25 30

Glu Gln Met Arg Gln Gln Leu Pro Thr Phe Leu Gln Gln
 35 40 45

25

(2) INFORMATION FOR SEQ ID NO: 592:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 592:

35

Met Gln Asn Pro Asp Thr Leu Ser Ala Met Ser Asn Pro Arg Ala Met
 1 5 10 15

40

Gln Ala Leu Leu Gln Ile Gln Gln Gly Leu Gln Thr Leu Ala Thr Glu
 20 25 30

Ala Pro Gly Leu Ile Pro Gly Phe Thr Pro Gly Leu Gly Ala Leu Gly
 35 40 45

45

Ser Thr Gly Gly Ser Ser Gly Thr Asn Gly Ser Asn Ala Thr Pro Ser
 50 55 60

Glu Asn Thr Ser Pro Thr Ala Gly Thr
 65 70

50

(2) INFORMATION FOR SEQ ID NO: 593:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 593:

60

658

Thr Gln Pro Gly His Gln Gln Phe Ile Gln Gln Met Leu Gln Ala Leu
 1 5 10 15
 Ala Gly Val Asn Pro Gln Leu Gln Asn Pro Glu Val Arg Phe Gln Gln
 5 20 25 30
 Gln Leu Gln Gln Leu Ser Ala Met Gly Phe Leu Asn Arg Glu Ala Asn
 35 40 45
 Leu Gln Ala Leu Ile Ala Thr Gly Gly Asp Ile Asn Ala Ala Ile Glu
 50 55 60
 Arg Leu Leu Gly Ser Gln Pro Ser
 65 70
 15

(2) INFORMATION FOR SEQ ID NO: 594:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 45 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 594:
 25 Arg Asn Pro Ala Met Met Gln Glu Met Met Arg Asn Gln Asp Arg Ala
 1 5 10 15
 Leu Ser Asn Leu Glu Ser Ile Pro Gly Gly Tyr Asn Ala Leu Arg Arg
 30 20 25 30
 Met Tyr Thr Asp Ile Gln Glu Pro Met Leu Ser Ala Ala
 35 40 45
 35

(2) INFORMATION FOR SEQ ID NO: 595:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 595:
 45 Gly Asn Pro Phe Ala Ser Leu Val Ser Asn Thr Ser Ser
 1 5 10

50 (2) INFORMATION FOR SEQ ID NO: 596:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 596:

Glu Asn Arg Asp Pro Leu Pro Asn Pro Trp Ala
 1 5 10
 60

(2) INFORMATION FOR SEQ ID NO: 597:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 597:
10 Gly Lys Ile Leu Lys Asp Gln Asp Thr Leu Ser Gln His Gly Ile His
1 5 10 15
15 Asp

(2) INFORMATION FOR SEQ ID NO: 598:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 598:
Gly Leu Thr Val His Leu Val Ile Lys Thr Gln Asn Arg Pro
1 5 10
30

(2) INFORMATION FOR SEQ ID NO: 599:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 599:
40 Ser Glu Leu Gln Ser Gln Met Gln Arg Gln Leu Leu Ser Asn Pro Glu
1 5 10 15
Met Met
45

(2) INFORMATION FOR SEQ ID NO: 600:

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 600:
55 Pro Glu Ile Ser His Met Leu Asn Asn Pro Asp Ile Met Arg
1 5 10
60

660

(2) INFORMATION FOR SEQ ID NO: 501:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501:

Arg Gln Leu Ile Met Ala Asn Pro Gln Met Gln Gln Leu Ile Gln Arg
 1 5 10 15
 Asn Pro

15

(2) INFORMATION FOR SEQ ID NO: 502:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502:

Asn Leu Cys His Val Asp Cys Gln Asp Leu Leu Asn Pro Asn Leu Leu
 1 5 10 15
 Ala Gly Ile His Cys Ala Lys Arg Ile Val Ser
 20 25

30

(2) INFORMATION FOR SEQ ID NO: 503:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503:

Leu Asp Gly Phe Glu Gly Tyr Ser Leu Ser Asp Trp Leu Cys Leu Ala
 1 5 10 15
 Phe Val Glu Ser Lys Phe Asn
 20

45

(2) INFORMATION FOR SEQ ID NO: 504:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 504:

Asn Glu Asn Ala Asp Gly Ser Phe Asp Tyr Gly Leu Phe Gln Ile Asn
 1 5 10 15
 Ser His Tyr Trp Cys Asn

60

661

20

5 (2) INFORMATION FOR SEQ ID NO: 605:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 605:

Asn Leu Cys His Val Asp Cys Gln Asp Leu Leu Asn Pro Asn Leu Leu
1 5 10 15

15 Ala Gly Ile His Cys Ala Lys Arg Ile Val Ser
20 25

20

(2) INFORMATION FOR SEQ ID NO: 606:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

25 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 606:

30 Ile Arg Glu Val Asn Glu Val Ile Gln Asn Pro Ala Thr
1 5 10

35 (2) INFORMATION FOR SEQ ID NO: 607:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 607:

Ile Thr Arg Ile Leu Leu Ser His Phe Asn Trp Asp Lys Glu Lys Leu
1 5 10 15

45 Met Glu Arg Tyr Phe Asp Gly Asn Leu Glu Lys Leu Phe Ala
20 25 30

50 (2) INFORMATION FOR SEQ ID NO: 608:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 608:

Asn Thr Arg Ser Ser Ala Gln Asp Met Pro Cys Gln Ile Cys Tyr Leu
1 5 10 15

60

662

Asn Tyr Pro Asn Ser Tyr Phe
20

5

(2) INFORMATION FOR SEQ ID NO: 609:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

10

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 609:

15

Cys Asp Ile Leu Val Asp Asp Asn Thr Val Met Arg Leu Ile Thr Asp
1 5 10 15

Ser Lys Val Lys Leu Lys Tyr Gln His Leu Ile Thr Asn Ser Phe Val
20 25 30

20

Glu Cys Asn Arg Leu Leu Lys Trp Cys Pro Ala Pro Asp Cys His His
35 40 45

Val Val Lys Val Gln Tyr Pro Asp Ala Lys Pro Val
50 55 60

25

(2) INFORMATION FOR SEQ ID NO: 610:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 610:

35

Cys Asp Ile Leu Val Asp Asp Asn Thr Val Met Arg Leu Ile Thr Asp
1 5 10 15

40

Ser Lys Val Lys Leu Lys Tyr Gln His Leu Ile Thr Asn Ser Phe Val
20 25 30

Glu Cys Asn Arg Leu Leu Lys Trp Cys Pro Ala Pro Asp Cys His His
35 40 45

45

Val Val Lys Val
50

50

(2) INFORMATION FOR SEQ ID NO: 611:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

55

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 611:

Gly Cys Asn His Met Val Cys Arg Asn Gln Asn Cys Lys Ala Glu Phe
1 5 10 15

60

663

Cys Trp Val Cys Leu Gly Pro Trp Glu Pro His Gly Ser Ala Trp Tyr
 20 25 30

5 Asn Cys Asn Arg Tyr Asn Glu Asp Asp Ala Lys Ala Ala Arg Asp Ala
 35 40 45

Gln Glu Arg Ser Arg Ala Ala Leu Gln Arg Tyr Leu
 50 55 60

10

(2) INFORMATION FOR SEQ ID NO: 612:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 612:

20 Phe Tyr Cys Asn Arg Tyr Met Asn His Met Gln Ser Leu Arg Phe Glu
 1 5 10 15

His Lys Leu Tyr Ala Gln Val Lys Gln Lys Met Glu Glu Met Gln Gln
 20 25 30

25

His Asn Met Ser Trp Ile Glu Val Gln Phe Leu Lys Lys Ala Val Asp
 35 40 45

30 Val Leu Cys Gln Cys Arg Ala Thr Leu Met Tyr Thr
 50 55 60

35 (2) INFORMATION FOR SEQ ID NO: 613:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 613:

Tyr Val Phe Ala Phe Tyr Leu Lys Lys Asn Asn Gln Ser Ile Ile Phe
 1 5 10 15

45 Glu Asn Asn Gln Ala Asp Leu Glu Asn Ala Thr Glu Val Leu Ser Gly
 20 25 30

Tyr Leu Glu Arg Asp Ile Ser Gln Asp Ser Leu Gln Asp Ile Lys Gln
 35 40 45

50

Lys Val Gln Asp Lys Tyr Arg Tyr Cys Glu Ser Arg
 50 55 60

55

(2) INFORMATION FOR SEQ ID NO: 614:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

60

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 614:

5 Thr Gly Leu Glu Cys Gly His Lys Phe Cys Met Gln Cys Trp Ser Glu
1 5 10 15
Tyr Leu Thr Thr Lys Ile Met Glu Glu Gly Met Gly Gln Thr Ile Ser
20 25 30
10 Cys Pro Ala His Gly
35

15 (2) INFORMATION FOR SEQ ID NO: 615:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 615:

25 Met Trp Gly Tyr Leu Phe Val Asp Ala Ala Trp Asn Phe Leu Gly Cys
1 5 10 15
Leu Ile Cys Gly Trp
20

30

(2) INFORMATION FOR SEQ ID NO: 616:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 616:

40 Met His Phe Ile Ser Ser Gly Asn Val Ser Ala Ile Arg Ser Ser Ile
1 5 10 15
Leu Leu Leu Arg Xaa Ser Leu Ser Tyr Leu Gly Asn Cys Leu Arg Val
20 25 30
45 Ser Ala Ile Phe Val Tyr Phe Leu Leu Phe Leu Leu Ser
35 40 45

50 (2) INFORMATION FOR SEQ ID NO: 617:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 617:

Met Asp Gln Ala Leu Arg Gly Ser Pro Ser Glu Gly Phe Ser Thr Asp
1 5 10 15

665

Pro Ser Pro Pro Gln Val Gly Arg Gln Ile Pro Ser Phe Pro Pro Trp
 20 25 30

Arg Arg Leu Val Leu Pro Lys Ala Ser Gly Cys Phe Leu Glu Arg Glu
 5 35 40 45

Trp Trp Leu Cys Val Phe Lys Leu Arg Thr Arg Pro Gly Ala Glu Ala
 50 55 60

10 His Ala Tyr Asn Ser Ser Ile Leu Gly Gly Arg Gly Lys Gly Ile Thr
 65 70 75 80

15

(2) INFORMATION FOR SEQ ID NO: 618:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 618:

25

Met Leu Pro Ala Leu Ala Ser Cys Cys His Phe Ser Pro Pro Glu Gln
 1 5 10 15

30

Ala Ala Arg Leu Lys Lys Leu Gln Glu Gln Glu Lys Gln Gln Lys Val
 20 25 30

Glu Phe Arg Lys Arg Met Glu Lys Glu Val Ser Asp Phe Ile Gln Asp
 35 40 45

35

Ser Gly Gln Ile Lys Lys Lys Phe Gln Pro Met Asn Lys Ile Glu Arg
 50 55 60

40

Ser Ile Leu His Asp Val Val Glu Val Ala Gly Leu Thr Ser Phe Ser
 65 70 75 80

Phe Gly Glu Asp Asp Asp Cys Arg Tyr Val Met Ile Phe Lys Lys Glu
 85 90 95

45

Phe Ala Pro Ser Asp Glu Glu Leu Asp Ser Tyr Arg Arg Gly Glu Glu
 100 105 110

Trp Asp Pro Gln Lys Ala Glu Glu Lys Arg Asn Xaa Lys Glu Leu Ala
 115 120 125

50

Gln Arg Gln
 130

55

(2) INFORMATION FOR SEQ ID NO: 619:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 amino acids

(B) TYPE: amino acid

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 619:

	Glu	Glu	Glu	Ala	Ala	Gln	Gln	Gly	Pro	Val	Val	Val	Ser	Pro	Ala	Ser
	1				5					10					15	
5	Asp	Tyr	Lys	Asp	Lys	Tyr	Ser	His	Leu	Ile	Gly	Lys	Gly	Ala	Ala	Lys
				20					25					30		
	Asp	Ala	Ala	His	Met	Leu	Gln	Ala	Asn	Lys	Thr	Tyr	Gly	Cys	Xaa	Pro
10			35					40					45			
	Val	Ala	Asn	Lys	Arg	Asp	Thr	Arg	Ser	Ile	Glu	Glu	Ala	Met	Asn	Glu
		50					55					60				
15	Ile	Arg	Ala	Lys	Lys	Arg	Leu	Arg	Gln	Ser	Gly	Glu				
	65					70					75					

20 (2) INFORMATION FOR SEQ ID NO: 620:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 620:

30 Pro Pro Arg Arg Pro Ala Gln Leu Pro Leu Thr Pro Gly Ala Gly Gln
1 5 10 15
Gly Ala Gly Arg Asp Lys Ala Ala Ala Ile Arg Ala His Pro Gly Ala
20 25 30

35 Pro Pro Leu Asn His Leu Leu Pro
35 40

40 (2) INFORMATION FOR SEQ ID NO: 621:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 621:

Ala Val Pro Gln Ala Gly Gly Lys Gln Val Phe Asp Leu Ser Pro Leu
1 5 10 15

50 Glu Leu Gly Tyr Val Arg Gly Met Cys Val Cys Val
20 25

55 (2) INFORMATION FOR SEQ ID NO: 622:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 207 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

667

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 622:

5 Met Leu Pro Ala Leu Ala Ser Cys Cys His Phe Ser Pro Pro Glu Gln
 1 5 10 15
 Ala Ala Arg Leu Lys Lys Leu Gln Glu Lys Gln Gln Lys Val
 20 25 30
 10 Glu Phe Arg Lys Arg Met Glu Lys Glu Val Ser Asp Phe Ile Gln Asp
 35 40 45
 Ser Gly Gln Ile Lys Lys Lys Phe Gln Pro Met Asn Lys Ile Glu Arg
 50 55 60
 15 Ser Ile Leu His Asp Val Val Glu Val Ala Gly Leu Thr Ser Phe Ser
 65 70 75 80
 Phe Gly Glu Asp Asp Asp Cys Arg Tyr Val Met Ile Phe Lys Lys Glu
 85 90 95
 20 Phe Ala Pro Ser Asp Glu Glu Leu Asp Ser Tyr Arg Arg Gly Glu Glu
 100 105 110
 Trp Asp Pro Gln Lys Ala Glu Glu Lys Arg Asn Xaa Lys Glu Leu Ala
 115 120 125
 Gln Arg Gln Glu Glu Glu Ala Ala Gln Gln Gly Pro Val Val Val Ser
 130 135 140
 30 Pro Ala Ser Asp Tyr Lys Asp Lys Tyr Ser His Leu Ile Gly Lys Gly
 145 150 155 160
 Ala Ala Lys Asp Ala Ala His Met Leu Gln Ala Asn Lys Thr Tyr Gly
 165 170 175
 35 Cys Xaa Pro Val Ala Asn Lys Arg Asp Thr Arg Ser Ile Glu Glu Ala
 180 185 190
 Met Asn Glu Ile Arg Ala Lys Lys Arg Leu Arg Gln Ser Gly Glu
 195 200 205
 40

(2) INFORMATION FOR SEQ ID NO: 623:

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 623:

55 Leu Leu Cys Pro Val Leu Asn Ser Gly Xaa Ser Trp Asn Phe Pro His
 1 5 10 15
 Pro Ser Gln Pro Glu Tyr Ser Phe His Gly Phe His Ser Thr Arg Leu
 20 25 30
 Trp Ile
 60

(2) INFORMATION FOR SEQ ID NO: 624:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 624:

Pro Ser Thr Pro Trp Phe Leu Phe Leu Leu Gly Leu Thr Cys Pro Phe
 1 5 10 15
 Ser Thr Ser His Pro Arg Trp Asp Ser Ile Pro Pro
 15 20 25

(2) INFORMATION FOR SEQ ID NO: 625:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 227 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 625:

Glu Leu Ser Ile Ser Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu
 1 5 10 15
 Tyr Thr Cys Ser Ile Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu
 20 25 30
 Val Thr Val Leu Gly Ile Pro Gln Lys Pro Ile Ile Thr Gly Tyr Lys
 35 40 45
 Ser Ser Leu Arg Glu Lys Asp Thr Ala Thr Leu Asn Cys Gln Ser Ser
 50 55 60
 Gly Ser Lys Pro Ala Ala Arg Leu Thr Trp Arg Lys Gly Asp Gln Glu
 40 65 70 75 80
 Leu His Gly Glu Pro Thr Arg Ile Gln Glu Asp Pro Asn Gly Lys Thr
 85 90 95
 Phe Thr Val Ser Ser Val Thr Phe Gln Val Thr Arg Glu Asp Asp
 45 100 105 110
 Gly Ala Ser Ile Val Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala
 115 120 125
 Asp Arg Ser Thr Ser Gln Arg Ile Glu Val Leu Tyr Thr Pro Thr Ala
 50 130 135 140
 Met Ile Arg Pro Asp Pro Pro His Pro Arg Glu Gly Gln Lys Leu Leu
 55 145 150 155 160
 Leu His Cys Glu Gly Arg Gly Asn Pro Val Pro Gln Gln Tyr Leu Trp
 165 170 175
 60 Glu Lys Glu Gly Ser Val Pro Pro Leu Lys Met Thr Gln Glu Ser Ala

669

180 185 190

Leu Ile Phe Pro Phe Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys
195 200 205

5 Thr Ala Thr Ser Asn Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn
210 215 220

Val Asn Asp
10 225

(2) INFORMATION FOR SEQ ID NO: 626:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 626:

Glu Leu Ser Ile Ser Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu
1 5 10 15

25 Tyr Thr Cys Ser Ile Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu
20 25 30

Val Thr Val Leu Gly Ile Pro Gln Lys Pro Ile Ile Thr Gly Tyr Lys
35 40 45

30 Ser Ser Leu Arg Glu Lys Asp Thr Ala Thr Leu Asn Cys Gln Ser Ser
50 55 60

35

(2) INFORMATION FOR SEQ ID NO: 627:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 627:

Cys Gln Ser Ser Gly Ser Lys Pro Ala Ala Arg Leu Thr Trp Arg Lys
1 5 10 15

50 Gly Asp Gln Glu Leu His Gly Glu Pro Thr Arg Ile Gln Glu Asp Pro
20 25 30

Asn Gly Lys Thr Phe Thr Val Ser Ser Ser Val Thr Phe Gln Val Thr
35 40 45

55 Arg Glu Asp Asp Gly Ala Ser Ile Val Cys Ser Val Asn His Glu Ser
50 55 60

Leu
60 65

(2) INFORMATION FOR SEQ ID NO: 628:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 628:

His Glu Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser Gln Arg Ile Glu
1 5 10 15

15

Val Leu Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp Pro Pro His Pro
20 25 30

20

Arg Glu Gly Gln Lys Leu Leu Leu His Cys Glu Gly Arg Gly Asn Pro
35 40 45

Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu
50 55

25

(2) INFORMATION FOR SEQ ID NO: 629:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 629:

Trp Glu Lys Glu Gly Ser Val Pro Pro Leu Lys Met Thr Gln Glu Ser
35 1 5 10 15

Ala Leu Ile Phe Pro Phe Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly
20 25 30

40

Cys Thr Ala Thr Ser Asn Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu
35 40 45

Asn Val Asn Asp
50

45

(2) INFORMATION FOR SEQ ID NO: 630:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 630:

55

Val Pro Glu Leu Pro Asp Arg Val His Gln Leu His Gln Ala Val Gln
1 5 10 15

60

Gly Cys Ala Leu Gly Arg Pro Gly Phe Pro Gly Gly Pro Thr His Ser
20 25 30

671

Gly His His Lys Ser His Pro Gly Pro Ala Gly Gly Asp Tyr Asn Arg
 35 40 45
 5 Cys Asp Arg Pro Gly Gln Val His Leu His Asn Pro Arg Gly Thr Gly
 50 55 60
 Arg Arg Gly Gln Leu His Pro Thr Ala Gly Pro Gly Val His Arg Arg
 65 70 75 80
 10 Ala Cys Pro Ser Gln Gln Leu Pro His Arg Leu Gly Pro Gly Val Pro
 85 90 95
 15 Cys Pro Ser Pro Ser Leu Thr Pro Val Leu Pro Ser Trp Thr Gln Ser
 100 105 110
 Trp Cys Gly Leu Pro Gly Tyr Thr Ser Ser Ser
 115 120

20

(2) INFORMATION FOR SEQ ID NO: 631:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 631:

30 Val His Gln Leu His Gln Ala Val Gln Gly Cys Ala Leu Gly Arg Pro
 1 5 10 15
 Gly Phe Pro Gly Gly Pro
 20

35

(2) INFORMATION FOR SEQ ID NO: 632:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 632:

45

Pro Thr His Ser Gly His His Lys Ser His Pro Gly Pro Ala Gly Gly
 1 5 10 15
 50 Asp Tyr Asn Arg Cys Asp Arg Pro Gly Gln Val His Leu His Asn Pro
 20 25 30
 Arg Gly Thr Gly Arg Arg Gly Gln Leu His
 35 40

55

(2) INFORMATION FOR SEQ ID NO: 633:

- 60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 amino acids

672

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 633:

5 Leu His Pro Thr Ala Gly Pro Gly Val His Arg Arg Ala Cys Pro Ser
 1 5 10 15
 Gln Gln Leu Pro His Arg Leu Gly Pro Gly Val Pro Cys Pro Ser Pro
 20 25 30
 10 Ser Leu Thr Pro Val Leu Pro Ser Trp Thr Gln Ser Trp Cys Gly Leu
 35 40 45
 Pro Gly Tyr Thr Ser Ser Ser
 15 50 55

(2) INFORMATION FOR SEQ ID NO: 634:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 276 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 634:

Ser Leu Arg Arg Pro Arg Ser Ala Ala Xaa Gln Thr Leu Thr Thr Phe
 1 5 10 15
 30 Leu Ser Ser Val Ser Ser Ala Ser Ser Ser Ala Leu Pro Gly Ser Arg
 20 25 30
 Glu Pro Cys Asp Pro Arg Ala Pro Pro Pro Pro Arg Ser Gly Ser Ala
 35 40 45
 35 Ala Ser Cys Cys Ser Cys Cys Cys Ser Cys Pro Arg Arg Arg Ala Pro
 50 55 60
 Leu Arg Ser Pro Arg Gly Ser Lys Arg Arg Ile Arg Gln Arg Glu Val
 40 65 70 75 80
 Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala Gly Val Pro
 85 90 95
 45 Gly Arg Asp Gly Ser Pro Gly Ala Asn Gly Ile Pro Gly Thr Pro Gly
 100 105 110
 Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys Gly Glu Cys Leu Arg
 115 120 125
 50 Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn Tyr Lys Gln Cys Ser Trp
 130 135 140
 Ser Ser Leu Asn Tyr Gly Ile Asp Leu Gly Lys Ile Ala Glu Cys Thr
 55 145 150 155 160
 Phe Thr Lys Met Arg Ser Asn Ser Ala Leu Arg Val Leu Phe Ser Gly
 165 170 175
 60 Ser Leu Arg Leu Lys Cys Arg Asn Ala Cys Cys Gln Arg Trp Tyr Phe

180 185 190

Thr Phe Asn Gly Ala Glu Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile
195 200 205

5 Ile Tyr Leu Asp Gln Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile
210 215 220

10 His Arg Thr Ser Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly
225 230 235 240

Leu Val Asp Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys
245 250 255

15 Gly Asp Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu
260 265 270

Glu Leu Pro Lys
275

20

(2) INFORMATION FOR SEQ ID NO: 635:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 635:

30

Ser Leu Arg Arg Pro Arg Ser Ala Ala Xaa Gln Thr Leu Thr Thr Phe
1 5 10 15

35

Leu Ser Ser Val Ser Ser Ala Ser Ser Ser Ala Leu Pro Gly Ser Arg
20 25 30

Glu Pro Cys Asp Pro Arg Ala Pro Pro Pro Arg Ser Gly Ser Ala
35 40 45

40

Ala Ser Cys Cys Ser Cys Cys Cys Ser Cys Pro Arg Arg
50 55 60

45

(2) INFORMATION FOR SEQ ID NO: 636:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 636:

Arg Ala Pro Leu Arg Ser Pro Arg Gly Ser Lys Arg Arg Ile Arg Gln
1 5 10 15

55

Arg Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala
20 25 30

60

Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Gly Ile Pro Gly
35 40 45

Thr Pro Gly Ile
50

5

(2) INFORMATION FOR SEQ ID NO: 637:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 637:

15 Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys Gly Glu
1 5 10 15

Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn Tyr Lys Gln
20 25 30

20 Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu Gly Lys Ile Ala
35 40 45

25 Glu Cys Thr Phe
50

(2) INFORMATION FOR SEQ ID NO: 638:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 638:

Phe Thr Lys Met Arg Ser Asn Ser Ala Leu Arg Val Leu Phe Ser Gly
1 5 10 15

40 Ser Leu Arg Leu Lys Cys Arg Asn Ala Cys Cys Gln Arg Trp Tyr Phe
20 25 30

Thr Phe Asn Gly Ala Glu Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile
35 40 45

45 Ile Tyr Leu Asp Gln Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile
50 55 60

50 His Arg
65

(2) INFORMATION FOR SEQ ID NO: 639:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 639:

675

Arg Thr Ser Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu
 1 5 10 15
 5 Val Asp Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly
 20 25 30
 Asp Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu
 35 40 45
 10 Leu Pro Lys
 50

15

(2) INFORMATION FOR SEQ ID NO: 640:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 640:

Thr Lys Lys Glu Asn Cys Arg Pro Ala Ser Leu Met Asn Ile Asp Thr
 1 5 10 15
 Lys Ile Leu Asn Lys Ile Leu Met Asn Gln
 20 25

30

(2) INFORMATION FOR SEQ ID NO: 641:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 214 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 641:

40 Met Cys Asn Leu Pro Ile Lys Val Val Cys Arg Ala Asn Ala Glu Tyr
 1 5 10 15
 Met Ser Pro Ser Gly Lys Val Pro Xaa Xaa His Val Gly Asn Gln Val
 20 25 30
 45 Val Ser Glu Leu Gly Pro Ile Val Gln Phe Val Lys Ala Lys Gly His
 35 40 45
 Ser Leu Ser Asp Gly Leu Glu Val Gln Lys Ala Glu Met Lys Ala
 50 55 60
 Tyr Met Glu Leu Val Asn Asn Met Leu Leu Thr Ala Glu Leu Tyr Leu
 65 70 75 80
 55 Gln Trp Cys Asp Glu Ala Thr Val Gly Xaa Ile Thr His Xaa Arg Tyr
 85 90 95
 Gly Ser Pro Tyr Pro Trp Pro Leu Xaa His Ile Leu Ala Tyr Gln Lys
 100 105 110

60

676

Gln Trp Glu Val Lys Arg Lys Xaa Lys Ala Ile Gly Trp Gly Lys Lys
 115 120 125
 5 Thr Leu Asp Gln Val Leu Glu Asp Val Asp Gln Cys Cys Gln Ala Leu
 130 135 140
 Ser Gln Arg Leu Gly Thr Gln Pro Tyr Phe Phe Asn Lys Gln Pro Thr
 145 150 155 160
 10 Glu Leu Asp Ala Leu Val Phe Gly His Leu Tyr Thr Ile Leu Thr Thr
 165 170 175
 Gln Leu Thr Asn Asp Glu Leu Ser Glu Lys Val Lys Asn Tyr Ser Asn
 180 185 190
 15 Leu Leu Ala Phe Cys Arg Arg Ile Glu Gln His Tyr Phe Glu Asp Arg
 195 200 205
 Gly Lys Gly Arg Leu Ser
 20 210

25 (2) INFORMATION FOR SEQ ID NO: 642:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 44 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 642:

Met Cys Asn Leu Pro Ile Lys Val Val Cys Arg Ala Asn Ala Glu Tyr
 1 5 10 15
 35 Met Ser Pro Ser Gly Lys Val Pro Xaa Xaa His Val Gly Asn Gln Val
 20 25 30
 Val Ser Glu Leu Gly Pro Ile Val Gln Phe Val Lys
 35 40
 40

(2) INFORMATION FOR SEQ ID NO: 643:
 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 44 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 643:
 50 Phe Val Lys Ala Lys Gly His Ser Leu Ser Asp Gly Leu Glu Glu Val
 1 5 10 15
 Gln Lys Ala Glu Met Lys Ala Tyr Met Glu Leu Val Asn Asn Met Leu
 55 20 25 30
 Leu Thr Ala Glu Leu Tyr Leu Gln Trp Cys Asp Glu
 35 40
 60

(2) INFORMATION FOR SEQ ID NO: 644:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 644:

5 Leu Gln Trp Cys Asp Glu Ala Thr Val Gly Xaa Ile Thr His Xaa Arg
 1 5 10 15
 Tyr Gly Ser Pro Tyr Pro Trp Pro Leu Xaa His Ile Leu Ala Tyr Gln
 20 25 30
 15 Lys Gln Trp Glu Val Lys Arg Lys Xaa Lys Ala Ile Gly Trp Gly Lys
 35 40 45
 Lys Thr Leu
 20 50

(2) INFORMATION FOR SEQ ID NO: 645:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 645:

25 Asp Gln Val Leu Glu Asp Val Asp Gln Cys Cys Gln Ala Leu Ser Gln
 1 5 10 15
 35 Arg Leu Gly Thr Gln Pro Tyr Phe Phe Asn Lys Gln Pro Thr Glu Leu
 20 25 30
 Asp Ala Leu Val Phe Gly His Leu Tyr Thr Ile
 35 40

(2) INFORMATION FOR SEQ ID NO: 646:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 646:

45 Leu Thr Thr Gln Leu Thr Asn Asp Glu Leu Ser Glu Lys Val Lys Asn
 1 5 10 15
 50 Tyr Ser Asn Leu Leu Ala Phe Cys Arg Arg Ile Glu Gln His Tyr Phe
 20 25 30
 Glu Asp Arg Gly Lys Gly Arg Leu Ser
 35 40

60

(2) INFORMATION FOR SEQ ID NO: 647:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 70 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 647:

10 Met Xaa Xaa Xaa Asn Ser His Ile Thr Ile Phe Thr Leu Asn Val Asn
1 5 10 15
Gly Leu Asn Ala Pro Asn Glu Arg His Arg Leu Ala Asn Trp Ile Gln
20 25 30
15 Ser Gln Asp Gln Val Cys Cys Ile Gln Glu Thr His Leu Thr Gly Arg
35 40 45
20 Asp Thr His Arg Leu Lys Ile Lys Gly Trp Arg Lys Ile Tyr Gln Ala
50 55 60
Asn Gly Lys Gln Lys Lys
65 70

25

(2) INFORMATION FOR SEQ ID NO: 648:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 28 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 648:

35 Phe Thr Leu Asn Val Asn Gly Leu Asn Ala Pro Asn Glu Arg His Arg
1 5 10 15
Leu Ala Asn Trp Ile Gln Ser Gln Asp Gln Val Cys
20 25

40

(2) INFORMATION FOR SEQ ID NO: 649:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 649:

50 Thr His Leu Thr Gly Arg Asp Thr His Arg Leu Lys Ile Lys Gly Trp
1 5 10 15
55 Arg

55

(2) INFORMATION FOR SEQ ID NO: 650:

60

679

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 650:

Gly Trp Arg Lys Ile Tyr Gln Ala Asn Gly Lys Gln Lys Lys
 1 5 10

10

(2) INFORMATION FOR SEQ ID NO: 651:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 651:

20 Ile Tyr His Leu His Ser Trp Ile Phe Phe His Phe Lys Arg Ala Phe
 1 5 10 15

Cys Met Cys Phe Ile Thr Met Lys Val Ile His Ala His Cys Ser Lys
 20 25 30

25

Leu Arg Lys Cys Xaa Asn Ala Gln Ile Ser Val Phe Cys Thr Thr Leu
 35 40 45

30 Thr Ala Ser Tyr Pro Thr
 50

(2) INFORMATION FOR SEQ ID NO: 652:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 652:

Ile Tyr His Leu His Ser Trp Ile Phe Phe His Phe Lys Arg Ala Phe
 1 5 10 15

45 Cys Met Cys Phe Ile Thr Met
 20

(2) INFORMATION FOR SEQ ID NO: 653:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 653:

Lys Val Ile His Ala His Cys Ser Lys Leu Arg Lys Cys Xaa Asn Ala
 1 5 10 15

60

680

Gln Ile Ser Val Phe Cys Thr Thr Leu Thr Ala Ser Tyr Pro Thr
 20 25 30

5

(2) INFORMATION FOR SEQ ID NO: 654:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 654:

Trp Asn Leu Leu Trp Tyr Phe Gln Arg Leu Arg Leu Pro Ser Ile Leu
 1 5 10 15

Pro Gly Leu Val Leu Ala Ser Cys Asp Gly Pro Ser Xaa Ser Gln Ala
 20 25 30

Pro Ser Pro Trp Leu Thr Pro Asp Pro Ala Ser Val Gln Val Arg Leu
 35 40 45

Leu Trp Asp Val Leu Thr Pro Asp Pro Asn
 50 55

25

(2) INFORMATION FOR SEQ ID NO: 655:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 655:

35

Gln Arg Gly Ile Tyr Arg Glu Ile Leu Phe Leu Thr Met Ala Ala Leu
 1 5 10 15

Gly Lys Asp His Val Asp Ile Val Ala Phe Asp Lys Lys Tyr Lys Ser
 20 25 30

40

Ala Phe Asn Lys Leu Ala Ser Ser Met Gly Lys Glu Glu Leu Arg His
 35 40 45

Arg Arg Ala Gln Met Pro
 50

45

50 (2) INFORMATION FOR SEQ ID NO: 656:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 656:

Trp Asn Leu Leu Trp Tyr Phe Gln Arg Leu Arg Leu Pro Ser Ile Leu
 1 5 10 15

60

681

Pro Gly Leu Val Leu Ala Ser
20

5

(2) INFORMATION FOR SEQ ID NO: 657:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 amino acids

10

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 657:

15

Glu Asp Asp Gly Phe Asn Arg Ser Ile His Glu Val Ile Leu Lys Asn
1 5 10 15

Ile Thr Trp Tyr Ser Glu Arg Val Leu Thr Glu Ile Ser Leu Gly Ser
20 25 30

20

Leu Leu Ile Leu Val Val Ile Arg Thr Ile Gln Tyr Asn Met Thr Arg
35 40 45

Thr Arg Asp Lys Tyr Leu His Thr Asn Cys Leu Ala Ala Leu Ala Asn
50 55 60

25

Met Ser Ala Gln Phe Arg Ser Leu His Gln Tyr Ala Ala Gln Arg Ile
65 70 75 80

30

Ile Ser Leu Phe Ser Leu Leu Ser Lys Lys His Asn Lys Val Leu Glu
85 90 95

Gln Ala Thr Gln Ser Leu Arg Gly Ser Leu Ser Ser Asn Asp Val Pro
100 105 110

35

Leu Pro Asp Tyr Ala Gln Asp Leu Asn Val Ile Glu Glu Val Ile Arg
115 120 125

Met Met Leu Glu Ile Ile Asn Ser Cys Leu Thr Asn Ser Leu His His
130 135 140

40

Asn Pro Asn Leu Val Tyr Ala Leu Leu Tyr Lys Arg Asp Leu Phe Glu
145 150 155 160

45

Gln Phe Arg Thr His Pro Ser Phe Gln Asp Ile Met Gln Asn Ile Asp
165 170 175

Leu Val Ile Ser Phe Phe Ser Ser Arg Leu Leu Gln Ala Gly Ser
180 185 190

50

(2) INFORMATION FOR SEQ ID NO: 658:

(i) SEQUENCE CHARACTERISTICS:

55

(A) LENGTH: 38 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 658:

60

Glu Asp Asp Gly Phe Asn Arg Ser Ile His Glu Val Ile Leu Lys Asn

682

1 5 10 15
 Ile Thr Trp Tyr Ser Glu Arg Val Leu Thr Glu Ile Ser Leu Gly Ser
 20 25 30
 5 Leu Leu Ile Leu Val Val
 35

10

(2) INFORMATION FOR SEQ ID NO: 659:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 amino acids
 15 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 659:

20 Arg Thr Ile Gln Tyr Asn Met Thr Arg Thr Arg Asp Lys Tyr Leu His
 1 5 10 15
 Thr Asn Cys Leu Ala Ala Leu Ala Asn Met Ser Ala Gln Phe Arg Ser
 20 25 30
 25 Leu His Gln Tyr Ala Ala Gln Arg Ile Ile Ser Leu Phe Ser Leu Leu
 35 40 45
 Ser Lys Lys His Asn
 50

30

(2) INFORMATION FOR SEQ ID NO: 660:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 660:

40

Ser Cys Leu Thr Asn Ser Leu His His Asn Pro Asn Leu Val Tyr Ala
 1 5 10 15
 45 Leu Leu Tyr Lys Arg Asp Leu Phe Glu Gln Phe Arg Thr His Pro Ser
 20 25 30
 Phe Gln Asp Ile Met Gln Asn Ile Asp Leu Val Ile Ser Phe Phe Ser
 35 40 45
 50 Ser Arg Leu Leu Gln Ala Gly Ser
 50 55

55

(2) INFORMATION FOR SEQ ID NO: 661:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 amino acids
 60 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 661:

5 Lys Lys His Asn Lys Val Leu Glu Gln Ala Thr Gln Ser Leu Arg Gly
 1 5 10 15
 Ser Leu Ser Ser Asn Asp Val Pro Leu Pro Asp Tyr Ala Gln Asp
 20 25 30

10

(2) INFORMATION FOR SEQ ID NO: 662:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 125 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 662:

20 Met Ala Asp Ile Gln Thr Glu Arg Ala Tyr Gln Lys Gln Pro Thr Ile
 1 5 10 15
 Phe Gln Asn Lys Lys Arg Val Leu Leu Gly Glu Thr Gly Lys Glu Lys
 20 25 30
 25 Leu Pro Arg Val Thr Asn Lys Asn Ile Gly Leu Gly Phe Lys Asp Thr
 35 40 45
 Pro Arg Arg Leu Leu Arg Gly Thr Tyr Ile Asp Lys Lys Cys Pro Phe
 50 55 60
 30 Thr Gly Asn Val Ser Ile Arg Gly Arg Ile Leu Ser Gly Val Val Thr
 65 70 75 80
 Gln Asp Glu Asp Ala Glu Asp His Cys His Pro Pro Arg Leu Ser Ala
 35 85 90 95
 Leu His Pro Gln Val Gln Pro Leu Arg Glu Ala Pro Gln Glu His Val
 100 105 110
 40 Cys Thr Pro Val Pro Leu Leu Gln Gly Arg Pro Asp Arg
 115 120 125

45 (2) INFORMATION FOR SEQ ID NO: 663:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 79 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 663:

55 Met Lys Met Gln Arg Thr Ile Val Ile Arg Arg Asp Tyr Leu His Tyr
 1 5 10 15
 Ile Arg Lys Tyr Asn Arg Phe Glu Lys Arg His Lys Asn Met Ser Val
 20 25 30
 60 His Leu Ser Pro Cys Phe Arg Asp Val Gln Ile Gly Asp Ile Val Thr
 35 40 45

684

Val Gly Glu Cys Arg Pro Leu Ser Lys Thr Val Arg Phe Asn Val Leu
50 55 60

5 Lys Val Thr Lys Ala Ala Gly Thr Lys Lys Gln Phe Gln Lys Phe
65 70 75

10 (2) INFORMATION FOR SEQ ID NO: 664:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

15 (C) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 664:

Met Ala Asp Ile Gln Thr Glu Arg Ala Tyr Gln Lys Gln Pro Thr Ile
1 5 10 15

20 Phe Gln Asn Lys Lys Arg Val Leu Leu Gly Glu Thr Gly Lys
20 25 30

25 (2) INFORMATION FOR SEQ ID NO: 665:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids

30 (B) TYPE: amino acid

(C) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 665:

Lys Leu Pro Arg Val Thr Asn Lys Asn Ile Gly Leu Gly Phe Lys Asp
1 5 10 15

Thr Pro Arg Arg Leu Leu Arg Gly Thr Tyr Ile Asp Lys Lys Cys Pro
20 25 30

40 Phe Thr Gly Asn Val Ser Ile Arg Gly Arg Ile Leu Ser Gly Val Val
35 40 45

Thr Gln Asp Glu Asp Ala Glu Asp His Cys
50 55

45 (2) INFORMATION FOR SEQ ID NO: 666:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids

(B) TYPE: amino acid

(C) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 666:

His Cys His Pro Pro Arg Leu Ser Ala Leu His Pro Gln Val Gln Pro
1 5 10 15

60 Leu Arg Glu Ala Pro Gln Glu His Val Cys Thr Pro Val Pro Leu Leu
20 25 30

685

Gln Gly Arg Pro Asp Arg
35

5

(2) INFORMATION FOR SEQ ID NO: 667:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 667:

15 Met Lys Met Gln Arg Thr Ile Val Ile Arg Arg Asp Tyr Leu His Tyr
1 5 10 15

Ile Arg Lys Tyr Asn Arg Phe Glu Lys Arg His Lys Asn Met Ser Val
20 25 30

20

His Leu Ser Pro
35

25

(2) INFORMATION FOR SEQ ID NO: 668:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 668:

35 Cys Phe Arg Asp Val Gln Ile Gly Asp Ile Val Thr Val Gly Glu Cys
1 5 10 15

Arg Pro Leu Ser Lys Thr Val Arg Phe Asn Val Leu Lys Val Thr Lys
20 25 30

40 Ala Ala Gly Thr Lys Lys Gln Phe Gln Lys Phe
35 40

45 (2) INFORMATION FOR SEQ ID NO: 669:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 669:

55 Pro Arg Arg Leu Leu Arg Gly Thr Tyr Ile Asp Lys Lys Cys Pro Phe
1 5 10 15

Thr Gly Asn Val Ser Ile Arg Gly Arg Ile Leu Ser Gly Val Val Thr
20 25 30

55

Gln

60

5 (2) INFORMATION FOR SEQ ID NO: 670:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 670:

Ile Phe Tyr Asp Ser Asp Trp Asn Pro Thr Val Asp Gln Gln Ala Met
 1 5 10 15

15 Asp Arg Ala His Arg Leu Gly Gln Thr Lys Gln Val Thr Val Tyr Arg
 20 25 30

Leu Ile Cys Lys Gly Thr Ile Glu Glu Arg Ile Leu Gln Arg Ala Lys
 35 40 45

20 Glu Lys Ser Glu Ile Gln Arg Met Val Ile Ser Gly
 50 55 60

25 (2) INFORMATION FOR SEQ ID NO: 671:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 amino acids

30 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 671:

Thr Arg Met Ile Asp Leu Leu Glu Glu Tyr Met Val Tyr Arg Lys His
 35 1 5 10 15

Thr Tyr Xaa Arg Leu Asp Gly Ser Ser Lys Ile Ser Glu Arg Arg Asp
 20 25 30

40 Met Val Ala Asp Phe Gln Asn Arg Asn Asp Ile Phe Val Phe Leu Leu
 35 40 45

Ser Thr Arg Ala Gly Gly Leu Gly Ile Asn Leu Thr Ala Xaa Asp Thr
 50 55 60

45 Val His Phe
 65

50 (2) INFORMATION FOR SEQ ID NO: 672:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

55 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 672:

Ile Phe Tyr Asp Ser Asp Trp Asn Pro Thr Val Asp Gln Gln Ala Met
 60 1 5 10 15

687

Asp Arg Ala His Arg Leu Gly Gln Thr Lys Gln Val Thr Val Tyr Arg
 20 25 30

5

10 (2) INFORMATION FOR SEQ ID NO: 673:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 673:

Val Tyr Arg Leu Ile Cys Lys Gly Thr Ile Glu Glu Arg Ile Leu Gln
 1 5 10 15

20

Arg Ala Lys Glu Lys Ser Glu Ile Gln Arg Met Val Ile Ser Gly
 20 25 30

25

(2) INFORMATION FOR SEQ ID NO: 674:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 674:

Thr Arg Met Ile Asp Leu Leu Glu Glu Tyr Met Val Tyr Arg Lys His
 1 5 10 15

35

Thr Tyr Xaa Arg Leu Asp Gly Ser Ser Lys Ile Ser Glu Arg Arg Asp
 20 25 30

40 Met

45 (2) INFORMATION FOR SEQ ID NO: 675:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 675:

Arg Arg Asp Met Val Ala Asp Phe Gln Asn Arg Asn Asp Ile Phe Val
 1 5 10 15

55

Phe Leu Leu Ser Thr Arg Ala Gly Gly Leu Gly Ile Asn Leu Thr Ala
 20 25 30

60

Xaa Asp Thr Val His Phe
 35

5 (2) INFORMATION FOR SEQ ID NO: 676:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 676:

Ile Phe Tyr Asp Ser Asp Trp Asn Pro Thr Val Asp Gln Gln Ala Met
1 5 10 15

15 Asp Arg Ala His Arg Leu Gly Gln Thr Lys Gln Val Thr Val Tyr Arg
20 25 30

Leu Ile Cys Lys Gly
35

20 (2) INFORMATION FOR SEQ ID NO: 677:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 677:

30 Ile Phe Tyr Asp Ser Asp Trp Asn Pro Thr Val Asp Gln Gln Ala Met
1 5 10 15

35 Asp Arg Ala His Arg Leu Gly Gln Thr Lys Gln Val Thr Val Tyr Arg
20 25 30

Leu Ile Cys Lys Gly
35

40 (2) INFORMATION FOR SEQ ID NO: 678:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 678:

50 Arg Leu Ile Cys Lys Gly Thr Ile Glu Glu Arg Ile Leu Gln Arg Ala
1 5 10 15

Lys Glu Lys Ser Glu Ile Gln Arg Met Val Ile Ser Gly
20 25

55

(2) INFORMATION FOR SEQ ID NO: 679:

60 (i) SEQUENCE CHARACTERISTICS:

689

(A) LENGTH: 364 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 679:

5 Met Ser Leu His Gly Lys Arg Lys Glu Ile Tyr Lys Tyr Glu Ala Pro
 1 5 10 15
 10 Trp Thr Val Tyr Ala Met Asn Trp Ser Val Arg Pro Asp Lys Arg Phe
 20 25 30
 Arg Leu Ala Leu Gly Ser Phe Val Glu Glu Tyr Asn Asn Lys Val Gln
 35 40 45
 15 Leu Val Gly Leu Asp Glu Glu Ser Ser Glu Phe Ile Cys Arg Asn Thr
 50 55 60
 Phe Asp His Pro Tyr Pro Thr Thr Lys Leu Met Trp Ile Pro Asp Thr
 65 70 75 80
 20 Lys Gly Val Tyr Pro Asp Leu Leu Ala Thr Ser Gly Asp Tyr Leu Arg
 85 90 95
 Val Trp Arg Val Gly Glu Thr Glu Thr Arg Leu Glu Cys Leu Leu Asn
 100 105 110
 25 Asn Asn Lys Asn Ser Asp Phe Cys Ala Pro Leu Thr Ser Phe Asp Trp
 115 120 125
 30 Asn Glu Val Asp Pro Tyr Leu Leu Gly Thr Ser Ser Ile Asp Thr Thr
 130 135 140
 Cys Thr Ile Trp Gly Leu Glu Thr Gly Gln Val Leu Gly Arg Val Asn
 145 150 155 160
 35 Leu Val Ser Gly His Val Lys Thr Gln Leu Ile Ala His Asp Lys Glu
 165 170 175
 Val Tyr Asp Ile Ala Phe Ser Arg Ala Gly Gly Gly Arg Asp Met Phe
 180 185 190
 40 Ala Ser Val Gly Ala Asp Gly Ser Val Arg Met Phe Asp Leu Arg His
 195 200 205
 45 Leu Glu His Ser Thr Ile Ile Tyr Glu Asp Pro Gln His His Pro Leu
 210 215 220
 Leu Arg Leu Cys Trp Asn Lys Gln Asp Pro Asn Tyr Leu Ala Thr Met
 225 230 235 240
 50 Ala Met Asp Gly Met Glu Val Val Ile Leu Asp Val Arg Val Pro Ala
 245 250 255
 His Leu Xaa Pro Gly Thr Thr Ile Glu His Val Ser Met Ala Leu Leu
 260 265 270
 Gly Pro His Ile His Pro Ala Thr Ser Ala Leu Gln Arg Met Thr Thr
 275 280 285
 60 Arg Leu Ser Ser Gly Thr Ser Ser Lys Cys Pro Glu Pro Leu Arg Thr

690

290 295 300

Leu Ser Trp Pro Thr Gln Leu Xaa Gly Glu Ile Asn Asn Val Gln Trp
 305 310 315 320

5 Ala Ser Thr Gln Pro Glu Leu Ser Pro Ser Ala Thr Thr Thr Ala Trp
 325 330 335

10 Arg Tyr Ser Glu Cys Ser Val Gly Gly Ala Val Pro Thr Arg Gln Gly
 340 345 350

Leu Leu Tyr Phe Leu Pro Leu Pro His Pro Gln Ser
 355 360

15

(2) INFORMATION FOR SEQ ID NO: 680:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 680:

25 Met Ser Leu His Gly Lys Arg Lys Glu Ile Tyr Lys Tyr Glu Ala Pro
 1 5 10 15

Trp Thr Val Tyr Ala Met Asn Trp Ser Val Arg Pro Asp Lys Arg Phe
 20 25 30

30 Arg Leu Ala Leu Gly Ser Phe Val Glu Glu Tyr Asn Asn Lys Val Gln
 35 40 45

35 Leu Val Gly Leu Asp Glu Glu Ser Ser Glu Phe Ile Cys Arg Asn Thr
 50 55 60

Phe Asp His Pro Tyr Pro Thr Thr Lys Leu Met Trp Ile Pro Asp Thr
 65 70 75 80

40 Lys Gly Val Tyr Pro Asp Leu Leu Ala Thr Ser Gly Asp Tyr Leu Arg
 85 90 95

Val Trp Arg Val Gly Glu Thr Glu Thr Arg Leu Glu Cys Leu Leu Asn
 100 105 110

45 Asn Asn Lys Asn Ser Asp Phe Cys Ala Pro Leu Thr Ser Phe Asp Trp
 115 120 125

50 Asn Glu Val Asp Pro Tyr Leu Leu
 130 135

55 (2) INFORMATION FOR SEQ ID NO: 681:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 681:

691

Ser Phe Asp Trp Asn Glu Val Asp Pro Tyr Leu Leu Gly Thr Ser Ser
 1 5 10 15
 5 Ile Asp Thr Thr Cys Thr Ile Trp Gly Leu Glu Thr Gly Gln Val Leu
 20 25 30
 Gly Arg Val Asn Leu Val Ser Gly His Val Lys Thr Gln Leu Ile Ala
 35 40 45
 10 His Asp Lys Glu Val Tyr Asp Ile Ala Phe Ser Arg Ala Gly Gly Gly
 50 55 60
 15 Arg Asp Met Phe Ala Ser Val Gly Ala Asp Gly Ser Val Arg Met Phe
 65 70 75 80
 Asp Leu Arg His Leu Glu His Ser Thr Ile Ile Tyr Glu Asp Pro Gln
 85 90 95
 20 His His Pro Leu Leu Arg Leu Cys Trp Asn Lys Gln Asp Pro Asn Tyr
 100 105 110
 Leu Ala Thr Met Ala Met Asp Gly Met Glu Val Val Ile Leu Asp Val
 115 120 125
 25 Arg Val Pro Ala His Leu Xaa Pro Gly Thr Thr Ile
 130 135 140

30

(2) INFORMATION FOR SEQ ID NO: 682:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 682:

35 Val Gly Ala Asp Gly Ser Val Arg Met Phe Asp Leu Arg His Leu Glu
 40 1 5 10 15
 His Ser Thr Ile Ile Tyr Glu Asp Pro Gln His His Pro Leu Leu Arg
 20 25 30
 45 Leu Cys Trp Asn Lys Gln Asp Pro Asn Tyr Leu Ala Thr Met Ala Met
 35 40 45
 Asp Gly Met Glu Val Val Ile Leu Asp Val Arg Val Pro Ala His Leu
 50 55 60
 50 Xaa Pro Gly Thr Thr Ile Glu His Val Ser Met Ala Leu Leu Gly Pro
 65 70 75 80
 His Ile His Pro Ala Thr Ser Ala Leu Gln Arg Met Thr Thr Arg Leu
 55 85 90 95
 Ser Ser Gly Thr Ser Ser Lys Cys Pro Glu Pro Leu Arg Thr Leu Ser
 100 105 110
 60 Trp Pro Thr Gln Leu Xaa Gly Glu Ile Asn Asn Val Gln Trp Ala Ser

692

115 120 125
 Thr Gln Pro Glu Leu Ser Pro Ser Ala Thr Thr Thr Ala Trp Arg Tyr
 130 135 140
 5 Ser Glu Cys Ser Val Gly Gly Ala Val Pro Thr Arg Gln Gly Leu Leu
 145 150 155 160
 Tyr Phe Leu Pro Leu Pro His Pro Gln Ser
 10 165 170

 (2) INFORMATION FOR SEQ ID NO: 683:
 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 286 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 683:
 Leu Tyr Ala Thr Ala Thr Val Ile Ser Ser Pro Ser Thr Glu Xaa Leu
 1 5 10 15
 25 Ser Gln Asp Gln Gly Asp Arg Ala Ser Leu Asp Ala Ala Asp Ser Gly
 20 25 30
 Arg Gly Ser Trp Thr Ser Cys Ser Ser Gly Ser His Asp Asn Ile Gln
 35 40 45
 30 Thr Ile Gln His Gln Arg Ser Trp Glu Thr Leu Pro Phe Gly His Thr
 50 55 60
 His Phe Asp Tyr Ser Gly Asp Pro Ala Gly Leu Trp Ala Ser Ser Ser
 35 65 70 75 80
 His Met Asp Gln Ile Met Phe Ser Asp His Ser Thr Lys Tyr Asn Arg
 85 90 95
 40 Gln Asn Gln Ser Arg Glu Ser Leu Glu Gln Ala Gln Ser Arg Ala Ser
 100 105 110
 Trp Ala Ser Ser Thr Gly Tyr Trp Gly Glu Asp Ser Glu Gly Asp Thr
 115 120 125
 45 Gly Thr Ile Lys Arg Arg Gly Gly Lys Asp Val Ser Ile Glu Ala Glu
 130 135 140
 Ser Ser Ser Leu Thr Ser Val Thr Thr Glu Glu Thr Lys Pro Val Pro
 50 145 150 155 160
 Met Pro Ala His Ile Ala Val Ala Ser Ser Thr Thr Lys Gly Leu Ile
 165 170 175
 55 Ala Arg Lys Glu Gly Arg Tyr Arg Glu Pro Pro Pro Thr Pro Pro Gly
 180 185 190
 Tyr Ile Gly Ile Pro Ile Thr Asp Phe Pro Glu Gly His Ser His Pro
 195 200 205
 60

693

Ala Arg Lys Pro Pro Asp Tyr Asn Val Ala Leu Gln Arg Ser Arg Met
 210 215 220

Val Ala Arg Ser Ser Asp Thr Ala Gly Pro Ser Ser Val Gln Gln Pro
 5 225 230 235 240

His Gly His Pro Thr Ser Ser Arg Pro Val Asn Lys Pro Gln Trp His
 245 250 255

10 Lys Xaa Asn Glu Ser Asp Pro Arg Leu Ala Pro Tyr Gln Ser Gln Gly
 260 265 270

Phe Ser Thr Glu Glu Asp Glu Asp Glu Gln Val Ser Ala Val
 15 275 280 285

(2) INFORMATION FOR SEQ ID NO: 684:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 684:

25 His Met Asp Gln Ile Met Phe Ser Asp His Ser Thr Lys Tyr Asn Arg
 1 5 10 15

Gln Asn Gln Ser Arg Glu Ser Leu Glu Gln Ala Gln Ser Arg Ala Ser
 30 20 25 30

Trp Ala Ser Ser Thr Gly Tyr Trp Gly Glu
 35 40

35

(2) INFORMATION FOR SEQ ID NO: 685:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 685:

45 Ser Val Thr Thr Glu Glu Thr Lys Pro Val Pro Met Pro Ala His Ile
 1 5 10 15

Ala Val Ala Ser Ser Thr Thr Lys Gly Leu Ile Ala Arg Lys Glu Gly
 20 25 30

50 Arg Tyr Arg Glu Pro Pro Pro Thr Pro Pro Gly Tyr Ile Gly Ile Pro
 35 40 45

Ile Thr Asp
 55 50

60

(2) INFORMATION FOR SEQ ID NO: 686:

694

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 686:

Val Ala Leu Gln Arg Ser Arg Met Val Ala Arg Ser Ser Asp Thr Ala
 1 5 10 15

10 Gly Pro Ser Ser Val Gln Gln Pro His Gly His Pro Thr Ser Ser Arg
 20 25 30

Pro Val Asn Lys Pro Gln Trp His Lys Xaa Asn Glu Ser Asp Pro Arg
 35 40 45

15 Leu Ala Pro Tyr Gln Ser Gln Gly Phe
 50 55

20

(2) INFORMATION FOR SEQ ID NO: 687:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

25 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 687:

30 Cys Leu Leu Phe Val Phe Val Ser Leu Gly Met Arg Cys Leu Phe Trp
 1 5 10 15

Thr Ile Val Tyr Asn Val Leu Tyr Leu Lys His Lys Cys Asn Thr Val
 20 25 30

35 Leu Leu Cys Tyr His Leu Cys Ser Ile
 35 40

40

(2) INFORMATION FOR SEQ ID NO: 688:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 amino acids

45 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 688:

50 Ala Cys Ser Lys Leu Ile Pro Ala Phe Glu Met Val Met Arg Ala Lys
 1 5 10 15

Asp Asn Val Tyr His Leu Asp Cys Phe Ala Cys Gln Leu Cys Asn Gln
 20 25 30

55 Arg Xaa Cys Val Gly Asp Lys Phe Phe Leu Lys Asn Asn Xaa Xaa Leu
 35 40 45

Cys Gln Thr Asp Tyr Glu Glu Gly Leu Met Lys Glu Gly Tyr Ala Pro
 50 55 60

60 Xaa Val Arg

695

65

5 (2) INFORMATION FOR SEQ ID NO: 689:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 689:

Ser Ala Leu Ser Glu Pro Gly Ala Pro Asp Arg Arg Arg Pro Cys Pro
 1 5 10 15

Glu Ser Val Pro Arg Arg Pro Asp Asp Glu Gln Trp Pro Pro Pro Thr
 20 25 30

Ala Leu Cys Leu Asp Val Ala Pro Leu Pro Pro Ser Ser
 35 40 45

25 (2) INFORMATION FOR SEQ ID NO: 690:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 690:

Pro Val Gly Tyr Leu Asp Lys Gln Val Pro Asp Thr Ser Val Gln Glu
 1 5 10 15

Thr Asp Arg Ile Leu Val Glu Lys Arg Cys Trp Asp Ile Ala Leu Gly
 20 25 30

Pro Leu Lys Gln Ile Pro Met Asn Leu Phe Ile
 35 40

40

(2) INFORMATION FOR SEQ ID NO: 691:

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 214 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 691:

Ala His Ala Ser Glu Ser Gly Glu Arg Trp Trp Ala Cys Cys Gly Val
 1 5 10 15

Arg Phe Gly Leu Arg Ser Ile Glu Ala Ile Gly Arg Ser Cys Cys His
 20 25 30

55

Asp Gly Pro Gly Gly Leu Val Ala Asn Arg Gly Arg Arg Phe Lys Trp
 35 40 45

60 Ala Ile Glu Leu Ser Gly Pro Gly Gly Ser Arg Gly Arg Ser Asp

696

50 55 60

Arg Gly Ser Gly Gln Gly Asp Ser Leu Tyr Pro Val Gly Tyr Leu Asp
65 70 75 80

5 Lys Gln Val Pro Asp Thr Ser Val Gln Glu Thr Asp Arg Ile Leu Val
 85 90 95

10 Glu Lys Arg Cys Trp Asp Ile Ala Leu Gly Pro Leu Lys Gln Ile Pro
 100 105 110

Met Asn Leu Phe Ile Met Tyr Met Ala Gly Asn Thr Ile Ser Ile Phe
 115 120 125

15 Pro Thr Met Met Val Cys Met Met Ala Trp Arg Pro Ile Gln Ala Leu
 130 135 140

Met Ala Ile Ser Ala Thr Phe Lys Met Leu Glu Ser Ser Ser Gln Lys
145 150 155 160

20 Phe Leu Gln Gly Leu Val Tyr Leu Ile Gly Asn Leu Met Gly Leu Ala
 165 170 175

25 Leu Ala Val Tyr Lys Cys Gln Ser Met Gly Leu Leu Pro Thr His Ala
 180 185 190

Ser Asp Trp Leu Ala Phe Ile Glu Pro Pro Glu Arg Met Glu Phe Ser
 195 200 205

30 Gly Gly Gly Leu Leu Leu
 210

35 (2) INFORMATION FOR SEQ ID NO: 692:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 amino acids

(B) TYPE: amino acid

40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 692:

Ala Thr Phe Lys Met Leu Glu Ser Ser Ser Gln Lys Phe Leu Gln Gly
1 5 10 15

45 Leu Val Tyr Leu Ile Gly Asn Leu Met Gly Leu Ala Leu Ala Val Tyr
 20 25 30

Lys Cys Gln Ser Met Gly Leu Leu Pro Thr His Ala Ser Asp
50 35 40 45

55 (2) INFORMATION FOR SEQ ID NO: 693:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 693:

697

Pro Val Gly Tyr Leu Asp Lys Gln Val Pro Asp Thr Ser Val Gln Glu
 1 5 10 15
 5 Thr Asp Arg Ile Leu Val Glu Lys Arg Cys Trp Asp Ile Ala Leu Gly
 20 25 30
 Pro Leu Lys Gln Ile Pro Met Asn Leu Phe Ile
 35 40

10

(2) INFORMATION FOR SEQ ID NO: 694:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 694:

20

Pro Thr Thr Lys Leu Asp Ile Met Glu Lys Lys Lys His Ile Gln Ile
 1 5 10 15

25

Arg Phe Pro Ser Phe Tyr His Lys Leu Val Asp Ser Gly Arg Met Arg
 20 25 30

Ser Lys Arg Glu Thr Arg Arg Glu Asp Ser Asp Thr Lys His Asn Leu
 35 40 45

30

35

(2) INFORMATION FOR SEQ ID NO: 695:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 695:

40

Thr Glu His Ile Ile Ala Val Met Ile Thr Glu Leu Arg Gly Lys Asp
 1 5 10 15

45

Ile Leu Ser Tyr Leu Glu Lys Asn Ile Ser Val Gln Met Thr Ile Ala
 20 25 30

50

Val Gly Thr Arg Met Pro Pro Lys Asn Phe Ser Arg Gly Ser Leu Val
 35 40 45

Phe Val Ser Ile Ser Phe Ile Val Leu Met Ile Ile Ser Ser Ala Trp
 50 55 60

55

Leu Ile Phe Tyr Phe Ile Gln Lys Ile Arg Tyr Thr Asn Ala Arg Asp
 65 70 75 80

Arg Asn Gln Arg Arg Leu Gly Asp Ala Ala Lys Lys Ala Ile Ser Lys
 85 90 95

60

698

Leu Thr Thr Arg Thr Val Lys Lys Gly Asp Lys Glu Thr Asp Pro Asp
 100 105 110
 5 Phe Asp His Cys Ala Val Cys Ile Glu Ser Tyr Lys Gln Asn Asp Val
 115 120 125
 Val Arg Ile Leu Pro Cys Lys His Val Phe His Lys Ser Cys Val Asp
 130 135 140
 10 Pro Trp Leu Ser Glu His Cys Thr Cys Pro Met Cys Lys Leu Asn Ile
 145 150 155 160
 Leu Lys Ala Leu Gly Ile Val
 165
 15

(2) INFORMATION FOR SEQ ID NO: 696:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 276 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 696:
 25 Met Thr His Pro Gly Thr Glu His Ile Ile Ala Val Met Ile Thr Glu
 1 5 10 15
 30 Leu Arg Gly Lys Asp Ile Leu Ser Tyr Leu Glu Lys Asn Ile Ser Val
 20 25 30
 Gln Met Thr Ile Ala Val Gly Thr Arg Met Pro Pro Lys Asn Phe Ser
 35 40 45
 35 Arg Gly Ser Leu Val Phe Val Ser Ile Ser Phe Ile Val Leu Met Ile
 50 55 60
 Ile Ser Ser Ala Trp Leu Ile Phe Tyr Phe Ile Gln Lys Ile Arg Tyr
 65 70 75 80
 40 Thr Asn Ala Arg Asp Arg Asn Gln Arg Arg Leu Gly Asp Ala Ala Lys
 85 90 95
 45 Lys Ala Ile Ser Lys Leu Thr Thr Arg Thr Val Lys Lys Gly Asp Lys
 100 105 110
 Glu Thr Asp Pro Asp Phe Asp His Cys Ala Val Cys Ile Glu Ser Tyr
 115 120 125
 50 Lys Gln Asn Asp Val Val Arg Ile Leu Pro Cys Lys His Val Phe His
 130 135 140
 Lys Ser Cys Val Asp Pro Trp Leu Ser Glu His Cys Thr Cys Pro Met
 145 150 155 160
 55 Cys Lys Leu Asn Ile Leu Lys Ala Leu Gly Ile Val Pro Asn Leu Pro
 165 170 175
 60 Cys Thr Asp Asn Val Ala Phe Asp Met Glu Arg Leu Thr Arg Thr Gln
 180 185 190

699

Ala Val Asn Arg Arg Ser Ala Leu Gly Asp Leu Ala Gly Asp Asn Ser
 195 200 205

5 Leu Gly Leu Glu Pro Leu Arg Thr Ser Gly Ile Ser Pro Leu Pro Gln
 210 215 220

Asp Gly Glu Leu Thr Pro Arg Thr Gly Glu Ile Asn Ile Ala Val Thr
 225 230 235 240

10 Lys Glu Trp Phe Ile Ile Ala Ser Phe Gly Leu Leu Ser Ala Leu Thr
 245 250 255

15 Leu Cys Tyr Met Ile Ile Arg Ala Thr Ala Ser Leu Asn Ala Asn Glu
 260 265 270

Val Glu Trp Phe
 275

20

(2) INFORMATION FOR SEQ ID NO: 697:

(i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 69 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 697:

30 Thr Glu His Ile Ile Ala Val Met Ile Thr Glu Leu Arg Gly Lys Asp
 1 5 10 15

Ile Leu Ser Tyr Leu Glu Lys Asn Ile Ser Val Gln Met Thr Ile Ala
 20 25 30

35 Val Gly Thr Arg Met Pro Pro Lys Asn Phe Ser Arg Gly Ser Leu Val
 35 40 45

40 Phe Val Ser Ile Ser Phe Ile Val Leu Met Ile Ile Ser Ser Ala Trp
 50 55 60

Leu Ile Phe Tyr Phe
 65

45

(2) INFORMATION FOR SEQ ID NO: 698:

(i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 58 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 698:

55 Ser Ile Ser Phe Ile Val Leu Met Ile Ile Ser Ser Ala Trp Leu Ile
 1 5 10 15

Phe Tyr Phe Ile Gln Lys Ile Arg Tyr Thr Asn Ala Arg Asp Arg Asn
 20 25 30

60

700

Gln Arg Arg Leu Gly Asp Ala Ala Lys Lys Ala Ile Ser Lys Leu Thr
 35 40 45

5 Thr Arg Thr Val Lys Lys Gly Asp Lys Glu
 50 55

10 (2) INFORMATION FOR SEQ ID NO: 699:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 699:

Val Lys Lys Gly Asp Lys Glu Thr Asp Pro Asp Phe Asp His Cys Ala
 1 5 10 15

20 Val Cys Ile Glu Ser Tyr Lys Gln Asn Asp Val Val Arg Ile Leu Pro
 20 25 30

Cys Lys His Val Phe His Lys Ser Cys Val Asp Pro Trp Leu Ser Glu
 35 40 45

25 His Cys Thr Cys Pro Met Cys Lys Leu Asn Ile Leu Lys Ala Leu Gly
 50 55 60

30 Ile Val
 65

35 (2) INFORMATION FOR SEQ ID NO: 700:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 700:

Met Thr His Pro Gly Thr Glu His Ile Ile Ala Val Met Ile Thr Glu
 1 5 10 15

45 Leu Arg Gly Lys Asp Ile Leu Ser Tyr Leu Glu Lys Asn Ile Ser Val
 20 25 30

Gln Met Thr Ile Ala Val Gly Thr Arg Met Pro Pro Lys Asn Phe Ser
 35 40 45

50 Arg Gly Ser Leu Val Phe Val Ser Ile Ser Phe Ile Val Leu Met Ile
 50 55 60

55 Ile Ser Ser Ala Trp Leu Ile Phe Tyr Phe Ile Gln Lys Ile Arg Tyr
 65 70 75 80

Thr Asn Ala Arg Asp Arg Asn Gln Arg Arg Leu Gly Asp Ala Ala Lys
 85 90 95

60 Lys Ala Ile Ser Lys Leu Thr Thr Arg Thr

701

100

105

5 (2) INFORMATION FOR SEQ ID NO: 701:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 701:

Ala Ala Lys Lys Ala Ile Ser Lys Leu Thr Thr Arg Thr Val Lys Lys
 1 5 10 15

15 Gly Asp Lys Glu Thr Asp Pro Asp Phe Asp His Cys Ala Val Cys Ile
 20 25 30

20 Glu Ser Tyr Lys Gln Asn Asp Val Val Arg Ile Leu Pro Cys Lys His
 35 40 45

Val Phe His Lys Ser Cys Val Asp Pro Trp Leu Ser Glu His Cys Thr
 50 55 60

25 Cys Pro Met Cys Lys Leu Asn Ile Leu Lys Ala Leu Gly Ile Val Pro
 65 70 75 80

Asn Leu Pro Cys

30

(2) INFORMATION FOR SEQ ID NO: 702:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 702:

Thr Gln Ala Val Asn Arg Arg Ser Ala Leu Gly Asp Leu Ala Gly Asp
 1 5 10 15

45 Asn Ser Leu Gly Leu Glu Pro Leu Arg Thr Ser Gly Ile Ser Pro Leu
 20 25 30

Pro Gln Asp Gly Glu Leu Thr Pro Arg Thr Gly Glu Ile Asn Ile Ala
 35 40 45

50 Val Thr Lys Glu Trp Phe Ile Ile Ala Ser Phe Gly Leu Leu Ser Ala
 50 55 60

Leu Thr Leu Cys Tyr Met Ile Ile Arg Ala Thr Ala Ser Leu Asn Ala
 65 70 75 80

55

Asn Glu Val Glu Trp Phe
 85

60

702

2) INFORMATION FOR SEQ ID NO: 703:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 341 amino acids

(B) TYPE: amino acid

(C) TOPOLOGY: linear

(2) SEQUENCE DESCRIPTION: SEQ ID NO: 703:

5
 10 Pro Leu His Gly Val Ala Asp His Leu Gly Cys Asp Pro Gln Thr Arg
 1 5 10 15
 Phe Phe Val Pro Pro Asn Ile Lys Gln Trp Ile Ala Leu Leu Gln Arg
 20 25 30
 15 Gly Asn Cys Thr Phe Lys Glu Lys Ile Ser Arg Ala Ala Phe His Asn
 35 40 45
 Ala Val Ala Val Val Ile Tyr Asn Asn Lys Ser Lys Glu Glu Pro Val
 50 55 60
 20 Thr Met Thr His Pro Gly Thr Glu His Ile Ile Ala Val Met Ile Thr
 65 70 75 80
 25 Glu Leu Arg Gly Lys Asp Ile Leu Ser Tyr Leu Glu Lys Asn Ile Ser
 85 90 95
 Val Glu Met Thr Ile Ala Val Gly Thr Arg Met Pro Pro Lys Asn Phe
 100 105 110
 30 Ser Arg Gly Ser Leu Val Phe Val Ser Ile Ser Phe Ile Val Leu Met
 115 120 125
 35 Ile Ile Ser Ser Ala Trp Leu Ile Phe Tyr Phe Ile Gln Lys Ile Arg
 130 135 140
 Tyr Thr Asn Ala Arg Asp Arg Asn Gln Arg Arg Leu Gly Asp Ala Ala
 145 150 155 160
 40 Lys Lys Ala Ile Ser Lys Leu Thr Thr Arg Thr Val Lys Lys Gly Asp
 165 170 175
 Lys Glu Thr Asp Pro Asp Phe Asp His Cys Ala Val Cys Ile Glu Ser
 180 185 190
 45 Tyr Lys Gln Asn Asp Val Val Arg Ile Leu Pro Cys Lys His Val Phe
 195 200 205
 50 His Lys Ser Cys Val Asp Pro Trp Leu Ser Glu His Cys Thr Cys Pro
 210 215 220
 Met Cys Lys Leu Asn Ile Leu Lys Ala Leu Gly Ile Val Pro Asn Leu
 225 230 235 240
 55 Pro Cys Thr Asp Asn Val Ala Phe Asp Met Glu Arg Leu Thr Arg Thr
 245 250 255
 Gln Ala Val Asn Arg Arg Ser Ala Leu Gly Asp Leu Ala Gly Asp Asn
 260 265 270
 60 Ser Leu Gly Leu Glu Pro Leu Arg Thr Ser Gly Ile Ser Pro Leu Pro

703

275 280 285

Gln Asp Gly Glu Leu Thr Pro Arg Thr Gly Glu Ile Asn Ile Ala Val
 290 295 300

5 Thr Lys Glu Trp Phe Ile Ile Ala Ser Phe Gly Leu Leu Ser Ala Leu
 305 310 315 320

10 Thr Leu Cys Tyr Met Ile Ile Arg Ala Thr Ala Ser Leu Asn Ala Asn
 325 330 335

Glu Val Glu Trp Phe
 340

15

(2) INFORMATION FOR SEQ ID NO: 704:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 704:

25 His Gly Val Ala Asp His Leu Gly Cys Asp Pro Gln Thr Arg Phe Phe
 1 5 10 15

Val Pro Pro Asn Ile Lys Gln Trp Ile Ala Leu Leu Gln Arg Gly Asn
 20 25 30

30 Cys Thr Phe Lys Glu Lys Ile Ser Arg Ala Ala Phe His Asn Ala Val
 35 40 45

Ala Val Val Ile Tyr Asn Asn Lys Ser Lys Glu Glu
 35 50 55 60

40 (2) INFORMATION FOR SEQ ID NO: 705:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 314 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 705:

Met Ser Gly Gln Gly Leu Ala Gly Phe Phe Ala Ser Val Ala Met Ile
 1 5 10 15

50 Cys Ala Ile Ala Ser Gly Ser Glu Leu Ser Glu Ser Ala Phe Gly Tyr
 20 25 30

Phe Ile Thr Ala Cys Ala Val Ile Ile Leu Thr Ile Ile Cys Tyr Leu
 35 40 45

55 Gly Leu Pro Arg Leu Glu Phe Tyr Arg Tyr Tyr Gln Gln Leu Lys Leu
 50 55 60

Glu Gly Pro Gly Glu Gln Glu Thr Lys Leu Asp Leu Ile Ser Lys Gly
 60 65 70 75 80

704

Glu Glu Pro Arg Ala Gly Lys Glu Glu Ser Gly Val Ser Val Ser Asn
 85 90 95
 5 Ser Gln Pro Thr Asn Glu Ser His Ser Ile Lys Ala Ile Leu Lys Asn
 100 105 110
 Ile Ser Val Leu Ala Phe Ser Val Cys Phe Ile Phe Thr Ile Thr Ile
 115 120 125
 10 Gly Met Phe Pro Ala Val Thr Val Glu Val Lys Ser Ser Ile Ala Gly
 130 135 140
 Ser Ser Thr Trp Glu Arg Tyr Phe Ile Pro Val Ser Cys Phe Leu Thr
 15 145 150 155 160
 Phe Asn Ile Phe Asp Trp Leu Gly Arg Ser Leu Thr Ala Val Phe Met
 165 170 175
 20 Trp Pro Gly Lys Asp Ser Arg Trp Leu Pro Ser Trp Xaa Leu Ala Arg
 180 185 190
 Leu Val Phe Val Pro Leu Leu Leu Leu Cys Asn Ile Lys Pro Arg Arg
 25 195 200 205
 Tyr Leu Thr Val Val Phe Glu His Asp Ala Trp Phe Ile Phe Phe Met
 210 215 220
 Ala Ala Phe Ala Phe Ser Asn Gly Tyr Leu Ala Ser Leu Cys Met Cys
 30 225 230 235 240
 Phe Gly Pro Lys Lys Val Lys Pro Ala Glu Ala Glu Thr Ala Glu Pro
 245 250 255
 35 Ser Trp Pro Ser Ser Cys Val Trp Val Trp His Trp Gly Leu Phe Ser
 260 265 270
 Pro Ser Cys Ser Gly Gln Leu Cys Asp Lys Gly Trp Thr Glu Gly Leu
 275 280 285
 40 Pro Ala Ser Leu Pro Val Cys Leu Leu Pro Leu Pro Ser Ala Arg Gly
 290 295 300
 Asp Pro Glu Trp Ser Gly Gly Phe Phe Phe
 45 305 310

50 (2) INFORMATION FOR SEQ ID NO: 706:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 706:

Met Ser Gly Gln Gly Leu Ala Gly Phe Phe Ala Ser Val Ala Met Ile
 1 5 10 15
 60 Cys Ala Ile Ala Ser Gly Ser Glu Leu Ser Glu Ser Ala Phe Gly Tyr

705

				20					25					30			
	Phe	Ile	Thr	Ala	Cys	Ala	Val	Ile	Ile	Leu	Thr	Ile	Ile	Cys	Tyr	Leu	
				35				40					45				
5																	
	Gly	Leu	Pro	Arg	Leu	Glu	Phe	Tyr	Arg	Tyr	Tyr	Gln	Gln	Leu	Lys	Leu	
		50					55					60					
10	Glu	Gly	Pro	Gly	Glu	Gln	Glu	Thr	Lys	Leu	Asp	Leu	Ile	Ser	Lys	Gly	
	65					70					75					80	
	Glu	Glu	Pro	Arg	Ala	Gly	Lys	Glu	Glu	Ser	Gly	Val	Ser	Val	Ser	Asn	
					85					90					95		
15	Ser	Gln	Pro	Thr	Asn	Glu	Ser	His	Ser	Ile							
				100					105								

20 (2) INFORMATION FOR SEQ ID NO: 707:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 707:

[illegible]

45

(2) INFORMATION FOR SEQ ID NO: 708:

50 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 708:

55 Thr Ile Gly Met Phe Pro Ala Val Thr Val Glu Val Lys Ser Ser Ile
1 5 10 15
Ala Gly Ser Ser Thr Trp Glu Arg Tyr Phe Ile Pro Val Ser Cys Phe
20 25 30
60

706

Leu Thr Phe Asn Ile Phe Asp Trp Leu Gly Arg Ser Leu Thr Ala Val
 35 40 45

5 Phe Met Trp Pro Gly Lys Asp Ser Arg Trp Leu Pro Ser Trp Xaa Leu
 50 55 60

Ala Arg Leu Val Phe Val Pro Leu Leu Leu Leu Cys Asn Ile Lys Pro
 65 70 75 80

10 Arg Arg Tyr Leu Thr Val Val Phe Glu His Asp Ala
 85 90

15

(2) INFORMATION FOR SEQ ID NO: 709:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 709:

25 Phe Gly Pro Lys Lys Val Lys Pro Ala Glu Ala Glu Thr Ala Glu Pro
 1 5 10 15

Ser Trp Pro Ser Ser Cys Val Trp Val Trp His Trp Gly Leu Phe Ser
 20 25 30

30 Pro Ser Cys Ser Gly Gln Leu Cys Asp Lys Gly Trp Thr Glu Gly Leu
 35 40 45

Pro Ala Ser Leu Pro Val Cys Leu Leu Pro Leu Pro Ser Ala Arg Gly
 50 55 60

35 Asp Pro Glu Trp Ser Gly Gly Phe Phe Phe
 65 70

40

(2) INFORMATION FOR SEQ ID NO: 710:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 710:

50 Asp Asp Asp Gly Phe Glu Ile Val Pro Ile Glu Asp Pro Ala Lys His
 1 5 10 15

Arg Ile Leu Asp Pro Glu Gly Leu Ala Leu Gly Ala Val Ile Ala Ser
 20 25 30

55 Ser Lys Lys Ala Lys Arg Asp Leu Ile Asp Asn Ser Phe Asn Arg Tyr
 35 40 45

Thr Phe Asn Glu Asp Glu Gly Glu Leu Pro Glu Trp Phe Val Gln Glu
 50 55 60

60

707

Glu Lys Gln His Arg Ile Arg Gln Leu Pro Val Gly Lys Lys Glu Val
 65 70 75 80
 5 Glu His Tyr Arg Lys Arg Trp Arg Glu Ile Asn Ala Arg Pro Ile Xaa
 85 90 95
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 100 105 110
 10 Leu Glu Gln Thr Arg Lys Lys Ala Glu Ala Val Val Asn Thr Val Asp
 115 120 125
 Ile Xaa Arg Thr Arg Glu Ser
 130 135
 15

(2) INFORMATION FOR SEQ ID NO: 711:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 711:
 25

Asp Asp Asp Gly Phe Glu Ile Val Pro Ile Glu Asp Pro Ala Lys His
 1 5 10 15
 30 Arg Ile Leu Asp Pro Glu Gly Leu Ala Leu Gly Ala Val Ile Ala Ser
 20 25 30
 Ser Lys Lys Ala Lys Arg Asp Leu Ile Asp Asn Ser Phe Asn Arg Tyr
 35 40 45
 35 Thr Phe
 50

(2) INFORMATION FOR SEQ ID NO: 712:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 712:

Lys Arg Trp Arg Glu Ile Asn Ala Arg Pro Ile Xaa Xaa Xaa Xaa Xaa
 1 5 10 15
 50 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 20 25 30
 Arg Lys Lys Ala Glu Ala Val Val Asn Thr Val Asp Ile Xaa Arg Thr
 35 40 45
 55 Arg Glu Ser
 50
 60

708

(2) INFORMATION FOR SEQ ID NO: 713:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 216 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 713:

5 Met Ile Lys Asp Lys Gly Arg Ala Arg Thr Ala Leu Thr Ser Ser Gln
 1 5 10 15
 Pro Ala His Leu Cys Pro Glu Asn Pro Leu Leu His Leu Lys Ala Ala
 20 25 30
 15 Val Lys Glu Lys Lys Arg Asn Lys Lys Lys Thr Ile Gly Ser Pro
 35 40 45
 Lys Arg Ile Gln Ser Pro Leu Asn Asn Lys Leu Leu Asn Ser Pro Ala
 20 50 55 60
 Lys Thr Leu Pro Gly Ala Cys Gly Ser Pro Gln Lys Leu Ile Asp Gly
 65 70 75 80
 25 Phe Leu Lys His Glu Gly Pro Pro Ala Glu Lys Pro Leu Glu Glu Leu
 85 90 95
 Ser Ala Ser Thr Ser Gly Val Pro Gly Leu Ser Ser Leu Gln Ser Asp
 100 105 110
 30 Pro Ala Gly Cys Val Arg Pro Pro Ala Pro Asn Leu Ala Gly Ala Val
 115 120 125
 Glu Phe Asn Asp Val Lys Thr Leu Leu Arg Glu Trp Ile Thr Thr Ile
 35 130 135 140
 Ser Asp Pro Met Glu Glu Asp Ile Leu Gln Val Val Lys Tyr Cys Thr
 145 150 155 160
 40 Asp Leu Ile Glu Glu Lys Asp Leu Glu Lys Leu Asp Leu Val Ile Lys
 165 170 175
 Tyr Met Lys Arg Leu Met Gln Gln Ser Val Glu Ser Val Trp Asn Met
 180 185 190
 45 Ala Phe Asp Phe Ile Leu Asp Asn Val Gln Val Val Leu Gln Gln Thr
 195 200 205
 Tyr Gly Ser Thr Leu Lys Val Thr
 50 210 215

(2) INFORMATION FOR SEQ ID NO: 714:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 714:

60

709

Met Ile Lys Asp Lys Gly Arg Ala Arg Thr Ala Leu Thr Ser Ser Gln
 1 5 10 15
 5 Pro Ala His Leu Cys Pro Glu Asn Pro Leu Leu His Leu Lys Ala Ala
 20 25 30
 Val Lys Glu Lys Lys Arg Asn Lys Lys Lys Thr Ile Gly Ser Pro
 35 40 45
 10 Lys Arg Ile Gln
 50

15

(2) INFORMATION FOR SEQ ID NO: 715:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 100 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 715:

25 Lys Arg Ile Gln Ser Pro Leu Asn Asn Lys Leu Leu Asn Ser Pro Ala
 1 5 10 15
 Lys Thr Leu Pro Gly Ala Cys Gly Ser Pro Gln Lys Leu Ile Asp Gly
 20 25 30
 30 Phe Leu Lys His Glu Gly Pro Pro Ala Glu Lys Pro Leu Glu Glu Leu
 35 40 45
 Ser Ala Ser Thr Ser Gly Val Pro Gly Leu Ser Ser Leu Gln Ser Asp
 50 55 60
 35 Pro Ala Gly Cys Val Arg Pro Pro Ala Pro Asn Leu Ala Gly Ala Val
 65 70 75 80
 40 Glu Phe Asn Asp Val Lys Thr Leu Leu Arg Glu Trp Ile Thr Thr Ile
 85 90 95
 Ser Asp Pro Met
 100

45

(2) INFORMATION FOR SEQ ID NO: 716:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 74 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 716:

55 Thr Ile Ser Asp Pro Met Glu Glu Asp Ile Leu Gln Val Val Lys Tyr
 1 5 10 15
 Cys Thr Asp Leu Ile Glu Glu Lys Asp Leu Glu Lys Leu Asp Leu Val
 20 25 30
 60

710

Ile Lys Tyr Met Lys Arg Leu Met Gln Gln Ser Val Glu Ser Val Trp
 35 40 45

5 Asn Met Ala Phe Asp Phe Ile Leu Asp Asn Val Gln Val Val Leu Gln
 50 55 60

Gln Thr Tyr Gly Ser Thr Leu Lys Val Thr
 65 70

10

(2) INFORMATION FOR SEQ ID NO: 717:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 717:

20 Phe Cys His Asp Cys Lys Phe Pro Glu Ala Ser Pro Ala Met Asn Cys
 1 5 10 15

Glu Pro

25

(2) INFORMATION FOR SEQ ID NO: 718:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 718:

35 Phe Cys His Asp Cys Lys Phe Pro Glu Ala Ser Pro Ala Met Asn Cys
 1 5 10 15

Glu Pro

40

(2) INFORMATION FOR SEQ ID NO: 719:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 719:

Pro Gln Pro Ser Asn Phe Pro Thr Thr Val Arg Asn Leu Pro Tyr Ser
 1 5 10 15

55 Gly Ala Gly Ala Gln Pro Pro Pro Ser Asn Cys
 20 25

60 (2) INFORMATION FOR SEQ ID NO: 720:

711

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 720:

5 Met Ala Ser Ser Val Pro Ala Gly Gly His Thr Arg Ala Gly Gly Ile
 1 5 10 15
 10 Phe Leu Ile Gly Lys Leu Asp Leu Glu Ala Ser Leu Phe Lys Ser Phe
 20 25 30
 15 Gln Trp Leu Pro Phe Val Leu Arg Lys Lys Cys Asn Phe Phe Cys Trp
 35 40 45
 Asp Ser Ser Ala His Ser Leu Pro Leu His Pro Leu Ser Ala Ser Cys
 50 55 60
 20 Ser Ala Pro Ala Cys His Ala Ser Asp Thr His Leu Leu Tyr Pro Ser
 65 70 75 80
 Thr Arg Ala Leu Cys Pro Ser Ile Phe Ala Trp Leu Val Ala Pro His
 85 90 95
 25 Ser Val Phe Arg Thr Asn Ala Pro Gly Pro Thr Pro Ser Ser Gln Ser
 100 105 110
 30 Ser Pro Val Phe Pro Val Phe Pro Val Ser Phe Met Ala Leu Ile Val
 115 120 125
 Cys Xaa Leu Val Cys Cys
 130

35

(2) INFORMATION FOR SEQ ID NO: 721:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 721:

40 Met Ala Ser Ser Val Pro Ala Gly Gly His Thr Arg Ala Gly Gly Ile
 1 5 10 15
 Phe Leu Ile Gly Lys Leu Asp Leu Glu Ala Ser Leu Phe Lys Ser Phe
 20 25 30
 50 Gln Trp Leu Pro Phe Val Leu Arg Lys Lys Cys Asn Phe Phe Cys Trp
 35 40 45
 Asp Ser Ser Ala His Ser Leu Pro Leu His Pro Leu Ser Ala Ser Cys
 50 55 60
 Ser Ala Pro Ala Cys His Ala
 65 70

60

712

(2) INFORMATION FOR SEQ ID NO: 722:

(i) SEQUENCE CHARACTERISTICS:

5

(A) LENGTH: 46 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 722:

10 Phe Ala Trp Leu Val Ala Pro His Ser Val Phe Arg Thr Asn Ala Pro
 1 5 10 15

Gly Pro Thr Pro Ser Ser Gln Ser Ser Pro Val Phe Pro Val Phe Pro
 20 25 30

15 Val Ser Phe Met Ala Leu Ile Val Cys Xaa Leu Val Cys Cys
 35 40 45

20

(2) INFORMATION FOR SEQ ID NO: 723:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 134 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 723:

30 Met Ala Ser Ser Val Pro Ala Gly Gly His Thr Arg Ala Gly Gly Ile
 1 5 10 15

Phe Leu Ile Gly Lys Leu Asp Leu Glu Ala Ser Leu Phe Lys Ser Phe
 20 25 30

35 Gln Trp Leu Pro Phe Val Leu Arg Lys Lys Cys Asn Phe Phe Cys Trp
 35 40 45

Asp Ser Ser Ala His Ser Leu Pro Leu His Pro Leu Ser Ala Ser Cys
 50 55 60

40 Ser Ala Pro Ala Cys His Ala Ser Asp Thr His Leu Leu Tyr Pro Ser
 65 70 75 80

45 Thr Arg Ala Leu Cys Pro Ser Ile Phe Ala Trp Leu Val Ala Pro His
 85 90 95

Ser Val Phe Arg Thr Asn Ala Pro Gly Pro Thr Pro Ser Ser Gln Ser
 100 105 110

50 Ser Pro Val Phe Pro Val Phe Pro Val Ser Phe Met Ala Leu Ile Val
 115 120 125

Cys Xaa Leu Val Cys Cys
 130

55

(2) INFORMATION FOR SEQ ID NO: 724:

60

(i) SEQUENCE CHARACTERISTICS:

713

(A) LENGTH: 286 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 724:

5 Met Ala Met Glu Gly Tyr Trp Arg Phe Leu Ala Leu Leu Gly Ser Ala
1 5 10 15

10 Leu Leu Val Gly Phe Leu Ser Val Ile Phe Ala Leu Val Trp Val Leu
20 25 30

His Tyr Arg Glu Gly Leu Gly Trp Asp Gly Ser Ala Leu Glu Phe Asn
35 40 45

15 Trp His Pro Val Leu Met Val Thr Gly Phe Val Phe Ile Gln Gly Ile
50 55 60

Ala Ile Ile Val Tyr Arg Leu Pro Trp Thr Trp Lys Cys Ser Lys Leu
65 70 75 80

20 Leu Met Lys Ser Ile His Ala Gly Leu Asn Ala Val Ala Ala Ile Leu
85 90 95

Ala Ile Ile Ser Val Val Ala Val Phe Glu Asn His Asn Val Asn Asn
100 105 110

25 Ile Ala Asn Met Tyr Ser Leu His Ser Trp Val Gly Leu Ile Ala Val
115 120 125

30 Ile Cys Tyr Leu Leu Gln Leu Leu Ser Gly Phe Ser Val Phe Leu Leu
130 135 140

Pro Trp Ala Pro Leu Ser Leu Arg Ala Phe Leu Met Pro Ile His Val
145 150 155 160

35 Tyr Ser Gly Ile Val Ile Phe Gly Thr Val Ile Ala Thr Ala Leu Met
165 170 175

Gly Leu Thr Glu Lys Leu Ile Phe Ser Leu Arg Asp Pro Ala Tyr Ser
180 185 190

40 Thr Phe Pro Pro Glu Gly Val Phe Val Asn Thr Leu Gly Leu Leu Ile
195 200 205

45 Leu Val Phe Gly Ala Leu Ile Phe Trp Ile Val Thr Arg Pro Gln Trp
210 215 220

Lys Arg Pro Lys Glu Pro Asn Ser Thr Ile Leu His Pro Asn Gly Gly
225 230 235 240

50 Thr Glu Gln Gly Ala Arg Gly Ser Met Pro Ala Tyr Ser Gly Asn Asn
245 250 255

Met Asp Lys Ser Asp Ser Glu Leu Asn Ser Glu Val Ala Ala Arg Lys
260 265 270

55 Arg Asn Leu Ala Leu Asp Glu Ala Gly Gln Arg Ser Thr Met
275 280 285

60

(2) INFORMATION FOR SEQ ID NO: 725:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 725:

10 Pro Gly Arg Ala Gly Pro Ser Pro Gly Leu Ser Leu Gln Leu Pro Ala
1 5 10 15
Glu Pro Gly His Pro Ala Gly Asn Leu Ala Pro Leu Thr Ser Arg Pro
20 25 30
15 Gln Pro Leu Cys Arg Ile Pro Ala Val Pro Gly
35 40

20

(2) INFORMATION FOR SEQ ID NO: 726:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 424 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 726:

30 Met Lys Leu Leu Gly Glu Cys Ser Ser Ser Ile Asp Ser Val Lys Arg
1 5 10 15
Leu Glu His Lys Leu Lys Glu Glu Glu Glu Ser Leu Pro Gly Phe Val
20 25 30
35 Asn Leu His Ser Thr Glu Thr Gln Thr Ala Gly Val Ile Asp Arg Trp
35 40 45
Glu Leu Leu Gln Ala Gln Ala Leu Ser Lys Glu Leu Arg Met Lys Gln
50 55 60
40 Asn Leu Gln Lys Trp Gln Gln Phe Asn Ser Asp Leu Asn Ser Ile Trp
65 70 75 80
45 Ala Trp Leu Gly Asp Thr Glu Glu Glu Leu Glu Gln Leu Gln Arg Leu
85 90 95
Glu Leu Ser Thr Asp Ile Gln Thr Ile Glu Leu Gln Ile Lys Lys Leu
100 105 110
50 Lys Glu Leu Gln Lys Ala Val Asp His Arg Lys Ala Ile Ile Leu Ser
115 120 125
Ile Asn Leu Cys Ser Pro Glu Phe Thr Gln Ala Asp Ser Lys Glu Ser
130 135 140
55 Arg Asp Leu Gln Asp Arg Leu Xaa Gln Met Asn Gly Arg Trp Asp Arg
145 150 155 160
Val Cys Ser Leu Leu Glu Glu Trp Arg Gly Leu Leu Gln Asp Ala Leu
165 170 175

715

Met Gln Cys Gln Gly Phe His Glu Met Ser His Gly Leu Leu Leu Met
 180 185 190

5 Leu Glu Asn Ile Asp Arg Arg Lys Asn Glu Ile Val Pro Ile Asp Ser
 195 200 205

Asn Leu Asp Ala Glu Ile Leu Gln Asp His His Lys Gln Leu Met Gln
 210 215 220

10 Ile Lys His Glu Leu Leu Glu Ser Gln Leu Arg Val Ala Ser Leu Gln
 225 230 235 240

Asp Met Ser Cys Gln Leu Leu Val Asn Ala Glu Gly Thr Asp Cys Leu
 245 250 255

15 Glu Ala Lys Glu Lys Val His Val Ile Gly Asn Arg Leu Lys Leu Leu
 260 265 270

20 Leu Lys Glu Val Ser Arg His Ile Lys Glu Leu Glu Lys Leu Leu Asp
 275 280 285

Val Ser Ser Ser Gln Gln Asp Leu Ser Ser Trp Ser Ser Ala Asp Glu
 290 295 300

25 Leu Asp Thr Ser Gly Ser Val Ser Pro Xaa Ser Gly Arg Ser Thr Pro
 305 310 315 320

Asn Arg Gln Lys Thr Pro Arg Gly Lys Cys Ser Leu Ser Gln Pro Gly
 325 330 335

30 Pro Ser Val Ser Ser Pro His Ser Arg Ser Thr Lys Gly Gly Ser Asp
 340 345 350

35 Ser Ser Leu Ser Glu Pro Xaa Pro Gly Arg Ser Gly Arg Gly Phe Leu
 355 360 365

Phe Arg Val Leu Arg Ala Ala Leu Pro Leu Gln Leu Leu Leu Leu
 370 375 380

40 Leu Ile Gly Leu Ala Cys Leu Val Pro Met Ser Glu Glu Asp Tyr Ser
 385 390 395 400

Cys Ala Leu Ser Asn Asn Phe Ala Arg Ser Phe His Pro Met Leu Arg
 405 410 415

45 Tyr Thr Asn Gly Pro Pro Pro Leu
 420

50

(2) INFORMATION FOR SEQ ID NO: 727:

- (i) SEQUENCE CHARACTERISTICS:
- 55 (A) LENGTH: 110 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 727:

60 Met Lys Leu Leu Gly Glu Cys Ser Ser Ser Ile Asp Ser Val Lys Arg

716

1 5 10 15
 Leu Glu His Lys Leu Lys Glu Glu Glu Glu Ser Leu Pro Gly Phe Val
 20 25 30
 5 Asn Leu His Ser Thr Glu Thr Gln Thr Ala Gly Val Ile Asp Arg Trp
 35 40 45
 10 Glu Leu Leu Gln Ala Gln Ala Leu Ser Lys Glu Leu Arg Met Lys Gln
 50 55 60
 Asn Leu Gln Lys Trp Gln Gln Phe Asn Ser Asp Leu Asn Ser Ile Trp
 65 70 75 80
 15 Ala Trp Leu Gly Asp Thr Glu Glu Glu Leu Glu Gln Leu Gln Arg Leu
 85 90 95
 Glu Leu Ser Thr Asp Ile Gln Thr Ile Glu Leu Gln Ile Lys
 100 105 110
 20

(2) INFORMATION FOR SEQ ID NO: 728:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 728:

30 Lys Leu Lys Glu Leu Gln Lys Ala Val Asp His Arg Lys Ala Ile Ile
 1 5 10 15
 35 Leu Ser Ile Asn Leu Cys Ser Pro Glu Phe Thr Gln Ala Asp Ser Lys
 20 25 30
 Glu Ser Arg Asp Leu Gln Asp Arg Leu Xaa Gln Met Asn Gly Arg Trp
 35 40 45
 40 Asp Arg Val Cys Ser Leu Leu Glu Glu Trp Arg Gly Leu Leu Gln Asp
 50 55 60
 Ala Leu Met Gln Cys Gln Gly Phe His Glu Met Ser His Gly Leu Leu
 65 70 75 80
 45 Leu Met Leu Glu Asn Ile Asp Arg Arg Lys Asn Glu Ile Val Pro Ile
 85 90 95
 Asp Ser Asn Leu Asp Ala Glu Ile Leu Gln Asp His His Lys Gln Leu
 100 105 110
 50 Met Gln Ile Lys His Glu Leu Leu Glu Ser Gln Leu Arg Val Ala Ser
 115 120 125
 55 Leu Gln Asp Met Ser Cys Gln Leu
 130 135

60 (2) INFORMATION FOR SEQ ID NO: 729:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 729:

Gln Asp Met Ser Cys Gln Leu Leu Val Asn Ala Glu Gly Thr Asp Cys
1 5 10 15

Leu Glu Ala Lys Glu Lys Val His Val Ile Gly Asn Arg Leu Lys Leu
20 25 30

Leu Leu Lys Glu Val Ser Arg His Ile Lys Glu Leu Glu Lys Leu Leu
35 40 45

Asp Val Ser Ser Ser Gln Gln Asp Leu Ser Ser Trp Ser Ser Ala Asp
50 55 60

Glu Leu Asp Thr Ser Gly Ser Val Ser Pro Xaa Ser Gly Arg Ser Thr
65 70 75 80

Pro Asn Arg Gln Lys Thr Pro Arg Gly Lys Cys Ser Leu Ser Gln Pro
85 90 95

Gly Pro Ser Val Ser Ser Pro His Ser
100 105

(2) INFORMATION FOR SEQ ID NO: 730:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 730:

Asp Ser Ser Leu Ser Glu Pro Xaa Pro Gly Arg Ser Gly Arg Gly Phe
1 5 10 15

Leu Phe Arg Val Leu Arg Ala Ala Leu Pro Leu Gln Leu Leu Leu Leu
20 25 30

Leu Leu Ile Gly Leu Ala Cys Leu Val Pro Met Ser Glu Glu Asp Tyr
35 40 45

Ser Cys Ala Leu Ser Asn Asn Phe Ala Arg Ser Phe His Pro Met Leu
50 55 60

Arg Tyr Thr Asn Gly Pro Pro Pro Leu
65 70

(2) INFORMATION FOR SEQ ID NO: 731:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 amino acids

(B) TYPE: amino acid

718

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 731:

5 Met Lys Leu Leu Ile Cys Gly Asn Tyr Leu Ala Pro Ser His Ser Glu
1 5 10 15

Ser Ser Arg Arg Cys Cys Leu Leu Cys Phe Tyr Pro Leu Cys Leu Glu
20 25 30

10 Ile Asn Phe Gly Met Lys Val Phe Leu Ser Met Pro Phe Leu Val Leu
35 40 45

Phe Gln Ser Leu Ile Gln Glu Asp
50 55

15

(2) INFORMATION FOR SEQ ID NO: 732:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 271 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 732:

25 Arg Ile Leu Leu Val Lys Tyr Ser Ala Asn Glu Glu Asn Lys Tyr Asp
1 5 10 15

30 Tyr Leu Pro Thr Thr Val Asn Val Cys Ser Glu Leu Val Lys Leu Val
20 25 30

Phe Cys Val Leu Val Ser Phe Cys Val Ile Lys Lys Asp His Gln Ser
35 40 45

35 Arg Asn Leu Lys Tyr Ala Ser Trp Lys Glu Phe Ser Asp Phe Met Lys
50 55 60

Trp Ser Ile Pro Ala Phe Leu Tyr Phe Leu Asp Asn Leu Ile Val Phe
65 70 75 80

40 Tyr Val Leu Ser Tyr Leu Gln Pro Ala Met Ala Val Ile Phe Ser Asn
85 90 95

45 Phe Ser Ile Ile Thr Thr Ala Leu Leu Phe Arg Ile Val Leu Lys Xaa
100 105 110

Arg Leu Asn Trp Ile Gln Trp Ala Ser Leu Leu Thr Leu Phe Leu Ser
115 120 125

50 Ile Val Ala Leu Thr Ala Gly Thr Lys Thr Leu Gln His Asn Leu Ala
130 135 140

Gly Arg Gly Phe His His Asp Ala Phe Phe Ser Pro Ser Asn Ser Cys
145 150 155 160

55 Leu Leu Phe Arg Asn Glu Cys Pro Arg Lys Asp Asn Cys Thr Ala Lys
165 170 175

60 Glu Trp Thr Phe Pro Glu Ala Lys Trp Asn Thr Thr Ala Arg Val Phe
180 185 190

719

Ser His Ile Arg Leu Gly Met Gly His Val Leu Ile Ile Val Gln Cys
 195 200 205

5 Phe Ile Ser Ser Met Ala Asn Ile Tyr Asn Glu Lys Ile Leu Lys Glu
 210 215 220

Gly Asn Gln Leu Thr Glu Xaa Ile Phe Ile Gln Asn Ser Lys Leu Tyr
 225 230 235 240

10 Phe Phe Gly Ile Leu Phe Asn Gly Leu Thr Leu Gly Leu Gln Arg Ser
 245 250 255

15 Asn Arg Asp Gln Ile Lys Asn Cys Gly Phe Phe Tyr Gly His Ser
 260 265 270

20 (2) INFORMATION FOR SEQ ID NO: 733:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 94 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 733:

Asn Ser Val Pro Asn Leu Gln Thr Leu Ala Val Leu Thr Glu Ala Ile
 1 5 10 15

30 Gly Pro Glu Pro Ala Ile Pro Arg Xaa Pro Arg Glu Pro Pro Val Ala
 20 25 30

Thr Ser Thr Pro Ala Thr Pro Ser Ala Gly Pro Gln Pro Leu Pro Thr
 35 40 45

35 Gly Thr Val Leu Val Pro Gly Gly Pro Ala Pro Pro Cys Leu Gly Glu
 50 55 60

40 Ala Trp Ala Leu Leu Leu Pro Pro Cys Arg Pro Ser Leu Thr Ser Cys
 65 70 75 80

Phe Trp Ser Pro Arg Pro Ser Pro Trp Lys Glu Thr Gly Val
 85 90

45

(2) INFORMATION FOR SEQ ID NO: 734:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 734:

50 Ala Leu Gln Leu Ala Phe Tyr Pro Asp Ala Val Glu Glu Trp Leu Glu
 1 5 10 15

Glu Asn Val His Pro Ser Leu Gln Arg Leu Gln Xaa Leu Leu Gln Asp
 20 25 30

60

720

Leu Ser Glu Val Ser Ala Pro Pro
 35 40

5

(2) INFORMATION FOR SEQ ID NO: 735:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 735:

15 Cys His Pro Pro Ala Leu Ala Gly Thr Leu Leu Arg Thr Pro Glu Gly
 1 5 10 15

Arg Ala His Ala Arg Gly Leu Leu Leu Glu Ala Gly Gly Ala
 20 25 30

20

(2) INFORMATION FOR SEQ ID NO: 736:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 736:

30 Gly Ser Ser Ser Thr Arg Ser Trp Phe Ser Thr Ser Ser Pro Gln Arg
 1 5 10 15

Ser Ala Ser Trp His Ser Gly Ala Pro Ser Cys Arg Ser Trp Arg Leu
 20 25 30

35

Pro Cys Ser Trp Leu Ser Thr Arg Met Pro Trp Arg Ser Gly Trp Arg
 35 40 45

40 Lys Thr Cys Thr Pro Ala Cys Ser Gly Cys Lys
 50 55

45 (2) INFORMATION FOR SEQ ID NO: 737:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 247 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 737:

50 Met Arg Pro Asp Trp Lys Ala Gly Ala Gly Pro Gly Gly Pro Pro Gln
 1 5 10 15

55 Lys Pro Ala Pro Ser Ser Gln Arg Lys Pro Pro Ala Arg Pro Ser Ala
 20 25 30

60 Ala Ala Ala Ala Ile Ala Val Ala Ala Ala Glu Glu Glu Arg Arg Leu
 35 40 45

721

Arg Gln Arg Asn Arg Leu Arg Leu Glu Glu Asp Lys Pro Ala Val Glu
 50 55 60
 5 Arg Cys Leu Glu Glu Leu Val Phe Gly Asp Val Glu Asn Asp Glu Asp
 65 70 75 80
 Ala Leu Leu Arg Arg Leu Arg Gly Pro Arg Val Gln Glu His Glu Asp
 85 90 95
 10 Ser Gly Asp Ser Glu Val Glu Asn Glu Ala Lys Gly Asn Phe Pro Pro
 100 105 110
 Gln Lys Lys Pro Val Trp Val Asp Glu Glu Asp Glu Asp Glu Glu Met
 115 120 125
 15 Val Asp Met Met Asn Asn Arg Phe Arg Lys Asp Met Met Lys Asn Ala
 130 135 140
 Ser Glu Ser Lys Leu Ser Lys Asp Asn Leu Lys Lys Arg Leu Lys Glu
 145 150 155 160
 Glu Phe Gln His Ala Met Gly Gly Val Pro Ala Trp Ala Glu Thr Thr
 165 170 175
 25 Lys Arg Lys Thr Ser Ser Asp Asp Glu Ser Glu Glu Asp Glu Asp Asp
 180 185 190
 Leu Leu Gln Arg Thr Gly Asn Phe Ile Ser Thr Ser Thr Ser Leu Pro
 195 200 205
 30 Arg Gly Ile Leu Lys Met Lys Asn Cys Gln His Ala Asn Ala Glu Arg
 210 215 220
 Pro Thr Val Ala Arg Ile Ser Ile Cys Ala Val Pro Ser Arg Cys Thr
 225 230 235 240
 Asp Cys Asp Gly Cys Trp Asp
 245

40

(2) INFORMATION FOR SEQ ID NO: 738:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 738:

50

Cys Leu Glu Glu Leu Val Phe Gly Asp Val Glu Asn Asp Glu Asp Ala
 1 5 10 15

55

Leu Leu Arg Arg Leu Arg Gly Pro Arg Val Gln Glu His Glu Asp Ser
 20 25 30

Gly Asp Ser Glu Val Glu Asn Glu Ala Lys Gly Asn Phe Pro Pro Gln
 35 40 45

60

Lys Lys Pro Val Trp Val Asp Glu Glu Asp Glu Asp Glu Glu Met Val
 50 55 60

722

Asp Met Met Asn Asn Arg Phe Arg Lys Asp Met Met Lys Asn Ala Ser
 65 70 75 80
 5 Glu Ser Lys Leu Ser Lys Asp Asn Leu Lys Lys Arg Leu Lys Glu Glu
 85 90 95
 Phe Gln His Ala Met Gly Gly Val Pro Ala Trp Ala Glu Thr Thr Lys
 100 105 110
 10 Arg Lys Thr Ser Ser Asp Asp Glu Ser Glu Glu Asp Glu Asp Asp Leu
 115 120 125
 Leu Gln Arg Thr Gly Asn Phe Ile Ser Thr Ser Thr Ser Leu Pro Arg
 130 135 140
 15 Gly Ile Leu Lys Met Lys Asn Cys Gln His Ala Asn Ala Glu Arg Pro
 145 150 155 160
 20 Thr Val Ala Arg Ile Ser Ile Cys Ala Val Pro Ser Arg Cys Thr Asp
 165 170 175
 Cys Asp Gly Cys
 180
 25

(2) INFORMATION FOR SEQ ID NO: 739:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 218 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 739:
 Leu Lys Glu Lys Ile Val Arg Ser Phe Glu Val Ser Pro Asp Gly Ser
 1 5 10 15
 40 Phe Leu Leu Ile Asn Gly Ile Ala Gly Tyr Leu His Leu Leu Ala Met
 20 25 30
 Lys Thr Lys Glu Leu Ile Gly Ser Met Lys Ile Asn Gly Arg Val Ala
 35 40 45
 45 Ala Ser Thr Phe Ser Ser Asp Ser Lys Lys Val Tyr Ala Ser Ser Gly
 50 55 60
 Asp Gly Glu Val Tyr Val Trp Asp Val Asn Ser Arg Lys Cys Leu Asn
 65 70 75 80
 50 Arg Phe Val Asp Glu Gly Ser Leu Tyr Gly Leu Ser Ile Ala Thr Ser
 85 90 95
 Arg Asn Gly Gln Tyr Val Ala Cys Gly Ser Asn Cys Gly Val Val Asn
 100 105 110
 Ile Tyr Asn Gln Asp Ser Cys Leu Gln Glu Thr Asn Pro Lys Pro Ile
 115 120 125
 60 Lys Ala Ile Met Asn Leu Val Thr Gly Val Thr Ser Leu Thr Phe Asn

723

130 135 140

Pro Thr Thr Glu Ile Leu Ala Ile Ala Ser Glu Lys Met Lys Glu Ala
 145 150 155 160

5 Val Arg Leu Val His Leu Pro Ser Cys Thr Val Phe Ser Asn Phe Pro
 165 170 175

10 Val Ile Lys Asn Lys Asn Ile Ser His Val His Thr Met Asp Phe Ser
 180 185 190

Pro Arg Ser Gly Tyr Phe Ala Leu Gly Asn Glu Lys Gly Lys Ala Leu
 195 200 205

15 Met Tyr Arg Leu His His Tyr Ser Asp Phe
 210 215

20 (2) INFORMATION FOR SEQ ID NO: 740:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 167 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 740:

Lys Ile Asn Gly Arg Val Ala Ala Ser Thr Phe Ser Ser Asp Ser Lys
 1 5 10 15

30 Lys Val Tyr Ala Ser Ser Gly Asp Gly Glu Val Tyr Val Trp Asp Val
 20 25 30

35 Asn Ser Arg Lys Cys Leu Asn Arg Phe Val Asp Glu Gly Ser Leu Tyr
 35 40 45

Gly Leu Ser Ile Ala Thr Ser Arg Asn Gly Gln Tyr Val Ala Cys Gly
 50 55 60

40 Ser Asn Cys Gly Val Val Asn Ile Tyr Asn Gln Asp Ser Cys Leu Gln
 65 70 75 80

Glu Thr Asn Pro Lys Pro Ile Lys Ala Ile Met Asn Leu Val Thr Gly
 85 90 95

45 Val Thr Ser Leu Thr Phe Asn Pro Thr Thr Glu Ile Leu Ala Ile Ala
 100 105 110

50 Ser Glu Lys Met Lys Glu Ala Val Arg Leu Val His Leu Pro Ser Cys
 115 120 125

Thr Val Phe Ser Asn Phe Pro Val Ile Lys Asn Lys Asn Ile Ser His
 130 135 140

55 Val His Thr Met Asp Phe Ser Pro Arg Ser Gly Tyr Phe Ala Leu Gly
 145 150 155 160

Asn Glu Lys Gly Lys Ala Leu
 165

60

(2) INFORMATION FOR SEQ ID NO: 741:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 741:

Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu Val
 1 5 10 15
 Gly Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Leu His Ser
 20 25 30
 Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly
 35 40 45
 Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu
 50 55 60
 Lys Pro Arg Tyr Ile Val His Leu Gly Gln His Asn Leu Gln Lys Glu
 65 70 75 80
 Glu Gly Cys Glu Gln Thr Arg Thr Ala Thr Glu Ser Phe Pro His Pro
 85 90 95
 Gly Phe Asn Asn Ser Leu Pro Asn Lys Asp His Arg Asn Asp Ile Met
 100 105 110
 Leu Val Lys Met Ala Ser Pro Val Ser Ile Thr Trp Ala Val Arg Pro
 115 120 125
 Leu Thr Leu Ser Ser Arg Cys Val Thr Ala Gly Thr Ser Cys Ser Phe
 130 135 140
 Pro Ala Gly Ala Ala Arg Pro Asp Pro Ser Tyr Ala Cys Leu Thr Pro
 145 150 155 160
 Cys Asp Ala Pro Thr Ser Pro Ser Leu Ser Thr Arg Ser Val Arg Thr
 165 170 175
 Pro Thr Pro Ala Thr Ser Gln Thr Pro Trp Cys Val Pro Ala Cys Arg
 180 185 190
 Lys Gly Ala Arg Thr Pro Ala Arg Val Thr Pro Gly Ala Leu Trp Ser
 195 200 205
 Val Thr Ser Leu Phe Lys Ala Leu Ser Pro Gly Ala Arg Ile Arg Val
 210 215 220
 Arg Ser Pro Glu Ser Leu Val Ser Thr Arg Lys Ser Ala Asn Met Trp
 225 230 235 240
 Thr Gly Ser Arg Arg Arg
 245

60

725

(2) INFORMATION FOR SEQ ID NO: 742:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 228 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 742:

5
 10 Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Leu His Ser Gln Pro
 1 5 10 15
 Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly Ala Thr
 20 25 30
 15 Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu Lys Pro
 35 40 45
 20 Arg Tyr Ile Val His Leu Gly Gln His Asn Leu Gln Lys Glu Glu Gly
 50 55 60
 Cys Glu Gln Thr Arg Thr Ala Thr Glu Ser Phe Pro His Pro Gly Phe
 65 70 75 80
 25 Asn Asn Ser Leu Pro Asn Lys Asp His Arg Asn Asp Ile Met Leu Val
 85 90 95
 Lys Met Ala Ser Pro Val Ser Ile Thr Trp Ala Val Arg Pro Leu Thr
 100 105 110
 30 Leu Ser Ser Arg Cys Val Thr Ala Gly Thr Ser Cys Ser Phe Pro Ala
 115 120 125
 Gly Ala Ala Arg Pro Asp Pro Ser Tyr Ala Cys Leu Thr Pro Cys Asp
 130 135 140
 35 Ala Pro Thr Ser Pro Ser Leu Ser Thr Arg Ser Val Arg Thr Pro Thr
 145 150 155 160
 40 Pro Ala Thr Ser Gln Thr Pro Trp Cys Val Pro Ala Cys Arg Lys Gly
 165 170 175
 Ala Arg Thr Pro Ala Arg Val Thr Pro Gly Ala Leu Trp Ser Val Thr
 180 185 190
 45 Ser Leu Phe Lys Ala Leu Ser Pro Gly Ala Arg Ile Arg Val Arg Ser
 195 200 205
 Pro Glu Ser Leu Val Ser Thr Arg Lys Ser Ala Asn Met Trp Thr Gly
 210 215 220
 50 Ser Arg Arg Arg
 225

55

(2) INFORMATION FOR SEQ ID NO: 743:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

60

726

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 743:

5 Cys Lys Leu His Ser Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr
 1 5 10 15
 Arg Leu Leu Cys Gly Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr
 20 25 30
 10 Ala Ala His Cys Leu Lys Pro Arg Tyr Ile Val His Leu Gly Gln His
 35 40 45
 Asn Leu Gln Lys Glu Glu Gly Cys Glu Gln Thr Arg Thr Ala Thr Glu
 50 55 60
 15 Ser Phe Pro His Pro Gly Phe Asn Asn Ser
 65 70

20

(2) INFORMATION FOR SEQ ID NO: 744:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 81 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 744:

30 Val Leu Gln Gly Arg Tyr Phe Ser Pro Ile Leu Glu Met Arg Arg Leu
 1 5 10 15
 Arg Pro Glu Gly Xaa Xaa Asn Leu Pro Gly Gly Ser Arg Ala Gln Lys
 20 25 30
 35 Glu Pro Arg Gln Asp Leu Thr Leu Val Leu Trp Pro His Cys Pro His
 35 40 45
 Phe Ala Met Thr Arg Ser Tyr Val Pro Thr Lys Gln Cys Met Val Gln
 50 55 60
 40 Gly Ser Phe Tyr Cys Ile Phe Ile Phe Lys Gly Pro Val Gln Asn Trp
 65 70 75 80
 45 Cys

50

(2) INFORMATION FOR SEQ ID NO: 745:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 211 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 745:

Met Pro Ile Ile Asp Gln Val Asn Pro Glu Leu His Asp Phe Met Gln
 1 5 10 15
 60 Ser Ala Glu Val Gly Thr Ile Phe Ala Leu Ser Trp Leu Ile Thr Trp

727

20 25 30
 Phe Gly His Val Leu Ser Asp Phe Arg His Val Val Arg Leu Tyr Asp
 35 40 45
 5 Phe Phe Leu Ala Cys His Pro Leu Met Pro Ile Tyr Phe Ala Ala Val
 50 55 60
 10 Ile Val Leu Tyr Arg Glu Gln Glu Val Leu Asp Cys Asp Cys Asp Met
 65 70 75 80
 Ala Ser Val His His Leu Leu Ser Gln Ile Pro Gln Asp Leu Pro Tyr
 85 90 95
 15 Glu Thr Leu Ile Ser Arg Xaa Glu Thr Phe Leu Phe Ser Phe Pro His
 100 105 110
 Pro Asn Leu Leu Gly Arg Pro Leu Pro Asn Ser Lys Leu Arg Gly Arg
 115 120 125
 20 Gln Pro Leu Leu Ser Lys Thr Leu Ser Trp His Gln Pro Ser Arg Gly
 130 135 140
 25 Leu Ile Trp Cys Cys Gly Ser Gly Xaa Arg Gly Leu Leu Arg Pro Glu
 145 150 155 160
 Asp Arg Thr Lys Asp Val Leu Thr Lys Pro Arg Thr Asn Arg Phe Val
 165 170 175
 30 Lys Leu Ala Val Met Gly Leu Thr Val Ala Leu Gly Ala Ala Ala Leu
 180 185 190
 Ala Val Val Lys Ser Ala Leu Glu Trp Ala Pro Lys Phe Gln Leu Gln
 195 200 205
 35 Leu Phe Pro
 210
 40
 (2) INFORMATION FOR SEQ ID NO: 745:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 746:
 50 Cys Pro Glu Phe Phe Ile Pro Ala Thr Leu Pro Cys Pro Phe Val Phe
 1 5 10 15
 Ala Phe Thr Ser Glu Ala Ser Ser Arg Ala Tyr Leu Thr Gln Arg Gly
 20 25 30
 55 Pro Gly Gly Leu Ala Gln Asn Leu Met Pro Leu Pro Val Gly Phe Trp
 35 40 45
 Met Gly Ser Leu Pro Pro Pro Trp Cys Trp Arg Lys Trp Val Ser Glu
 50 55 60
 60

728

Ala Cys Ser Cys Phe Cys
65 70

5

(2) INFORMATION FOR SEQ ID NO: 747:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

10

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 747:

15 Gly Phe Gly Ser Val Ser Ala Ala Gly Arg Arg Ser Gly Gly Thr Trp
1 5 10 15

Gln Pro Val Gln
20

20

(2) INFORMATION FOR SEQ ID NO: 748:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 748:

30 Pro Gly Gly Leu Ala Val Gly Ser Arg Trp Trp Ser Arg Ser Leu Thr
1 5 10 15

35

(2) INFORMATION FOR SEQ ID NO: 749:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 749:

45

Leu Glu Pro Ser Arg Gln Arg Arg Pro Arg Arg Arg Gly Gly Thr Ser
1 5 10 15

50 Arg Pro Glu Thr Asp Gln Arg Ala Lys Cys Trp Arg Gln Leu
20 25 30

55

(2) INFORMATION FOR SEQ ID NO: 750:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 750:

729

Val Cys Leu Arg Cys Gln Asn Arg Met Glu Asn
 1 5 10

5

(2) INFORMATION FOR SEQ ID NO: 751:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 367 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 751:

15 Met Ala Ala Cys Thr Ala Arg Arg Pro Gly Arg Gly Gln Pro Leu Val
 1 5 10 15

Val Pro Val Ala Asp Xaa Gly Pro Val Ala Lys Ala Ala Leu Cys Ala
 20 25 30

Ala Xaa Ala Gly Ala Phe Ser Pro Ala Ser Thr Thr Thr Arg Arg
 35 40 45

25 His Leu Ser Ser Arg Asn Arg Pro Glu Gly Lys Val Leu Glu Thr Val
 50 55 60

Gly Val Phe Glu Val Pro Lys Gln Asn Gly Lys Tyr Glu Thr Gly Gln
 65 70 75 80

30 Leu Phe Leu His Ser Ile Phe Gly Tyr Arg Gly Val Val Leu Phe Pro
 85 90 95

Trp Gln Ala Arg Leu Xaa Asp Arg Asp Val Ala Ser Ala Ala Pro Glu
 100 105 110

35 Lys Ala Glu Asn Pro Ala Gly His Gly Ser Lys Glu Val Lys Gly Lys
 115 120 125

40 Thr His Thr Tyr Tyr Gln Val Leu Ile Asp Ala Arg Asp Cys Pro His
 130 135 140

Ile Ser Gln Arg Ser Gln Thr Glu Ala Val Thr Phe Leu Ala Asn His
 145 150 155 160

45 Asp Asp Ser Arg Ala Leu Tyr Ala Ile Pro Gly Leu Asp Tyr Val Ser
 165 170 175

His Glu Asp Ile Leu Pro Tyr Thr Ser Thr Asp Gln Val Pro Ile Gln
 180 185 190

50 His Glu Leu Phe Glu Arg Phe Leu Leu Tyr Asp Gln Thr Lys Ala Pro
 195 200 205

Pro Phe Val Ala Arg Glu Thr Leu Arg Ala Trp Gln Glu Lys Asn His
 210 215 220

55 Pro Trp Leu Glu Leu Ser Asp Val His Arg Glu Thr Thr Glu Asn Ile
 225 230 235 240

60 Arg Val Thr Val Ile Pro Phe Tyr Met Gly Met Arg Glu Ala Gln Asn

730

245 250 255

Ser His Val Tyr Trp Trp Arg Tyr Cys Ile Arg Leu Glu Asn Leu Asp
260 265 270

5 Ser Asp Val Val Gln Leu Arg Glu Arg His Trp Arg Ile Phe Ser Leu
275 280 285

10 Ser Gly Thr Leu Glu Thr Val Arg Gly Arg Gly Val Val Gly Arg Glu
290 295 300

Pro Val Leu Ser Lys Glu Gln Pro Ala Phe Gln Tyr Ser Ser His Val
305 310 315 320

15 Ser Leu Gln Ala Ser Ser Gly His Met Trp Gly Thr Phe Arg Phe Glu
325 330 335

Arg Pro Asp Gly Ser His Phe Asp Val Arg Ile Pro Pro Phe Ser Leu
340 345 350

20 Glu Ser Asn Lys Asp Glu Lys Thr Pro Pro Ser Gly Leu His Trp
355 360 365

25

(2) INFORMATION FOR SEQ ID NO: 752:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 752:

35 Met Ala Ala Cys Thr Ala Arg Arg Pro Gly Arg Gly Gln Pro Leu Val
1 5 10 15

Val Pro Val Ala Asp Xaa Gly Pro Val Ala Lys Ala Ala Leu Cys Ala
20 25 30

40 Ala

45

(2) INFORMATION FOR SEQ ID NO: 753:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 753:

55 Met Ala Ala Cys Thr Ala Arg Arg Pro Gly Arg Gly Gln Pro Leu Val
1 5 10 15

Val Pro Val Ala Asp Xaa Gly Pro Val Ala Lys Ala Ala Leu Cys Ala
20 25 30

Ala

60

(2) INFORMATION FOR SEQ ID NO: 754:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 754:

Met Ala Ala Cys Thr Ala Arg Arg Pro Gly Arg Gly Gln Pro Leu Val
1 5 10 15

15 Val Pro Val Ala Asp Xaa Gly Pro Val Ala Lys Ala Ala Leu Cys Ala
20 25 30

Ala

20

(2) INFORMATION FOR SEQ ID NO: 755:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 755:

Met Ala Ala Cys Thr Ala Arg Arg Pro Gly Arg Gly Gln Pro Leu Val
1 5 10 15

35 Val Pro Val Ala Asp Xaa Gly Pro Val Ala Lys Ala Ala Leu Cys Ala
20 25 30

Ala

40

(2) INFORMATION FOR SEQ ID NO: 756:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 756:

50 Met Ala Ala Cys Thr Ala Arg Arg Pro Gly Arg Gly Gln Pro Leu Val
1 5 10 15

Val Pro Val Ala Asp Xaa Gly Pro Val Ala Lys Ala Ala Leu Cys Ala
20 25 30

55

Ala

60

(2) INFORMATION FOR SEQ ID NO: 757:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 757:

5 Val Leu Glu Thr Val Gly Val Phe Glu Val Pro Lys Gln Asn Gly Lys
 10 1 5 10 15
 Tyr Glu Thr Gly Gln Leu Phe Leu His Ser Ile Phe Gly Tyr Arg Gly
 20 25 30
 15 Val Val Leu
 35

20 (2) INFORMATION FOR SEQ ID NO: 758:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 758:

25 Gly Leu Asp Tyr Val Ser His Glu Asp Ile Leu Pro Tyr Thr Ser Thr
 30 1 5 10 15

35 (2) INFORMATION FOR SEQ ID NO: 759:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 759:

40 Asp Val His Arg Glu Thr Thr Glu Asn Ile Arg Val Thr Val Ile Pro
 45 1 5 10 15
 Phe Tyr Met

50 (2) INFORMATION FOR SEQ ID NO: 760:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 760:

55 Trp Trp Arg Tyr Cys Ile Arg Leu Glu Asn Leu Asp Ser Asp Val Val
 60

733

1 5 10 15

Gln Leu Arg Glu Arg
20

5

(2) INFORMATION FOR SEQ ID NO: 761:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 761:

15

Pro Ala Phe Gln Tyr Ser Ser His Val Ser Leu Gln Ala Ser Ser Gly
1 5 10 15

His Met Trp Gly Thr Phe Arg Phe Glu Arg
20 25

20

(2) INFORMATION FOR SEQ ID NO: 762:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 762:

Ser Leu Cys Cys Pro Glu Gly Ala Glu Gly Cys
1 5 10

35

(2) INFORMATION FOR SEQ ID NO: 763:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 763:

Gln Leu Lys Lys Thr His Tyr Asp Arg Pro Cys Pro
1 5 10

50

(2) INFORMATION FOR SEQ ID NO: 764:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 764:

Gln Leu Lys Lys Thr His Tyr Asp Arg Pro Cys Pro
1 5 10

60

(2) INFORMATION FOR SEQ ID NO: 765:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 765:

Ala Gln Arg Lys Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu
 1 5 10 15

Met Glu Trp Thr Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys
 15 20 25 30

Phe Arg Arg Leu Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile Val
 35 40 45

Met Phe Thr Ala Leu Gln Leu His Arg Gln Cys Val Val Cys Lys Gln
 50 55 60

Ala Asp Glu Glu Phe Gln Ile Leu Ala Asn Ser Trp Arg Tyr Ser Ser
 65 70 75 80

Ala Phe Thr Asn Arg Ile Phe Phe Ala Met Val Asp Phe Asp Glu Gly
 85 90 95

Ser Asp Val Phe Gln Met Leu Asn Met Asn Ser Ala Pro Thr Phe Ile
 100 105 110

Asn Phe Pro Ala Lys Gly Lys Pro Lys Arg Gly Asp Thr Tyr Glu Leu
 115 120 125

Gln Val Arg Gly Phe Ser Ala Glu Gln Ile Ala Arg Trp Ile Ala Asp
 130 135 140

Arg Thr Asp Val Asn Ile Arg Val Ile Arg Pro Pro Asn Met Ala Ala
 145 150 155 160

Arg Trp Arg Phe Trp Cys Val Ser Val Thr
 165 170

45

(2) INFORMATION FOR SEQ ID NO: 766:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 766:

Met Val Val Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser
 55 1 5 10 15

60

(2) INFORMATION FOR SEQ ID NO: 767:

735

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 767:

Ala Gln Arg Lys Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu
 1 5 10 15

10

15 (2) INFORMATION FOR SEQ ID NO: 768:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 768:

Met Glu Trp Thr Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys
 1 5 10 15

25

Phe

30

(2) INFORMATION FOR SEQ ID NO: 769:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 769:

40

Arg Arg Leu Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile Val Met
 1 5 10 15

Phe Thr Ala Leu Gln Leu His Arg Gln Cys Val Val Cys Lys Gln Ala
 20 25 30

45

Asp Glu Glu Phe Gln Ile Leu Ala Asn Ser Trp Arg Tyr Ser Ser Ala
 35 40 45

Phe Thr Asn Arg Ile Phe Phe Ala
 50 55

50

(2) INFORMATION FOR SEQ ID NO: 770:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 770:

736

Met Val Asp Phe Asp Glu Gly Ser Asp Val Phe Gln Met Leu Asn Met
 1 5 10 15

5 Asn Ser Ala Pro Thr Phe Ile Asn Phe Pro Ala Lys Gly Lys Pro
 20 25 30

10 (2) INFORMATION FOR SEQ ID NO: 771:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 771:

Lys Arg Gly Asp Thr Tyr Glu Leu Gln Val Arg Gly Phe Ser Ala Glu
 1 5 10 15

20 Gln Ile Ala Arg Trp Ile Ala Asp Arg Thr Asp Val Asn Ile Arg Val
 20 25 30

Ile Arg Pro Pro Asn
 35

25

(2) INFORMATION FOR SEQ ID NO: 772:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 44 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 772:

Tyr Ala Gly Pro Leu Met Leu Gly Leu Leu Ala Val Ile Gly Gly
 1 5 10 15

40 Leu Val Tyr Leu Arg Arg Val Ile Trp Asn Phe Ser Leu Ile Lys Leu
 20 25 30

Asp Gly Leu Leu Gln Leu Cys Val Leu Cys Leu Leu
 35 40

45

(2) INFORMATION FOR SEQ ID NO: 773:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 773:

55 Asp Ala Val Phe Lys Gly Phe Ser Asp Cys Leu Leu Lys Leu Gly Asp
 1 5 10 15

Ser

60

(2) INFORMATION FOR SEQ ID NO: 774:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 774:

10

Cys Gln Glu Gly Ala Lys Asp Met Trp Asp Lys Leu Arg Lys Glu Ser
 1 5 10 15

15

Lys Asn Leu Asn
 20

(2) INFORMATION FOR SEQ ID NO: 775:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 775:

Val Leu Leu Val Ser Leu Ser Ala Ala Leu Ala Thr Trp Leu Ser Phe
 1 5 10 15

30

35

(2) INFORMATION FOR SEQ ID NO: 776:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 776:

Met Gly Leu Lys Leu Asn Gly Arg Tyr Ile Ser Leu Ile Leu Ala Val
 1 5 10 15

45

Gln Ile Ala Tyr Leu Val Gln Ala Val Arg Ala Ala Gly Lys Cys Asp
 20 25 30

50

Ala Val Phe Lys Gly Phe Ser Asp Cys Leu Leu Lys Leu Gly Asp Ser
 35 40 45

55

(2) INFORMATION FOR SEQ ID NO: 777:

60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 amino acids

738

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 777:

5 Pro Ala Ala Trp Asp Asp Lys Thr Asn Ile Lys Thr Val Cys Thr Tyr
 1 5 10 15

Trp Glu Asp Phe His Ser Cys Thr Val Thr Ala Leu Thr Asp Cys Gln
 20 25 30

10 Glu Gly Ala Lys Asp Met Trp Asp Lys Leu Arg Lys Glu Ser Lys Asn
 35 40 45

Leu Asn Ile Gln Gly Ser Leu Phe Glu Leu Cys Gly Ser Gly Asn Gly
 15 50 55 60

Ala Ala Gly Ser Leu Leu Pro Ala Phe Pro Val Leu Leu Val Ser Leu
 65 70 75 80

20 Ser Ala Ala Leu Ala Thr Trp Leu Ser Phe
 85 90

25 (2) INFORMATION FOR SEQ ID NO: 778:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 143 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 778:

Met Gly Leu Lys Leu Asn Gly Arg Tyr Ile Ser Leu Ile Leu Ala Val
 1 5 10 15

35 Gln Ile Ala Tyr Leu Val Gln Ala Val Arg Ala Ala Gly Lys Cys Asp
 20 25 30

Ala Val Phe Lys Gly Phe Ser Asp Cys Leu Leu Lys Leu Gly Asp Ser
 40 35 40 45

Xaa Xaa Xaa Xaa Xaa Pro Ala Ala Trp Asp Asp Lys Thr Asn Ile Lys
 50 55 60

45 Thr Val Cys Thr Tyr Trp Glu Asp Phe His Ser Cys Thr Val Thr Ala
 65 70 75 80

Leu Thr Asp Cys Gln Glu Gly Ala Lys Asp Met Trp Asp Lys Leu Arg
 85 90 95

50 Lys Glu Ser Lys Asn Leu Asn Ile Gln Gly Ser Leu Phe Glu Leu Cys
 100 105 110

55 Gly Ser Gly Asn Gly Ala Ala Gly Ser Leu Leu Pro Ala Phe Pro Val
 115 120 125

Leu Leu Val Ser Leu Ser Ala Ala Leu Ala Thr Trp Leu Ser Phe
 130 135 140

60

(2) INFORMATION FOR SEQ ID NO: 779:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 779:

Met Asn Ser Ala Ala Gly Phe Ser His Leu Asp Arg Arg Glu Arg Val
 1 5 10 15
 Leu Lys Leu Gly Glu Ser Phe Glu Lys Gln Pro Arg Cys Ala Ser Thr
 20 25 30
 Leu Cys

(2) INFORMATION FOR SEQ ID NO: 780:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 780:

Thr Ile Tyr Pro Thr Glu Glu Glu Leu Gln Ala Val Gln Lys Ile Val
 1 5 10 15
 Ser Ile Thr Glu Arg Ala Leu Lys Leu Val Ser Asp
 20 25

(2) INFORMATION FOR SEQ ID NO: 781:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 781:

Arg Ala Leu Lys Gly Val Leu Arg Val Gly Val Leu Ala Lys Gly Leu
 1 5 10 15
 Leu Leu Arg Gly Asp Arg Asn Val Asn Leu Val Leu Leu Cys
 20 25 30

(2) INFORMATION FOR SEQ ID NO: 782:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 782:

740

Ala Leu Ala Ala Leu Arg His Ala Lys Trp Phe Gln Ala Arg Ala Asn
 1 5 10 15
 5 Gly Leu Gln Ser Cys Val Ile Ile Ile Arg Ile Leu Arg Asp Leu Cys
 20 25 30
 Gln Arg Val Pro Thr Trp Ser
 35

10

(2) INFORMATION FOR SEQ ID NO: 783:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 783:

20 Gly Asp Ala Leu Arg Arg Val Phe Glu Cys Ile Ser Ser Gly Ile Ile
 1 5 10 15
 Leu

25

(2) INFORMATION FOR SEQ ID NO: 784:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 784:

35 Leu Ala Phe Arg Gln Ile His Lys Val Leu Gly Met Asp Pro Leu Pro
 1 5 10 15

40

(2) INFORMATION FOR SEQ ID NO: 785:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 342 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 785:

Thr Ile Tyr Pro Thr Glu Glu Glu Leu Gln Ala Val Gln Lys Ile Val
 1 5 10 15
 55 Ser Ile Thr Glu Arg Ala Leu Lys Leu Val Ser Asp Ser Leu Ser Glu
 20 25 30
 His Glu Lys Asn Lys Asn Lys Glu Gly Asp Asp Lys Lys Glu Gly Gly
 35 40 45

60

741

Lys Asp Arg Ala Leu Lys Gly Val Leu Arg Val Gly Val Leu Ala Lys
 50 55 60
 Gly Leu Leu Leu Arg Gly Asp Arg Asn Val Asn Leu Val Leu Leu Cys
 5 65 70 75 80
 Ser Glu Lys Pro Ser Lys Thr Leu Leu Ser Arg Ile Ala Glu Asn Leu
 85 90 95
 10 Pro Lys Gln Leu Ala Val Ile Ser Pro Glu Lys Tyr Asp Ile Lys Cys
 100 105 110
 Ala Val Ser Glu Ala Ala Ile Ile Leu Asn Ser Cys Val Glu Pro Lys
 115 120 125
 15 Met Gln Val Thr Ile Thr Leu Thr Ser Pro Ile Ile Arg Glu Glu Asn
 130 135 140
 Met Arg Glu Gly Asp Val Thr Ser Gly Met Val Lys Asp Pro Pro Asp
 20 145 150 155 160
 Val Leu Asp Arg Gln Lys Cys Leu Asp Ala Leu Ala Ala Leu Arg His
 165 170 175
 25 Ala Lys Trp Phe Gln Ala Arg Ala Asn Gly Leu Gln Ser Cys Val Ile
 180 185 190
 Ile Ile Arg Ile Leu Arg Asp Leu Cys Gln Arg Val Pro Thr Trp Ser
 195 200 205
 30 Asp Phe Pro Ser Trp Ala Met Glu Leu Leu Val Glu Lys Ala Ile Ser
 210 215 220
 Ser Ala Ser Ser Pro Gln Ser Pro Gly Asp Ala Leu Arg Arg Val Phe
 35 225 230 235 240
 Glu Cys Ile Ser Ser Gly Ile Ile Leu Lys Gly Ser Pro Gly Leu Leu
 245 250 255
 40 Asp Pro Cys Glu Lys Asp Pro Phe Asp Thr Leu Ala Thr Met Thr Asp
 260 265 270
 Gln Gln Arg Glu Asp Ile Thr Ser Ser Ala Gln Phe Ala Leu Arg Leu
 275 280 285
 45 Leu Ala Phe Arg Gln Ile His Lys Val Leu Gly Met Asp Pro Leu Pro
 290 295 300
 Gln Met Ser Gln Arg Phe Asn Ile His Asn Asn Arg Lys Arg Arg Arg
 50 305 310 315 320
 Asp Ser Asp Gly Val Asp Gly Phe Glu Ala Glu Gly Lys Lys Asp Lys
 325 330 335
 55 Lys Asp Tyr Asp Asn Phe
 340

60 (2) INFORMATION FOR SEQ ID NO: 786:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 786:

Met Gly Ser Gln His Ser Ala Ala Ala Arg Pro Ser Ser Cys Arg Arg
 1 5 10 15
 Lys Gln Glu Asp Asp Arg Asp Gly
 20

(2) INFORMATION FOR SEQ ID NO: 787:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 787:

Leu Leu Ala Glu Arg Glu Gln Glu Glu Ala Ile Ala Gln Phe Pro Tyr
 1 5 10 15
 Val Glu Phe Thr Gly Arg Asp Ser Ile Thr Cys Leu Thr Cys
 20 25 30

(2) INFORMATION FOR SEQ ID NO: 788:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 788:

Gln Gly Thr Gly Tyr Ile Pro Thr Glu Gln Val Asn Glu Leu Val Ala
 1 5 10 15
 Leu Ile Pro His Ser Asp Gln Arg Leu Arg Pro Gln Arg Thr Lys Gln
 20 25 30
 Tyr Val

(2) INFORMATION FOR SEQ ID NO: 789:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 789:

Ala Arg Leu Asn Val Gly Arg Glu Ser Leu Lys Arg Glu Met Leu Lys
 1 5 10 15

743

Ser Gln Gly Val Lys Val Ser Glu Ser Pro Met Gly Ala Arg His Ser
20 25 30

5 Ser Trp Pro Glu Gly Ala Ala Phe Cys Lys Lys Val Gln Gly Ala Gln
35 40 45

Met Gln Phe Pro Pro Arg Arg
50 55

10

(2) INFORMATION FOR SEQ ID NO: 790:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 790:

Ala Arg Leu Asn Val Gly Arg Glu Ser Leu Lys Arg Glu Met Leu
1 5 10 15

25

(2) INFORMATION FOR SEQ ID NO: 791:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 791:

35 Leu Lys Ser Gln Gly Val Lys Val Ser Glu Ser Pro Met Gly Ala Arg
1 5 10 15

His Ser Ser Trp
20

40

(2) INFORMATION FOR SEQ ID NO: 792:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 792:

50 Ala Phe Cys Lys Lys Val Gln Gly Ala Gln Met Gln Phe Pro Pro Arg
1 5 10 15

Arg

55

(2) INFORMATION FOR SEQ ID NO: 793:

60 (i) SEQUENCE CHARACTERISTICS:

744

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 793:

5

Ala Phe Cys Lys Lys Val Gln Gly Ala Gln Met Gln Phe Pro Pro Arg
 1 5 10 15

Arg

10

(2) INFORMATION FOR SEQ ID NO: 794:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 794:

Val Gln Val Leu Glu Gln Leu Thr Asn Asn Ala Val Ala Glu Ser Arg
 1 5 10 15

25

Phe Asn Asp Ala Ala Tyr Tyr Tyr Trp Met Leu Ser Met Gln Cys Leu
 20 25 30

Asp Ile Ala Gln Asp
 35

30

(2) INFORMATION FOR SEQ ID NO: 795:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 795:

40

Pro Ala Gln Lys Asp Thr Met Leu Gly Lys Phe Tyr His Phe Gln Arg
 1 5 10 15

45

Leu Ala Glu Leu Tyr His Gly Tyr His Ala Ile His Arg His Thr Glu
 20 25 30

Asp Pro

50

(2) INFORMATION FOR SEQ ID NO: 796:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 796:

60

Leu Ala Lys Gln Ser Lys Ala Leu Gly Ala Tyr Arg Leu Ala Arg His

745

1 5 10 15
 Ala Tyr Asp Lys Leu Arg Gly Leu Tyr Ile Pro
 20 25
 5

(2) INFORMATION FOR SEQ ID NO: 797:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 797:

15 Ala Arg Phe Gln Lys Ser Ile Glu Leu Gly Thr Leu Thr Ile Arg Ala
 1 5 10 15
 Lys Pro Phe His Asp Ser Glu Glu Leu Val Pro Leu Cys Tyr Arg Cys
 20 20 25 30
 Ser Thr Asn Asn
 35
 25

(2) INFORMATION FOR SEQ ID NO: 798:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 73 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 798:

35 Pro Leu Leu Asn Asn Leu Gly Asn Val Cys Ile Asn Cys Arg Gln Pro
 1 5 10 15
 Phe Ile Phe Ser Ala Ser Ser Tyr Asp Val Leu His Leu Val Glu Phe
 20 25 30
 40 Tyr Leu Glu Glu Gly Ile Thr Asp Glu Glu Ala Ile Ser Leu Ile Asp
 35 40 45
 Leu Glu Val Leu Arg Pro Lys Arg Asp Asp Arg Gln Leu Glu Ile Cys
 45 50 55 60
 Lys Gln Gln Leu Pro Asp Ser Cys Gly
 65 70
 50

(2) INFORMATION FOR SEQ ID NO: 799:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 799:

60 Met Pro Tyr Ala Gln Trp Leu Ala Glu Asn Asp Arg Phe Glu Glu Ala

746

1 5 10 15
Gln Lys Ala Phe His Lys Ala Gly Arg Gln Arg Glu Ala
 20 25
5

(2) INFORMATION FOR SEQ ID NO: 800:

10 (i) SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 36 amino acids

 (B) TYPE: amino acid

 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 800:

Phe Ser Val His Arg Pro Glu Thr Leu Phe Asn Ile Ser Arg Phe Leu
1 5 10 15
20 Leu His Ser Leu Pro Lys Asp Thr Pro Ser Gly Ile Ser Lys Val Lys
 20 25 30
Ile Leu Phe Thr
 35
25

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>161</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit March 27, 1997	Accession Number 97979
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>162</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit April 4, 1997	Accession Number 97974
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit") 	

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>162</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <p style="text-align: center;">American Type Culture Collection</p>	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit May 29, 1997	Accession Number 209080
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>164</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <p style="text-align: center;">American Type Culture Collection</p>	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit December 3, 1997	Accession Number 209511
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>167</u> . line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit April 4, 1997	Accession Number 97975
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications. e.g., "Accession Number of Deposit") 	

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>167</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <p style="text-align: center;">American Type Culture Collection</p>	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit <u>May 29, 1997</u>	Accession Number <u>209081</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit") 	

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(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page 171, line N/A	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit April 4, 1997	Accession Number 97976
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>172</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <u>---</u>	
Name of depositary institution <p style="text-align: center;">American Type Culture Collection</p>	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit <u>April 4, 1997</u>	Accession Number <u>97977</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <u>---</u>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications. e.g., "Accession Number of Deposit")	
<div style="display: flex; justify-content: space-between;"><div style="width: 48%;"><p>For receiving Office use only</p><div style="border: 1px solid black; padding: 5px;"><input checked="" type="checkbox"/> This sheet was received with the international application <p style="text-align: center;">Patricia Smith Paternal Specialist USPTO Operations</p></div><div style="border: 1px solid black; padding: 5px; margin-top: 5px;">Authorized officer <p style="font-size: 1.2em; margin-top: 10px;">04 JUN 1998</p></div></div><div style="width: 48%;"><p>For International Bureau use only</p><div style="border: 1px solid black; padding: 5px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div><div style="border: 1px solid black; padding: 5px; margin-top: 5px;">Authorized officer</div></div></div>	

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>172</u> . line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <u> </u>	
Name of depositary institution <p style="text-align: center;">American Type Culture Collection</p>	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit May 29, 1997	Accession Number 209082
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <u> </u>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>176</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <p style="text-align: center;">American Type Culture Collection</p>	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit April 28, 1997	Accession Number 209007
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit") 	
<div style="display: flex; justify-content: space-between;"><div style="width: 45%; border: 1px solid black; padding: 5px;"><p style="text-align: center;">For receiving Office use only</p><div style="display: flex; justify-content: space-between;"><div><input checked="" type="checkbox"/> This sheet was received with the international application</div><div><input type="checkbox"/> This sheet was received by the International Bureau on:</div></div><div style="display: flex; justify-content: space-between;"><div>Authorized officer 04 JUN 1998</div><div>17-10NS</div></div></div><div style="width: 45%; border: 1px solid black; padding: 5px;"><p style="text-align: center;">For International Bureau use only</p><div style="display: flex; justify-content: space-between;"><div><input type="checkbox"/> This sheet was received by the International Bureau on:</div><div></div></div><div style="display: flex; justify-content: space-between;"><div>Authorized officer</div><div></div></div></div></div>	

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>176</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <p style="text-align: center;">American Type Culture Collection</p>	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit May 29, 1997	Accession Number 209083
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>179</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit April 28, 1997	Accession Number 209008
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable) The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>179</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit May 29, 1997	Accession Number 209084
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>180</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <p style="text-align: center;">American Type Culture Collection</p>	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit April 28, 1997	Accession Number 209010
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable) The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>180</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <p style="text-align: center;">American Type Culture Collection</p>	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit <u>May 29, 1997</u>	Accession Number <u>209085</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit") 	
<div style="display: flex; justify-content: space-between;"><div style="width: 45%;"><p>For receiving Office use only</p><div style="border: 1px solid black; padding: 5px;"><input type="checkbox"/> This sheet was received with the international application <p style="text-align: center;">John Smith Specialist Operations</p></div><div style="border: 1px solid black; padding: 5px;">Authorized officer <p style="text-align: center;">04 JUN 1998</p></div></div><div style="width: 45%;"><p>For International Bureau use only</p><div style="border: 1px solid black; padding: 5px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div><div style="border: 1px solid black; padding: 5px;">Authorized officer</div></div></div>	

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>182</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit April 28, 1997	Accession Number 209009
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable) The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications. e.g., "Accession Number of Deposit")	

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>186</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <p style="text-align: center;">American Type Culture Collection</p>	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit <u>April 28, 1997</u>	Accession Number <u>209011</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit") 	
<div style="display: flex; justify-content: space-between;"><div style="width: 45%;">For receiving Office use only <input checked="" type="checkbox"/> This sheet was received with the international application by the Specialist WIPO-PCT Operations Authorized officer <p style="font-size: 1.2em;">04 JUN 1998</p></div><div style="width: 45%;">For International Bureau use only <input type="checkbox"/> This sheet was received by the International Bureau on: Authorized officer</div></div>	

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>174</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit April 7, 1998	Accession Number 209746
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable) The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	
<div style="text-align: center;">For receiving Office use only</div> <div style="border: 1px solid black; padding: 5px; margin-top: 5px;"><input checked="" type="checkbox"/> This sheet was received with the international application <div style="text-align: right;">DRC</div></div> <div style="border: 1px solid black; padding: 5px; margin-top: 5px;">Authorized officer <div style="text-align: center; font-size: 1.2em; font-weight: bold;">64 JUN 1998</div></div>	<div style="text-align: center;">For International Bureau use only</div> <div style="border: 1px solid black; padding: 5px; margin-top: 5px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border: 1px solid black; padding: 5px; margin-top: 5px;">Authorized officer</div>

What Is Claimed Is:

1. An isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence at least 95% identical to a sequence selected from the group consisting of:

(a) a polynucleotide fragment of SEQ ID NO:X or a polynucleotide fragment of the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

(b) a polynucleotide encoding a polypeptide fragment of SEQ ID NO:Y or a polypeptide fragment encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

(c) a polynucleotide encoding a polypeptide domain of SEQ ID NO:Y or a polypeptide domain encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

(d) a polynucleotide encoding a polypeptide epitope of SEQ ID NO:Y or a polypeptide epitope encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

(e) a polynucleotide encoding a polypeptide of SEQ ID NO:Y or the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X, having biological activity;

(f) a polynucleotide which is a variant of SEQ ID NO:X;

(g) a polynucleotide which is an allelic variant of SEQ ID NO:X;

(h) a polynucleotide which encodes a species homologue of the SEQ ID NO:Y;

(i) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(h), wherein said polynucleotide does not hybridize under stringent conditions to a nucleic acid molecule having a nucleotide sequence of only A residues or of only T residues.

2. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding a secreted protein.

3. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding the sequence identified as SEQ ID NO:Y or the polypeptide encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X.

4. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises the entire nucleotide sequence of SEQ ID NO:X or the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X.
5. The isolated nucleic acid molecule of claim 2, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.
6. The isolated nucleic acid molecule of claim 3, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.
7. A recombinant vector comprising the isolated nucleic acid molecule of claim 1.
8. A method of making a recombinant host cell comprising the isolated nucleic acid molecule of claim 1.
9. A recombinant host cell produced by the method of claim 8.
10. The recombinant host cell of claim 9 comprising vector sequences.
11. An isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence selected from the group consisting of:
 - (a) a polypeptide fragment of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;
 - (b) a polypeptide fragment of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z, having biological activity;
 - (c) a polypeptide domain of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;
 - (d) a polypeptide epitope of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;
 - (e) a secreted form of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;
 - (f) a full length protein of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

- (g) a variant of SEQ ID NO:Y;
- (h) an allelic variant of SEQ ID NO:Y; or
- (i) a species homologue of the SEQ ID NO:Y.

12. The isolated polypeptide of claim 11, wherein the secreted form or the full length protein comprises sequential amino acid deletions from either the C-terminus or the N-terminus.

13. An isolated antibody that binds specifically to the isolated polypeptide of claim 11.

14. A recombinant host cell that expresses the isolated polypeptide of claim 11.

15. A method of making an isolated polypeptide comprising:

- (a) culturing the recombinant host cell of claim 14 under conditions such that said polypeptide is expressed; and
- (b) recovering said polypeptide.

16. The polypeptide produced by claim 15.

17. A method for preventing, treating, or ameliorating a medical condition, comprising administering to a mammalian subject a therapeutically effective amount of the polypeptide of claim 11 or the polynucleotide of claim 1.

18. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:

- (a) determining the presence or absence of a mutation in the polynucleotide of claim 1; and
- (b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or absence of said mutation.

19. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:

- (a) determining the presence or amount of expression of the polypeptide of claim 11 in a biological sample; and
- (b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or amount of expression of the polypeptide.

20. A method for identifying a binding partner to the polypeptide of claim 11 comprising:

- (a) contacting the polypeptide of claim 11 with a binding partner; and
- (b) determining whether the binding partner effects an activity of the polypeptide.

21. The gene corresponding to the cDNA sequence of SEQ ID NO:Y.

22. A method of identifying an activity in a biological assay, wherein the method comprises:

- (a) expressing SEQ ID NO:X in a cell;
- (b) isolating the supernatant;
- (c) detecting an activity in a biological assay; and
- (d) identifying the protein in the supernatant having the activity.

23. The product produced by the method of claim 22.

PATENT COOPERATION TREATY

PCT

DECLARATION OF NON-ESTABLISHMENT OF INTERNATIONAL SEARCH REPORT

(PCT Article 17(2)(a) and Rule 39)

Applicant's or agent's file reference PZ007PCT	IMPORTANT DECLARATION	Date of mailing (day/month/year) 14 OCT 1998
International application No. PCT/US98/11422	International filing date (day/month/year) 04 JUNE 1998	(Earliest) Priority Date (day/month/year) 06 JUNE 1997
International Patent Classification (IPC) or both national classification and IPC Please See Continuation Sheet.		
Applicant HUMAN GENOME SCIENCES, INC.		

This International Searching Authority hereby declares, according to Article 17(2)(a), that no international search report will be established on the international application for the reasons indicated below.

1. ☐ The subject matter of the international application relates to:
 - a. ☐ scientific theories.
 - b. ☐ mathematical theories.
 - c. ☐ plant varieties.
 - d. ☐ animal varieties.
 - e. ☐ essentially biological processes for the production of plants and animals, other than microbiological processes and the products of such processes.
 - f. ☐ schemes, rules or methods of doing business.
 - g. ☐ schemes, rules or methods of performing purely mental acts.
 - h. ☐ schemes, rules or methods of playing games.
 - i. ☐ methods for treatment of the human body by surgery or therapy.
 - j. ☐ methods for treatment of the animal body by surgery or therapy.
 - k. ☐ diagnostic methods practiced on the human or animal body.
 - l. ☐ mere presentations of information.
 - m. ☐ computer programs for which this International Searching Authority is not equipped to search prior art.
2. ☐ The failure of the following parts of the international application to comply with prescribed requirements prevents a meaningful search from being carried out:

☐ the description
 ☐ the claims
 ☐ the drawings
3. ☒ The failure of the nucleotide and/or amino acid sequence listing to comply with the prescribed requirements prevents a meaningful search from being carried out:

☒ it does not comply with the prescribed standard
☒ it is not in the prescribed machine readable form
4. Further comments:
Please See Continuation Sheet.

Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231	Authorized officer BRIAN R. STANTON
Facsimile No. (703) 305-3230	Telephone No. (703) 308-0196

**DECLARATION OF NON-ESTABLISHMENT OF
INTERNATIONAL SEARCH REPORT**

International application No.
PCT/US98/11422

The International Patent Classification (IPC) or National Classification and IPC are as listed below:

IPC(6): A01N 37/18, 43/04; C12Q 1/00, 1/02, 1/68; C12N 5/00, 5/06, 15/00, 15/06, 15/09, 15/10, 15/11; G01N 33/53

US CL.: 435, 4, 7.1, 69.1, 70.1, 71.1, 172.3, 243, 320.1, 325, 410; 514/2, 44; 530/350, 387.1

4. Further Comments (Continued):

Applicant has not responded to the invitation to pay additional fees mailed on 04 August 1998. Therefore, the search would be conducted on the first appearing invention which includes claims 1-10, 14, and 15 in so far as these claims are drawn to the first ten (10) appearing nucleotide sequences. However, no meaningful search could be carried out on these sequences because the CRF that was received for this case on 15 June 1998 was technically defective and could not be used to conduct a search of the prior art.